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L3 ANSWER 1 OF 21 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2002:343948 BIOSIS

DOCUMENT NUMBER: PREV200200343948

TITLE: Analysis of differential gene expression in peripheral
blood eosinophils of atopic dermatitis patients.

AUTHOR(S): Ogawa, Kaoru (1); Hashida, Ryoichi (1); Itoh, Mikito (1);
Miyagawa, Masami (1); Sugita, Yuji (1); Takahashi, Eiki;
Tsujiimoto, Gozoh; Katsunuma, Toshio; Akasawa, Akira;
Matsumoto, Kenji; Saito, Hirohisa

CORPORATE SOURCE: (1) Genox Research, Inc, 907 Nogawa, Miyamae-ku, Kawasaki,
Kanagawa, 216-0001 Japan

SOURCE: FASEB Journal, (March 20, 2002) Vol. 16, No. 4, pp. A674.
<http://www.fasebj.org/>. print.

Meeting Info.: Annual Meeting of the Professional Research
Scientists on Experimental Biology New Orleans, Louisiana,
USA April 20-24, 2002

ISSN: 0892-6638.

DOCUMENT TYPE: Conference

LANGUAGE: English

AB To identify the genes related to atopic dermatitis (AD), we compared
differentially expressed genes in peripheral blood eosinophils from AD
patients and healthy volunteers. RNA was prepared from peripheral blood
eosinophils, and gene expression was monitored by fluorescent
differential

display (FDD) and real-time PCR (ABI PRISM 7700). Approximately 20 new
genes and **ESTs** (expressed sequence tags) were expressed at

higher levels in eosinophils of AD patients than in those of healthy volunteers. The functions of most of these genes are unknown.

Nonetheless,

we analyzed the relationship between the expression of each gene and clinical markers such as the number of eosinophils and the amount of IgE. There was **no correlation** between gene expression and clinical markers. Multivariate studies of the gene expression data in

each

sample showed a very high coefficient of relation among the copy numbers of each gene. The genes under investigation were also expressed in cultured blood eosinophils after IL-4 stimulation. We were able to estimate the function of some of the sequences by scanning the human genome database.

L3 ANSWER 2 OF 21 LIFESCI COPYRIGHT 2002 CSA
ACCESSION NUMBER: 2002:54239 LIFESCI
TITLE: Breeding Biology of Brant on Banks Island, Northwest Territories, Canada
AUTHOR: Cotter, R.C.; Hines, J.E.
CORPORATE SOURCE: Canadian Wildlife Service, 1141 route de l'Eglise, Sainte-Foy, Quebec G1V 4H5, Canada; E-mail: richard.cotter@ec.gc.ca
SOURCE: Arctic, (2001:200) vol. 54, no. 4, pp. 357-366. ISSN: 0004-0843.
DOCUMENT TYPE: Journal
FILE SEGMENT: D
LANGUAGE: English
SUMMARY LANGUAGE: English; French

AB The numbers of brant (*Branta bernicla*) in the Pacific Flyway are relatively small compared to other populations of arctic geese and have declined from historic levels. Little information is available on brant from Banks Island, although the size of the island and its location in the western Canadian Arctic make it a potentially important nesting area for this species. In 1992-93, we documented the distribution of nesting brant on the southern half of Banks Island through aerial surveys and carried out ground studies at the colonies to document nesting chronology and reproductive parameters. Ten colonies were found in 1992 ($n = 159$ nests) and 42 colonies (including seven colonies that had been active in 1992) and five solitary nests were found in 1993 ($n = 514$ nests). Two-thirds (67%) of the nesting locations supported 10 or fewer nests. Most colonies (36 of 45) were located on small islands (mean = 248 m super(2)) in inland lakes or large ponds, and the remaining colonies ($n = 9$) were located on the mainland near active snowy owl (*Nyctea scandiaca*) nests. In 1993, when June temperatures were milder and snow melted sooner than in 1992, mean date of clutch initiation was significantly earlier (12 June vs. 20 June in 1992; $p < 0.001$) and mean clutch size was significantly larger (3.8 vs. 3.5 in 1992; $p = 0.02$). An index of productivity for the 21 414 km super(2) area surveyed in both years was much higher in 1993 (1339 young) than in the very late spring of 1992 (347 young). The number of adult brant on the survey area was similar in both years, and the lower productivity in 1992 was due primarily to fewer pairs' nesting that year. Smaller clutch size and lower nesting success may also have lowered productivity in 1992, but their effects appeared to be secondary. **No correlation** was found between colony size and clutch size, mean number of goslings hatched, or the percentage of nests that proved successful. Original Abstract: Le nombre de bernaches cravants (*Branta bernicla*) dans la voie migratoire du Pacifique est

relativement faible quand on le compare aux autres populations d'oies de l'Arctique, et il a diminue par rapport a ses niveaux historiques. On a peu de renseignements sur la bernache de l'ile Banks, meme si la taille de l'ile et son emplacement dans l'Arctique canadien occidental pourraient faire une aire de nidification importante pour cette espece. En 1992 et 1993, on a consigne au moyen de releves aeriens la distribution des bernaches qui nichaient dans la moitie sud de l'ile Banks, et on a effectue des etudes sur le terrain, la ou se trouvaient les colonies, afin de consigner la chronologie de nidification et les parametres de reproduction. En 1992, on a trouve 10 colonies (n = 159 nids) et, en 1993, 42 colonies (y compris sept qui avaient ete actives en 1992), ainsi que cinq nids solitaires (n = 514 nids). Deux tiers (67 p. cent) des sites de nidification accueillaienent 10 nids ou moins. La plupart des colonies (36 sur 45) se trouvaient sur des ilots (moyenne = 248 m super(2)) situes dans des lacs ou de grands etangs de l'ile, tandis que le reste (n = 9) etaient situees sur la terre ferme pres de nids actifs de harfangs des neiges (*Nyctea scandiaca*). En 1993, avec des temperatures en juin plus douces et une fonte nivale plus rapide qu'en 1992, la date moyenne du debut de la couvee a ete nettement plus hative (le 12 juin par rapport au 20 juin en 1992; $p < 0,001$) et la taille moyenne de la couvee a ete nettement plus grande (3,8 par rapport a 3,5 en 1992; $p = 0,02$). Un index de productivite pour les 21 414 km super(2) de la zone de releves des deux annees etait beaucoup plus eleve en 1993 (1339 petits) qu'au cours du printemps tres tardif de 1992 (347 petits). Le nombre de bernaches cravants adultes dans la zone des releves etait semblable dans les deux annees, et la productivite plus faible en 1992 etait surtout due a un nombre moindre de paires ayant fait un nid cette annee-la. La taille plus petite de la couvee et le taux de reussite plus faible quant a l'etablissement du nid pourraient aussi expliquer la baisse de productivite de 1992, mais ces effets paraissent secondaires. On n'a trouve aucune correlation entre la taille de la colonie et la taille de la couvee, le nombre moyen d'oisons eclos, ou le pourcentage de nids ou la reproduction a reussi.

L3 ANSWER 3 OF 21 MEDLINE DUPLICATE 1
 ACCESSION NUMBER: 2001042989 MEDLINE
 DOCUMENT NUMBER: 20511958 PubMed ID: 11056228
 TITLE: Endometrial stripe thickness in tubal and intrauterine pregnancies.
 AUTHOR: Levigur M; Tsai T; Kang K; Feldman J; Kory L A
 CORPORATE SOURCE: Department of Obstetrics and Gynecology, Jacobi Medical Center, Albert Einstein School of Medicine, Bronx, New York, USA.. mlevigur@maimonidesmed.org
 SOURCE: FERTILITY AND STERILITY, (2000 Nov) 74 (5) 889-91.
 Journal code: 0372772. ISSN: 0015-0282.
 PUB. COUNTRY: United States
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200012
 ENTRY DATE: Entered STN: 20010322
 Last Updated on STN: 20010322
 Entered Medline: 20001207
 AB OBJECTIVE: To evaluate endometrial stripe thickness (EST) among patients with tubal pregnancy (TP) and intrauterine pregnancy (IUP).

DESIGN: Historical cohort. SETTING: City hospital. PATIENT(S):
 Ninety-four
 women suspected to have TP. INTERVENTION(S): Serum betaHCG and
 sonographic
EST measurements. MAIN OUTCOME MEASURE(S): Comparison of age,
 gestational age (GA), **EST**, and log beta HCG. RESULT(S): The two
 groups of women, 65 with TP and 29 with IUP, had similar mean ages
 (+/-SD)
 of 28.6 +/- 5.7 and 28.6 +/- 6.1, respectively. The median values of GA
 in
 the 2 groups were similar, 46.6 and 44.6 d, respectively. The mean values
 for **EST** (+/-SD), adjusted for GA, were significantly different:
 9.9 +/- 5.9 mm in the TP group and 12.6 +/- 5.3 mm in the IUP group. The
 mean values (+/-SD) of log beta HCG in the 2 groups also differed
 significantly: 6.90 +/- 1.29 and 7.52 +/- 0.97, respectively. **No**
correlation was found between **EST** and GA or log beta HCG
 within either group. CONCLUSION(S): The mean **EST** in women with
 TP was significantly smaller than in women with IUP. The wide range of
EST values and their overlap precludes the utilization of
EST as a single feature in the diagnosis of a tubal pregnancy.

L3 ANSWER 4 OF 21 MEDLINE DUPLICATE 2
 ACCESSION NUMBER: 97465607 MEDLINE
 DOCUMENT NUMBER: 97465607 PubMed ID: 9326327
 TITLE: Molecular definition of 22q11 deletions in 151
 velo-cardio-facial syndrome patients.
 AUTHOR: Carlson C; Sirotkin H; Pandita R; Goldberg R; McKie J;
 Wadey R; Patanjali S R; Weissman S M; Anyane-Yeboah K;
 Warburton D; Scambler P; Shprintzen R; Kucherlapati R;
 Morrow B E
 CORPORATE SOURCE: Department of Molecular Genetics, Albert Einstein College
 of Medicine, Bronx, New York 10461, USA.
 CONTRACT NUMBER: PO-1 (NICHD)
 HD 34980-01
 SOURCE: AMERICAN JOURNAL OF HUMAN GENETICS, (1997 Sep) 61 (3)
 620-9.
 Journal code: 0370475. ISSN: 0002-9297.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199710
 ENTRY DATE: Entered STN: 19971105
 Last Updated on STN: 20020125
 Entered Medline: 19971022
 AB Velo-cardio-facial syndrome (VCFS) is a relatively common developmental
 disorder characterized by craniofacial anomalies and conotruncal heart
 defects. Many VCFS patients have hemizygous deletions for a part of
 22q11,
 suggesting that haploinsufficiency in this region is responsible for its
 etiology. Because most cases of VCFS are sporadic, portions of 22q11 may
 be prone to rearrangement. To understand the molecular basis for
 chromosomal deletions, we defined the extent of the deletion, by
 genotyping 151 VCFS patients and performing haplotype analysis on 105,
 using 15 consecutive polymorphic markers in 22q11. We found that 83% had
 a
 deletion and >90% of these had a similar approximately 3 Mb deletion,
 suggesting that sequences flanking the common breakpoints are susceptible
 to rearrangement. We found **no correlation** between the
 presence or size of the deletion and the phenotype. To further define the
 chromosomal breakpoints among the VCFS patients, we developed somatic

hybrid cell lines from a set of VCFS patients. An 11-kb resolution physical map of a 1,080-kb region that includes deletion breakpoints was constructed, incorporating genes and expressed sequence tags (**ESTs**) isolated by the hybridization selection method. The ordered markers were used to examine the two separated copies of chromosome 22 in the somatic hybrid cell lines. In some cases, we were able to map the chromosome breakpoints within a single cosmid. A 480-kb critical region for VCFS has been delineated, including the genes for GSCL, CTP, CLTD, HIRA, and TMVCF, as well as a number of novel ordered **ESTs**.

L3 ANSWER 5 OF 21 MEDLINE DUPLICATE 3
 ACCESSION NUMBER: 97468008 MEDLINE
 DOCUMENT NUMBER: 97468008 PubMed ID: 9327152
 TITLE: Prognostic implications of c-Ki-ras2 mutations in patients with advanced colorectal cancer treated with 5-fluorouracil and interferon: a study of the eastern cooperative oncology group (EST 2292).
 COMMENT: Comment in: Cancer J Sci Am. 1997 Sep-Oct;3(5):271-2
 AUTHOR: Wadler S; Bajaj R; Neuberg D; Agarwal V; Haynes H; Benson A
 B 3rd
 CORPORATE SOURCE: Albert Einstein College of Medicine, Bronx, New York, USA.
 CONTRACT NUMBER: CA14958 (NCI)
 CA17145 (NCI)
 CA23318 (NCI)
 +
 SOURCE: CANCER JOURNAL FROM SCIENTIFIC AMERICAN, (1997 Sep-Oct) 3 (5) 284-8.
 Journal code: 9513568. ISSN: 1081-4442.
 PUB. COUNTRY: United States
 (CLINICAL TRIAL)
 (CLINICAL TRIAL, PHASE I)
 (CLINICAL TRIAL, PHASE II)
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199710
 ENTRY DATE: Entered STN: 19971224
 Last Updated on STN: 19971224
 Entered Medline: 19971029
 AB PURPOSE: Mutations in c-Ki-ras2 (ras) occur in about 40% of patients with colorectal cancers and occur early in the pathogenesis of this disease.
 To evaluate the prognostic value of mutations in ras, the Eastern Cooperative Oncology Group (ECOG) conducted a retrospective study (**EST 2292**) to determine the frequency of mutations in patients with advanced colorectal cancer, and to determine whether ras mutations were associated with altered response to therapy and survival. PATIENTS AND METHODS: Patients were enrolled from four studies: P-Z289, an ECOG phase II trial of 5-fluorouracil (5-FU) and interferon (IFN) in patients with advanced colorectal cancer; P-Z991, an ECOG phase I trial of 5-FU and IFN in patients with advanced malignancies; and two trials from the Albert Einstein College of Medicine in patients with advanced colorectal cancer treated with 5-FU and either IFN-alpha or IFN-beta. All patients had advanced colorectal carcinoma and had sufficient histologic material

available for analysis for the presence and type of ras, using polymerase chain reaction and dot-blot analysis with sets of probes sufficient to detect all the common mutations of ras at codons 12, 13, and 61. RESULTS: Seventy-two patients were enrolled in this trial. Mutations in ras were detected in 25 (35%), including 17 (23%) in codon 12, four (6%) in codon 13, and four (6%) in codon 61. There was **no correlation** between the presence of a ras mutation and age, sex, Dukes' stage, histology, or tumor markers. Thirty-one of 72 patients (43%) responded to therapy with 5-FU and IFN, and 10 of 31 responders (32%) and 15 of 41 nonresponders (37%) had mutations in ras. There was no difference in response rates or overall survival between the groups with and without ras mutations. CONCLUSIONS: It is unlikely that ras mutations will have significant prognostic value for either response to therapy or survival in patients with colorectal carcinomas treated with 5-FU and IFN.

L3 ANSWER 6 OF 21 MEDLINE DUPLICATE 4
 ACCESSION NUMBER: 96381889 MEDLINE
 DOCUMENT NUMBER: 96381889 PubMed ID: 8789902
 TITLE: Gallbladder function and recurrent stones of the biliary tract in patients after endoscopic sphincterotomy.
 COMMENT: Comment in: Scand J Gastroenterol. 1997 Jan;32(1):95-6
 AUTHOR: Lai K H; Peng N J; Cheng J S; Lo G H; Wang E M; Wang N M; Huang R L; Chang C F; Lin C K; Chen S M
 CORPORATE SOURCE: Division of Gastroenterology, Veterans General Hospital-Kaohsiung, Taiwan.
 SOURCE: SCANDINAVIAN JOURNAL OF GASTROENTEROLOGY, (1996 Jun) 31 (6)
 612-5.
 Journal code: 0060105. ISSN: 0036-5521.
 PUB. COUNTRY: Norway
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199611
 ENTRY DATE: Entered STN: 19961219
 Last Updated on STN: 19980206
 Entered Medline: 19961113
 AB BACKGROUND: Change in gallbladder function may occur in patients with an intact gallbladder after endoscopic sphincterotomy (**EST**). This study was designed to evaluate the factors influencing gallbladder filling after **EST** and the correlation between gallbladder function and stone recurrence. METHODS: Sixty Chinese patients with symptomatic choledocholithiasis and an intact gallbladder received **EST** to clear the bile ducts. They were further investigated with sphincter of Oddi manometry (SOM), quantitative cholescintigraphy (QC), and long-term clinical follow-up. RESULTS: Fifty-six of the 60 patients in the study group were confirmed to have a loss of sphincteric function by SOM. QC showed normal gallbladder filling in 35 of these patients and delayed or non-filling in 21 patients. A significantly higher incidence of normal gallbladder filling occurred in patients with juxtapapillary diverticulum than in those without ($P < 0.02$), but preexisting cholecystolithiasis had no effect on it. During the follow-up period (median, 32 months; range, 9-54 months) 10 of 56 patients developed recurrent choledocholithiasis. There was **no correlation** between the status of gallbladder filling, preexisting cholecystolithiasis, and recurrent stones, but 9 of the 10 patients with recurrent stones had a juxtapapillary diverticulum. Repeated endoscopic treatment was satisfactory in eight patients, and only two patients received

cholecystectomy. CONCLUSIONS: **EST** does not alter gallbladder function in most patients. Juxtapapillary diverticulum may facilitate gallbladder filling after **EST**, but it is also a possible factor for recurrent choledocholithiasis.

L3 ANSWER 7 OF 21 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1996:187667 BIOSIS

DOCUMENT NUMBER: PREV199698743796

TITLE: Isozymatic differentiation in local population of Glycine soja Sieb. and Zucc.

AUTHOR(S): Li Jun, Tao Yun; Zheng Shi-Zhang; Zhou Ji-Lun

CORPORATE SOURCE: Ecol. Res. Program, Fudan Univ., Shanghai 200433 China

SOURCE: Acta Botanica Sinica, (1995) Vol. 37, No. 9, pp. 669-676.
ISSN: 0577-7496.

DOCUMENT TYPE: Article

LANGUAGE: Chinese

SUMMARY LANGUAGE: Chinese; English

AB The biochemical genetic structure and variation among local population of Glycine soja Sieb. & Zucc. were investigated based on isozyme analysis using the techniques of polyacrylamide gel electrophoresis. The isoenzyme zymography of 6 enzymes viz malate dehydrogenase (MDH), peroxidase (PER), adenosine triphosphatase (ATPase), amylase (AMY), esterase (**EST**) and isocitric dehydrogenase (IDH) of 14 culture seedlings were respectively compared. Isozymatic analysis revealed high genetic variation

in the population of G. soja. MDH, PER, ATPase, AMY are polymorphic. ATPase has the highest polymorphic index (PI=0.1582). **EST** and IDH are monomorphic for all populations. The average population heterozygosity (He) was 0.3141, and the average genetic distance (Da) among the 14 samples is 0.1512. Cluster analysis and canonical analysis showed **no correlation** existed between the population's biochemical genetic structure and its environment. It was concluded that mutation could be the major cause of the high enzymatic polymorphism in population; and the mechanism that keeps the polymorphism could be random drift sampling strategy for conservation of crop genetic resources was also put forward.

L3 ANSWER 8 OF 21 MEDLINE

DUPLICATE 5

ACCESSION NUMBER: 95220659 MEDLINE

DOCUMENT NUMBER: 95220659 PubMed ID: 7705622

TITLE: Variation in sperm displacement and its association with accessory gland protein loci in Drosophila melanogaster.

AUTHOR: Clark A G; Aguade M; Prout T; Harshman L G; Langley C H

CORPORATE SOURCE: Department of Biology, Pennsylvania State University, University Park 16802.

SOURCE: GENETICS, (1995 Jan) 139 (1) 189-201.

Journal code: 0374636. ISSN: 0016-6731.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199505

ENTRY DATE: Entered STN: 19950518

Last Updated on STN: 19950518

Entered Medline: 19950511

AB Genes that influence mating and/or fertilization success may be targets for strong natural selection. If females remate frequently relative to the

duration of sperm storage and rate of sperm use, sperm displacement may be

an important component of male reproductive success. Although it has long

been known that mutant laboratory stocks of *Drosophila* differ in sperm displacement, the magnitude of the naturally occurring genetic variation in this character has not been systematically quantified. Here we report the results of a screen for variation in sperm displacement among 152 lines of *Drosophila melanogaster* that were made homozygous for second and/or third chromosomes recovered from natural populations. Sperm displacement was assayed by scoring the progeny of *cn;bw* females that had been mated sequentially to *cn;bw* and tested males in either order. Highly significant differences were seen in both the ability to displace sperm that is resident in the female's reproductive tract and in the ability to resist displacement by subsequent sperm. Most lines exhibited nearly complete displacement, having nearly all progeny sired by the second male, but several lines had as few as half the progeny fathered by the second male. Lines that were identified in the screen for naturally occurring variation in sperm displacement were also characterized for single-strand conformation polymorphisms (SSCP) at seven accessory gland protein (Acp) genes, Glucose dehydrogenase (Gld), and Esterase-6 (**Est-6**). Acp genes encode proteins that are in some cases known to be transmitted to the female in the seminal fluid and are likely candidates for genes that might mediate the phenomenon of sperm displacement. Significant associations were found between particular Acp alleles at four different loci (Acp26Aa/Ab, Acp29B, Acp36DE and Acp53E) and the ability of males to resist displacement by subsequent sperm. There was **no correlation** between the ability to displace resident sperm and the ability to resist being displaced by subsequent sperm. This lack of correlation, and the association of Acp alleles with resisting subsequent sperm only, suggests that different mechanisms mediate the two components of sperm displacement.

L3 ANSWER 9 OF 21 MEDLINE DUPLICATE 6
 ACCESSION NUMBER: 93273358 MEDLINE
 DOCUMENT NUMBER: 93273358 PubMed ID: 8500836
 TITLE: Lack of correlation between mating activity and EST-1 polymorphism in three natural and laboratory populations of *Drosophila bipectinata*.
 AUTHOR: Naseerulla M K; Hegde S N
 CORPORATE SOURCE: Department of Studies in Zoology, University of Mysore, Manasagangotri, India.
 SOURCE: INDIAN JOURNAL OF EXPERIMENTAL BIOLOGY, (1993 Mar) 31 (3) 215-8.
 Journal code: 0233411. ISSN: 0019-5189.
 PUB. COUNTRY: India
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199306
 ENTRY DATE: Entered STN: 19930716
 Last Updated on STN: 19930716
 Entered Medline: 19930630
 AB **Est-1** polymorphism and mating activity have been studied in three natural populations of *D. bipectinata* and after 10 generations of their maintenance in the laboratory. The results indicate that the enzyme **Est-1** variation was not significant within natural populations within F10 generation and also between different natural populations and F10 generation indicating the role of balancing selection in the maintenance of enzyme polymorphism in both natural and laboratory conditions. On the other hand, there was variability in the mating activity within natural populations and within F10 generation and also between natural population and F10 generation. However, there was

no correlation between **Est-1** polymorphism and mating activity.

L3 ANSWER 10 OF 21 MEDLINE DUPLICATE 7
ACCESSION NUMBER: 93021858 MEDLINE
DOCUMENT NUMBER: 93021858 PubMed ID: 1404979
TITLE: Extracorporeal shock wave lithotripsy (ESWL) for common bile duct stones.
AUTHOR: Okushima K; Nakazawa S; Yamao K; Yoshino J; Inui K; Yamachika H; Kishi K
CORPORATE SOURCE: Department of Internal Medicine, Second Hospital, Fujita Health University School of Medicine, Nagoya.
SOURCE: NIPPON SHOKAKIBYO GAKKAI ZASSHI. JAPANESE JOURNAL OF GASTROENTEROLOGY, (1992 Aug) 89 (8) 1512-9.
Journal code: 2984683R. ISSN: 0446-6586.
PUB. COUNTRY: Japan
LANGUAGE: Japanese
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199211
ENTRY DATE: Entered STN: 19930122
Last Updated on STN: 19930122
Entered Medline: 19921103

AB We treated twenty-three patients with common bile duct stones (12 female, 11 male, mean age: 67.1 years) by Extracorporeal Shock Wave Lithotripsy (ESWL). The stones were focused by ultrasonic or choledochographic localization. The twenty-three patients received 53 ESWL treatments consisting of mean 2357 shocks per treatment at mean 18 kV. We performed ESWL in five cases with endoscopically unextractable common bile duct stones after endoscopic sphincterotomy (**EST**). In these cases, ESWL permitted stone disintegration and successful endoscopic extraction of the fragments. We performed ESWL in eighteen cases with common bile duct stones without **EST**. In fifteen of the eighteen cases (83%), fragmentation was achieved. The stone fragments were spontaneously discharged in ten cases (56%) after a median of 4 days following ESWL. In five cases, adjunct endoscopic procedures were performed. The complete fragmentation and the clearance rate for stones of diameter of less than 10 mm were higher than that for stones of diameter of more than 11 mm. In the cases with the stones of diameter of more than 10 mm, there is a very strong possibility that complete clearance is achieved by ESWL alone. **No correlation** was obtained for the effective results according to pretreatment number of stones. In eight of thirteen cases (62%) with gall bladder stones, complete clearance was achieved without **EST**. ESWL without **EST** can be thought as a rational treatment for preserving the function of papilla of Vater in the case of cholecysto-choledocholithiasis.

L3 ANSWER 11 OF 21 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1993:234945 BIOSIS
DOCUMENT NUMBER: PREV199395126120
TITLE: Soil respiration in barley (*Hordeum vulgare* L.) and fallow fields.
AUTHOR(S): Rochette, P. (1); Desjardins, R. L. (1); Gregorich, E. G. (1); Pattey, E. (1); Lessard, R.
CORPORATE SOURCE: (1) Centre Land Biol. Resources Res., Res. Branch, Agric. Canada, Ottawa, ON K1A 0C6 Canada
SOURCE: Canadian Journal of Soil Science, (1992) Vol. 72, No. 4, pp. 591-603.
ISSN: 0008-4271.
DOCUMENT TYPE: Article
LANGUAGE: English

SUMMARY LANGUAGE: English; French

AB A study was carried out to quantify the diurnal variation of soil respiration in fallow and barley fields and to assess the impact of atmospheric CO₂ concentration (C) and crop photosynthesis on soil respiration rates under field conditions. Soil respiration rate was measured twice a day (06:00 and 13:00 h **EST**) for 69 consecutive days at Ottawa, Ontario, Canada, during the 1990 growing season. Measurements were taken on fallow and under a barley (*Hordeum vulgare* L. 'Leger') crop using a dynamic closed chamber system. Crop net photosynthesis was obtained by subtracting soil respiration from the vertical CO₂ fluxes above the crop which was obtained using the eddy correlation technique. Afternoon soil respiration averaged 22 and 17%

more

than that in the morning on fallow and barley soils, respectively.

No correlation was found between atmospheric CO₂ concentration and morning respiration rates. The two daily respiration measurements on fallow soil could be fit to the same function of soil temperature despite important differences in C at the time of measurement.

These results indicate that soil temperature might account for the differences in R between morning and afternoon, and that the effect of C need not be considered for the modelling of the soil respiration diurnal cycle. Respiration in soil under barley was 25% lower than in fallow

soil.

Soil under barley was estimated to have at least 199 g C m⁻² more than fallow soil at the time of harvest due to the lower soil respiration and to the input of carbon by barley root residues. High correlations were obtained between crop photosynthesis and soil respiration rates during vegetative and reproductive periods, confirming that the biotic plant component is an important factor controlling soil respiration rates in cropped fields.

L3 ANSWER 12 OF 21 MEDLINE

ACCESSION NUMBER: 89117232 MEDLINE

DOCUMENT NUMBER: 89117232 PubMed ID: 3219003

TITLE: [Calculation of the slope of the ST/HR segment].
Calculo de la pendiente segmento ST/FC.

AUTHOR: Martinez Sanchez J; Galvan Montiel O; Palomar Lever A;
Elizalde Gonzalez J J

CORPORATE SOURCE: Laboratorio de Pruebas, Hospital ABC (British Cowdray) de Mexico, D.F.

SOURCE: ARCHIVOS DEL INSTITUTO DE CARDIOLOGIA DE MEXICO, (1988 Sep-Oct) 58 (5) 409-13.

Journal code: 0400463. ISSN: 0020-3785.

PUB. COUNTRY: Mexico

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: Spanish

FILE SEGMENT: Priority Journals

ENTRY MONTH: 198902

ENTRY DATE: Entered STN: 19900308

Last Updated on STN: 19900308

Entered Medline: 19890224

AB Several methods for evaluation of exercise stress testing (**EST**) have been described in order to analyze the relationship between ST segment changes and heart rate. The ST/HR slope has demonstrated to be worthwhile in identifying severe coronary artery disease (CAD). We applied

this method in patients catalogued as borderline in the traditional exercise test to find out if they could be considered to have a severe CAD. The patients were divided into two groups: the A, which included 41 patients with borderline **EST**, and the group B with 41 patients

with normal **EST**. Age, risk factors, double product and ST/HR slope were evaluated. The testing was done on a treadmill with the Bruce protocol. Four patients in group A had ST/HR slope greater than 6.0 mu Volt/beat/min (two of them with borderline **EST**). Whereas all patients in group B had ST/HR slope values less than 6.0. We concluded this is a sensitive method for discrimination between normal and borderline **EST**. We found **no correlation** among age, sex, risk factors, double product and ST/HR slope. Approximately 10 percent of borderline **EST** would be underestimated with the traditional method. The calculation of the slope obtained its maximum applicability in patients with almost maximum **EST**.

L3 ANSWER 13 OF 21 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1989:133193 BIOSIS
DOCUMENT NUMBER: BA87:67846
TITLE: MEASUREMENT OF THE ST-HR SLOPE DURING STRESS TEST.
AUTHOR(S): MARTINEZ SANCHEZ J; GALVAN MONTIEL O; PALOMAR LEVER A;
ELIZALDE GONZALEZ J J
CORPORATE SOURCE: LAB. DE PRUEBAS DE ESFUERZO DEL HOSP. ABC DE MEXICO, MEX.,
D.F.
SOURCE: ARCH INST CARDIOL MEX, (1988) 58 (5), 409-413.
CODEN: AICMA2. ISSN: 0365-3080.
FILE SEGMENT: BA; OLD
LANGUAGE: Spanish

AB Several methods for evaluation of exercise stress testing (**EST**) have been described in order to analyze the relationship between ST segment changes and heart rate. The ST/HR slope has demonstrated to be worthwhile in identifying severe coronary artery disease (CAD). We applied this method in patients catalogued as borderline in the traditional exercise testings to find out if they could be considered to have a severe

CAD. The patients were divided into two groups: The A, which included 41 patients with borderline **EST**, and the group B with 41 patients with normal **EST**. Age, risk factors, double product and ST/HR slope were evaluated. The testing was made in a treadmill with the Bruce protocol. Four patients in group A had ST/HR slope > 6.0 u Volt/beat/min (two of them with borderline **EST**). Whereas all patients in group B had ST/HR slope values less than 6.0. We concluded this is a sensitivity method for discrimination between normal and borderline **EST**. We found **no correlation** among age, sex, risk factors, double product and ST/HR slope. Approximately 10 percent of borderline **EST** would be under estimated with the traditional method. The calculation of the slope obtained its maximum applicability in patients with almost maximum **EST**.

L3 ANSWER 14 OF 21 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1988:482183 BIOSIS
DOCUMENT NUMBER: BA86:113493
TITLE: ALLOZYME VARIATION IN POPULATIONS OF THE DOG WHELK
NUCELLA-LAPILLUS PROSOBRANCHIA MURIACEA FROM THE SOUTH
WEST PENINSULA OF ENGLAND UK.
AUTHOR(S): DAY A J; BAYNE B L
CORPORATE SOURCE: PLYMOUTH MARINE LAB., WEST HOE, PLYMOUTH PL1 3DH, DEVON,
ENGL.
SOURCE: MAR BIOL (BERL), (1988) 99 (1), 93-100.
CODEN: MBIOAJ. ISSN: 0025-3162.
FILE SEGMENT: BA; OLD
LANGUAGE: English

AB Four populations of the predatory gastropod *Nucella lapillus* were sampled at sites around the South West Peninsula of England in 1986, and analyzed for allozyme variation at 18 enzyme loci. Two of these loci, .alpha.Gpd-1 and Hk-1, exhibited sex-specific phenotypes. An absolute locus association

was observed between two other loci, Mdh-1 and **Est-3**. This association was only found at one site (Prawle), and it is suggested that the presence of chromosomal polymorphisms could explain this finding. As

a measure of overall similarity, Nei's genetic identity statistic, I, was calculated; the mean for all populations was 0.989, with values ranging from 0.981 to 0.997. Although similar on this gross level, considerable interpopulation variation was evident. Observed mean heterozygosity (per locus) ranged from 0.043 to 0.104 (mean 0.074). Populations differed also in the loci at which significant heterozygote deficits were seen (of the seven deficits recorded only those at the Pep-1 locus were consistent across sites) and in the presence of rare alleles undetected elsewhere. The variation observed showed **no correlation** to shell morphology or geographical distance and confirmed the conclusion that species of the genus *Nucella* show considerable disjunct variation.

L3 ANSWER 15 OF 21 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1985:434082 BIOSIS

DOCUMENT NUMBER: BA80:104074

TITLE: TEMPORAL VARIATION OF ALLELE FREQUENCIES IN POPULATIONS OF AKODON-DOLORES RODENTIA CRICETIDAE.

AUTHOR(S): APFELBAUM L I; BLANCO A

CORPORATE SOURCE: CATEDRA QUIMICA BIOL., FAC. CIENCIAS MED., UNIV. NACL. CORDOBA, 5016 CORDOBA, ARGENTINA.

SOURCE: THEOR APPL GENET, (1985) 70 (5), 569-572.
CODEN: THAGA6. ISSN: 0040-5752.

FILE SEGMENT: BA; OLD

LANGUAGE: English

AB Six population samples of the South American cricetid rodent *Akodon dolores* were collected at the same site at six-month intervals over a three year period. Changes in density were detected. Seven out of 18 loci analyzed by means of starch gel electrophoresis were polymorphic. Only

two of these loci (**Est-4** and G6pdh) showed statistically significant variation in allele frequencies following a seasonal pattern. There was **no correlation** between allele frequencies and population density. When animals were grouped into two classes according to body weight, a clear difference in allele distribution at the **Est-4** and G6pdh loci was observed between individuals 39 g or less and those heavier than 39 g. As the first group comprises predominantly younger animals, the data indicate that changes in the age-structure of population, rather than density variations, are responsible for the cyclic pattern of allele frequencies fluctuations.

L3 ANSWER 16 OF 21

MEDLINE

DUPLICATE 8

ACCESSION NUMBER: 85051025 MEDLINE

DOCUMENT NUMBER: 85051025 PubMed ID: 6094151

TITLE: Secretion of luteinizing hormone (LH) and pituitary receptors for LH-releasing hormone as modified by the proestrous surge of progesterone.

AUTHOR: Witcher J A; Nearhoof K F; Freeman M E

CONTRACT NUMBER: HD-00231 (NICHD)

SOURCE: ENDOCRINOLOGY, (1984 Dec) 115 (6) 2189-94.
Journal code: 0375040. ISSN: 0013-7227.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 198412
ENTRY DATE: Entered STN: 19900320
Last Updated on STN: 19970203
Entered Medline: 19841227

AB Pituitary glands of proestrous (PRO) rats display enhanced LH secretory response to LHRH when compared to pituitary glands of estrous (EST) rats. In addition proestrous pituitary glands display a self-potentiating (priming) response to LHRH, whereas estrous pituitary glands do not. This study addresses the role of the proestrous surge of progesterone in converting the proestrous-like LH secretory responses of the pituitary gland to those of estrus. Anterior pituitary glands were obtained from PRO and EST rats. In addition, Pro rats were treated with pentobarbital alone (PRO/PB) or with pentobarbital plus progesterone (PRO/PB-P4). Pentobarbital was given to prevent proestrous surges of LH and progesterone. Pentobarbital-treated animals were killed the day after treatment, estrus. Pituitary glands from each group were tested for LH secretory response in a superfusion chamber with exposure

of

two 15-min pulses of 10 nM LHRH separated by 90 min, or assayed for LHRH receptor content using iodinated D-Ala6-LHRH. Anterior pituitary glands from PRO rats secreted higher levels of LH than EST rats in response to an LHRH pulse. Only PRO anterior pituitary glands secreted priming responses to LHRH. Though anterior pituitary glands obtained from pentobarbital-treated rats showed LH responses of similar magnitude to anterior pituitary glands of PRO rats after initial LHRH challenge, they did not display priming responses. Progesterone replacement (PRO/PB-P4) led to depressed secretory responses when compared to PRO pituitary

glands

similar to EST rats. LHRH receptor concentrations in pituitary glands of EST rats was lower than those in pituitary glands of PRO rats. Depression of pituitary LHRH receptor concentration from proestrus to estrus was prevented by pentobarbital-treatment on

proestrus.

Estrus-like depression of receptor concentration was restored after progesterone treatment (PRO/PB-P4). These data suggest the LHRH receptor depression on estrus is a consequence of the secretion of progesterone on proestrus. Further, the declining magnitude of the in vitro LH-secretory response to LHRH follows a declining LHRH receptor concentration; however no correlation exists between receptor number and ability to prime.

L3 ANSWER 17 OF 21 MEDLINE
ACCESSION NUMBER: 85069993 MEDLINE
DOCUMENT NUMBER: 85069993 PubMed ID: 6391223
TITLE: Parasitological, serological, and clinical studies of Wuchereria bancrofti in Limbe, Haiti.
AUTHOR: Raccurt C P; Mojon M; Hodges W H
SOURCE: AMERICAN JOURNAL OF TROPICAL MEDICINE AND HYGIENE, (1984 Nov) 33 (6) 1124-9.
Journal code: 0370507. ISSN: 0002-9637.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 198501
ENTRY DATE: Entered STN: 19900320
Last Updated on STN: 19900320
Entered Medline: 19850114

AB A survey for *Wuchereria bancrofti* in Limbe, Haiti (**est.** pop. = 10,500) revealed that 17% (231/1,450) had a patent infection. Nearly half of those surveyed harbored fewer than 10 microfilariae (mf) per 20 mm³ of finger-prick blood; the median mf density for females and males was 12.4 and 9.5, respectively. Parasitemias occurred as early as age 4. Antibody titers greater than or equal to 1:20 against adult *D. viteae* antigen were observed in 38% of microfilaremic individuals and in 29% of amicrofilaremic individuals. Peak antibody responsiveness (40%) was observed between 5 and 9 years of age. In all age groups there was **no correlation** between mf density and antibody titer. Among the mf carriers, 5.6% had no clinical symptoms. Lymphangitis was a common feature with 14.3% having lymphedema, 8.2% with edema of the lower extremities, and 1.3% reporting episodes of chyluria. Genital involvement among women was rare, but in males 5.4% had genital swelling and 4.5% had hydroceles. *Culex pipiens quinquefasciatus* (Say) was observed to support the complete development of *W. bancrofti* in Limbe.

L3 ANSWER 18 OF 21 MEDLINE DUPLICATE 9
ACCESSION NUMBER: 84161323 MEDLINE
DOCUMENT NUMBER: 84161323 PubMed ID: 6706678
TITLE: Population genetics of the tree hole mosquito *Aedes triseriatus*: **no correlation** between **Est-6** and larval habitat.
AUTHOR: Matthews T C
CONTRACT NUMBER: AI-02753 (NIAID)
SOURCE: HEREDITY, (1984 Feb) 52 (Pt 1) 133-9.
Journal code: 0373007. ISSN: 0018-067X.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198405
ENTRY DATE: Entered STN: 19900319
Last Updated on STN: 20000303
Entered Medline: 19840502

L3 ANSWER 19 OF 21 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1983:169308 BIOSIS
DOCUMENT NUMBER: BA75:19308
TITLE: THE SEROLOGICAL DETECTION OF ANTIBODIES TO AVIAN ENCEPHALOMYELITIS VIRUS.
AUTHOR(S): AHMED A A S; EL-AZM I M A; AYOUB N N K; EL-TOUKHI B I M
CORPORATE SOURCE: DEP. OF AVIAN AND AQUATIC ANIMAL MED., FAC. OF VET. MED., ALEXANDRIA UNIV., EDFINA, BEHERA, EGYPT.
SOURCE: AVIAN PATHOL, (1982) 11 (2), 253-262.
CODEN: AVPADN. ISSN: 0307-9457.
FILE SEGMENT: BA; OLD
LANGUAGE: English

AB An avian encephalomyelitis virus (AEV) antigen, prepared from the gastrointestinal tract of infected chick embryos and partially purified and concentrated by chloroform and polyethylene glycol treatments, exhibited the highest reactivity in the agar-gel precipitin test (AGPT). Antigen used in the passive hemagglutination test (PHAT) that was purified and concentrated yielded higher antibody titers than when untreated crude antigens were used. The use of the AGPT, PHAT and embryo susceptibility test (**EST**) on chicken breeding flocks with and without a history of previous vaccination against AEV revealed that the PHAT was more sensitive in detecting AEV antibodies than the AGPT. The sensitivity of the PHAT was nearly equal to the **EST**. **No correlation** was found between the results of the AGPT and the

immune status of a flock judged by the **EST**.

L3 ANSWER 20 OF 21 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS
INC.DUPLICATE

10

ACCESSION NUMBER: 1981:190944 BIOSIS
DOCUMENT NUMBER: BA71:60936
TITLE: THE FUNCTION OF THE PITUITARY THYROIDAL AXIS IN
ACROMEGALIC PATIENTS VS. PATIENTS WITH HYPER PROLACTINEMIA AND A
PITUITARY TUMOR.
AUTHOR(S): KLIJN J G M; LAMBERTS S W J; DOCTER R; DE JONG F H; VAN
DONGEN K J; BIRKENHAGER J C
CORPORATE SOURCE: DEP. OF MED. 111 , UNIV. HOSP. 'DIJKZIGT', ERASMUS UNIV.,
DR MOLEWATERPLEIN 40, 3015 GD ROTTERDAM, NETHERLANDS.
SOURCE: CLIN ENDOCRINOL, (1980) 13 (6), 577-586.
CODEN: CLECAP. ISSN: 0300-0664.
FILE SEGMENT: BA; OLD
LANGUAGE: English

AB The function of the pituitary thyroidal axis was examined in 53 of 62 patients with hyperprolactinemia and a pituitary tumor and in 40 of 44 acromegalic patients, in whom 1 or more indices of the pituitary thyroid function were determined before treatment. In the patients with hyperprolactinemia and a pituitary tumor, sellar + extrasellar tissue (**EST**) size showed a significant negative correlation with the response of TSH [thyrotropin] to TRH [thyroliberin] (.DELTA.TSH) as well as with the circulating T4 [thyroxine] and T3 [triiodothyronine] levels. These correlations were not present in the acromegalic patients. In the prolactinoma group, a sharp decrease in mean serum T4 and T3 levels was found at sellar + **EST** sizes exceeding 3 cm². In 23 patients with a sellar + **EST** size of 3 cm² or more, 13 (57%) showed a T4 level of less than 6 .mu.g/dl against none of the 28 patients with a sellar + **EST** size of less than 3 cm². For T3 using a limit of 120 ng/dl, the corresponding numbers were 8 of 13 (62%) and none of the 10 patients, respectively. A positive correlation was observed between .DELTA.TSH and the T3 levels but not between .DELTA.TSH and T4, while in the acromegalic patients there was **no correlation** between TSH reserve and T3 or T4. In the patients with hyperprolactinemia and a pituitary tumor, positive correlations between basal TSH and .DELTA.TSH as well as between T4 and T3 levels were observed. These correlations were not found in the acromegalic patients. Thyroid function appears to be independent

of

pituitary tumor size in patients with acromegaly but not in patients with hyperprolactinemia and a pituitary tumor. In acromegalic patients, the high incidence of an impaired TSH response (without hyperthyroidism and independent of tumor size) may be caused by suppression of TSH secretion rather than by destruction of thyrotrophic cells.

L3 ANSWER 21 OF 21 MEDLINE

ACCESSION NUMBER: 76087718 MEDLINE
DOCUMENT NUMBER: 76087718 PubMed ID: 54163
TITLE: Esterase polymorphism and sensitivity to Dursban organophosphorus insecticide in Culex pipiens pipiens populations.
AUTHOR: Pasteur N; Sinigra G
SOURCE: BIOCHEMICAL GENETICS, (1975 Dec) 13 (11-12) 789-803.
Journal code: 0126611. ISSN: 0006-2928.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals

ENTRY MONTH: 197602
ENTRY DATE: Entered STN: 19900313
Last Updated on STN: 19900313
Entered Medline: 19760227

AB Esterase polymorphism and Dursban
(O,O-dimethyl-2-pyridylphosphorothioate)
sensitivity have been investigated in 12 natural populations and three
laboratory strains of *Culex pipiens pipiens*. This mosquito has two
esterase loci, **Est-1** and **Est-2**, which were shown to
code esterases of the B group (aliesterases) but not cholinesterases.
No correlation between **Est-1** polymorphism and
Dursban sensitivity was found, but the increase of the **Est**
-2(0.64) allele in the populations less sensitive to Dursban was highly
significant ($r = -0.9850$ for 6 df).

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(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
19:04:09

ON 08 JUL 2002

L1 13496 S EST
L2 34 S L1(S) (NO#(W) CORRELAT?)
L3 21 DUP REM L2 (13 DUPLICATES REMOVED)

=> s l1(s) (mRNA or cDNA or polynucleotide#)

L4 3375 L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)

=> s l4(s) (protein or peptide)

3 FILES SEARCHED...

L5 1972 L4(S) (PROTEIN OR PEPTIDE)

=> s l5(express?)

MISSING OPERATOR 'L25(EXPRESS?)'

The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> s l5(s) (express?)

L6 1748 L5(S) (EXPRESS?)

=> s l6(s) database#

L7 775 L6(S) DATABASE#

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
19:04:09

ON 08 JUL 2002

L1 13496 S EST
L2 34 S L1(S) (NO#(W) CORRELAT?)
L3 21 DUP REM L2 (13 DUPLICATES REMOVED)
L4 3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5 1972 S L4(S) (PROTEIN OR PEPTIDE)
L6 1748 S L5(S) (EXPRESS?)
L7 775 S L6(S) DATABASE#

=> dup rem l7

PROCESSING COMPLETED FOR L7
L8 355 DUP REM L7 (420 DUPLICATES REMOVED)

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L8 ANSWER 1 OF 355 MEDLINE
ACCESSION NUMBER: 2002328673 IN-PROCESS
DOCUMENT NUMBER: 22056133 PubMed ID: 12060780
TITLE: Identification of gene expression profile of dorsal root
ganglion in the rat peripheral axotomy model of
neuropathic pain.
AUTHOR: Xiao Hua-Sheng; Huang Qiu-Hua; Zhang Fang-Xiong; Bao Lan;
Lu Ying-Jin; Guo Chao; Yang Liang; Huang Wein-Jing; Fu
Gang; Xu Shu-Hua; Cheng Xi-Ping; Yan Qing; Zhu Zhi-Dong;
Zhang Xin; Chen Zhu; Han Ze-Guang; Zhang Xu
CORPORATE SOURCE: Laboratory of Sensory System, Institute of Neuroscience,
Shanghai Institutes for Biological Sciences, Chinese
Academy of Sciences, 320 Yue Yang Road, Shanghai 200031,
China.
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE
UNITED STATES OF AMERICA, (2002 Jun 11) 99 (12) 8360-5.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
OTHER SOURCE: GENBANK-BG662484; GENBANK-BG662485; GENBANK-BG662486;
GENBANK-BG662487; GENBANK-BG662488; GENBANK-BG662489;
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GENBANK-BG663402; GENBANK-BG663403; GENBANK-BG663404;
GENBANK-BG663405; GENBANK-BG663406; GENBANK-BG663407;
GENBANK-BG663408; GENBANK-BG663409; GENBANK-BG663410;
GENBANK-BG663411; GENBANK-BG663412; GENBANK-BG663413;
GENBANK-BG663414; GENBANK-BG663415; GENBANK-BG663416;
GENBANK-BG663417; GENBANK-BG663418; GENBANK-BG663419;
GENBANK-BG663420; GENBANK-BG663421; GENBANK-BG663422;
GENBANK-BG663423; GENBANK-BG663424; GENBANK-BG663425;
GENBANK-BG663426; GENBANK-BG663427; GENBANK-BG663428;
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GENBANK-BG663456; GENBANK-BG663457; GENBANK-BG663458;
GENBANK-BG663459; GENBANK-BG663460; GENBANK-BG663461;
GENBANK-BG663462; GENBANK-BG663463; GENBANK-BG663464;
GENBANK-BG663465; GENBANK-BG663466; GENBANK-BG663467;
GENBANK-BG663468; GENBANK-BG663469; GENBANK-BG663470;
GENBANK-BG663471; GENBANK-BG663472; GENBANK-BG663473;
GENBANK-BG663474; GENBANK-BG663475; GENBANK-BG663476;
GENBANK-BG663477; GENBANK-BG663478; GENBANK-BG663479;
GENBANK-BG663480; GENBANK-BG663481; GENBANK-BG663482;
GENBANK-BG663483

ENTRY DATE:

Entered STN: 20020620

Last Updated on STN: 20020620

L8 ANSWER 2 OF 355

MEDLINE

DUPLICATE 1

ACCESSION NUMBER: 2002326077

IN-PROCESS

DOCUMENT NUMBER: 22064257 PubMed ID: 12069307
TITLE: Purification and identification of a tributyltin-binding protein from serum of Japanese flounder, *Paralichthys olivaceus*.
AUTHOR: Shimasaki Yohei; Oshima Yuji; Yokota Yoshiko; Kitano Takeshi; Nakao Miki; Kawabata Shun-ichiro; Imada Nobuyoshi;
CORPORATE SOURCE: Honjo Tsuneo
LABORATORY OF MARINE BIOCHEMISTRY, GRADUATE SCHOOL OF BIORESOURCE AND BIOENVIRONMENTAL SCIENCES, KYUSHU UNIVERSITY, FUKUOKA, JAPAN.
SOURCE: ENVIRONMENTAL TOXICOLOGY AND CHEMISTRY / SETAC, (2002 Jun) 21 (6) 1229-35.
JOURNAL CODE: 8308958. ISSN: 0730-7268.
PUB. COUNTRY: United States
JOURNAL; ARTICLE; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; PRIORITY JOURNALS
ENTRY DATE: Entered STN: 20020619
Last Updated on STN: 20020619

L8 ANSWER 3 OF 355 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2002299254 IN-PROCESS
DOCUMENT NUMBER: 22035872 PubMed ID: 12040005
TITLE: Identification of Gasz, an Evolutionarily Conserved Gene Expressed Exclusively in Germ Cells and Encoding a Protein with Four Ankyrin Repeats, a Sterile-alpha Motif, and a Basic Leucine Zipper.
AUTHOR: Yan Wei; Rajkovic Aleksandar; Viveiros Maria M; Burns Kathleen H; Eppig John J; Matzuk Martin M
CORPORATE SOURCE: DEPARTMENTS OF PATHOLOGY (W.Y., M.M.M.), DEPARTMENT OF MOLECULAR AND CELLULAR BIOLOGY (M.M.M.), DEPARTMENT OF MOLECULAR AND HUMAN GENETICS (M.M.M., K.H.B.), DEPARTMENT OF OBSTETRICS AND GYNECOLOGY (A.R.), BAYLOR COLLEGE OF MEDICINE, HOUSTON, TEXAS 77030.
SOURCE: MOLECULAR ENDOCRINOLOGY, (2002 Jun) 16 (6) 1168-84.
JOURNAL CODE: 8801431. ISSN: 0888-8809.
PUB. COUNTRY: United States
JOURNAL; ARTICLE; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; PRIORITY JOURNALS
ENTRY DATE: Entered STN: 20020602
Last Updated on STN: 20020602

L8 ANSWER 4 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:370545 BIOSIS
DOCUMENT NUMBER: PREV200200370545
TITLE: DCAL-1: A novel dendritic cell-associated C-type lectin regulated by CD40.
AUTHOR(S): Ryan, Elizabeth J. (1); Marshall, Aaron J.; Magaletti, Dario M. (1); Olson, N. Eric (1); Clark, Edward A. (1)
CORPORATE SOURCE: (1) Microbiology, University of Washington, Seattle, WA USA
SOURCE: FASEB Journal, (March 22, 2002) Vol. 16, No. 5, pp. A1056.
<http://www.fasebj.org/>. print.
Meeting Info.: Annual Meeting of Professional Research Scientists on Experimental Biology New Orleans, Louisiana, USA April 20-24, 2002
ISSN: 0892-6638.
DOCUMENT TYPE: Conference
LANGUAGE: English

L8 ANSWER 5 OF 355 MEDLINE DUPLICATE 3

ACCESSION NUMBER: 2002190233 MEDLINE

DOCUMENT NUMBER: 21920758 PubMed ID: 11923246

TITLE: Transcriptional profile of rat extraocular muscle by serial analysis of gene expression.

AUTHOR: Cheng Georgiana; Porter John D

CORPORATE SOURCE: Department of Ophthalmology, Case Western Reserve University, Cleveland, OH 44106-5068, USA.

CONTRACT NUMBER: P30-EY11370 (NEI)
R01-EY09834 (NEI)
R01-EY12779 (NEI)

SOURCE: INVESTIGATIVE OPHTHALMOLOGY AND VISUAL SCIENCE, (2002 Apr) 43 (4) 1048-58.
Journal code: 7703701. ISSN: 0146-0404.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200204

ENTRY DATE: Entered STN: 20020403
Last Updated on STN: 20020430
Entered Medline: 20020429

L8 ANSWER 6 OF 355 MEDLINE

ACCESSION NUMBER: 2002303792 MEDLINE

DOCUMENT NUMBER: 22040342 PubMed ID: 12045154

TITLE: A subtracted cDNA library from the zebrafish (Danio rerio) embryonic inner ear.

AUTHOR: Coimbra Roney S; Weil Dominique; Brottier Phillipe; Blanchard Stephane; Levi Michael; Hardelin Jean-Pierre; Weissenbach Jean; Petit Christine

CORPORATE SOURCE: Unite de Genetique des Deficits Sensoriels, Centre National de la Recherche Scientifique Unite de Recherche Associer (URA) 1968, Institut Pasteur, 75724 Paris cedex 15, France.

SOURCE: GENOME RESEARCH, (2002 Jun) 12 (6) 1007-11.
Journal code: 9518021. ISSN: 1088-9051.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AL714032; GENBANK-AL714033; GENBANK-AL714034;
GENBANK-AL714035; GENBANK-AL714036; GENBANK-AL714037;
GENBANK-AL714038; GENBANK-AL714039; GENBANK-AL714040;
GENBANK-AL714041; GENBANK-AL714042; GENBANK-AL714043;
GENBANK-AL714044; GENBANK-AL714045; GENBANK-AL714046;
GENBANK-AL714047; GENBANK-AL714048; GENBANK-AL714049;
GENBANK-AL714050; GENBANK-AL714051; GENBANK-AL714052;
GENBANK-AL714053; GENBANK-AL714054; GENBANK-AL714055;
GENBANK-AL714056; GENBANK-AL714057; GENBANK-AL714058;
GENBANK-AL714059; GENBANK-AL714060; GENBANK-AL714061;
GENBANK-AL714062; GENBANK-AL714063; GENBANK-AL714064;
GENBANK-AL714065; GENBANK-AL714066; GENBANK-AL714067;
GENBANK-AL714068; GENBANK-AL714069; GENBANK-AL714070;
GENBANK-AL714071; GENBANK-AL714072; GENBANK-AL714073;
GENBANK-AL714074; GENBANK-AL714075; GENBANK-AL714076;
GENBANK-AL714077; GENBANK-AL714078; GENBANK-AL714079;
GENBANK-AL714080; GENBANK-AL714081; GENBANK-AL714082;

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

GENBANK-AL714998; GENBANK-AL714999; GENBANK-AL715000;
GENBANK-AL715001; GENBANK-AL715002; GENBANK-AL715003;
GENBANK-AL715004; GENBANK-AL715005; GENBANK-AL715006;
GENBANK-AL715007; GENBANK-AL715008; GENBANK-AL715009;
GENBANK-AL715010; GENBANK-AL715011; GENBANK-AL715012;
GENBANK-AL715013; GENBANK-AL715014; GENBANK-AL715015;
GENBANK-AL715016; GENBANK-AL715017; GENBANK-AL715018;
GENBANK-AL715019; GENBANK-AL715020; GENBANK-AL715021;
GENBANK-AL715022; GENBANK-AL715023; GENBANK-AL715024;
GENBANK-AL715025; GENBANK-AL715026; GENBANK-AL715027;
GENBANK-AL715028; GENBANK-AL715029; GENBANK-AL715030;
GENBANK-AL715031

ENTRY MONTH: 200207
ENTRY DATE: Entered STN: 20020605
Last Updated on STN: 20020702
Entered Medline: 20020701

L8 ANSWER 7 OF 355 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 2002272413 IN-PROCESS
DOCUMENT NUMBER: 22007746 PubMed ID: 12010494
TITLE: The Pneumocystis carinii drug target S-adenosyl-L-methionine:sterol C-24 methyl transferase has a unique substrate preference.
AUTHOR: Kaneshiro Edna S; Rosenfeld Jill A; Basselin-Eiweida Mireille; Stringer James R; Keely Scott P; Smulian A George; Giner Jose-Luis
CORPORATE SOURCE: Department of Biological Sciences, University of Cincinnati, Cincinnati, OH 45221-0006, USA.
SOURCE: MOLECULAR MICROBIOLOGY, (2002 May) 44 (4) 989-99.
Journal code: 8712028. ISSN: 0950-382X.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020516
Last Updated on STN: 20020516

L8 ANSWER 8 OF 355 MEDLINE DUPLICATE 5
ACCESSION NUMBER: 2002131925 MEDLINE
DOCUMENT NUMBER: 21856591 PubMed ID: 11867573
TITLE: Gene expression profile of native human retinal pigment epithelium.
AUTHOR: Buraczynska Monika; Mears Alan J; Zareparsa Sepideh; Farjo Rafal; Filippova Elena; Yuan Yukun; MacNee Sean P; Hughes Bret; Swaroop Anand
CORPORATE SOURCE: Department of Ophthalmology and Visual Sciences, W.K. Kellogg Eye Center, University of Michigan, 1000 Wall Street, Ann Arbor, MI 48105, USA.
CONTRACT NUMBER: EY 07003 (NEI)
EY 07961 (NEI)
EY 11115 (NEI)
M01 RR 00042 (NCRR)
SOURCE: INVESTIGATIVE OPHTHALMOLOGY AND VISUAL SCIENCE, (2002 Mar) 43 (3) 603-7.
Journal code: 7703701. ISSN: 0146-0404.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200203
ENTRY DATE: Entered STN: 20020228

Last Updated on STN: 20020403
Entered Medline: 20020328

L8 ANSWER 9 OF 355 MEDLINE DUPLICATE 6
ACCESSION NUMBER: 2002302237 MEDLINE
DOCUMENT NUMBER: 22039529 PubMed ID: 12043562
TITLE: Molecular cloning, characterization, chromosomal assignment, genomic organization and verification of SFRS12(SRrp508), a novel member of human SR protein superfamily and a human homolog of rat SRrp86.
AUTHOR: Zhang De-Li; Sun Xiao-Jing; Ling Lun-Jiang; Chen Run-Sheng;
CORPORATE SOURCE: Ma Da-Long
Peking University Center for Human Disease Genomics, China
National Center for Human Genome Research, Beijing 100083, China.. delizhang@bjmu.edu
SOURCE: I CHUAN HSUEH PAO. ACTA GENETICA SINICA, (2002 May) 29 (5) 377-83.
Journal code: 7900784. ISSN: 0379-4172.
PUB. COUNTRY: China
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: Chinese
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF459094
ENTRY MONTH: 200207
ENTRY DATE: Entered STN: 20020605
Last Updated on STN: 20020704
Entered Medline: 20020703

L8 ANSWER 10 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:306444 BIOSIS
DOCUMENT NUMBER: PREV200200306444
TITLE: Establishing connections between microarray expression data and chemotherapeutic cancer pharmacology.
AUTHOR(S): Wallqvist, Anders (1); Rabow, Alfred A.; Shoemaker, Robert H.; Sausville, Edward A.; Covell, David G.
CORPORATE SOURCE: (1) Science Applications International Corporation, Frederick, MD, 21702 USA
SOURCE: Molecular Cancer Therapeutics, (March, 2002) Vol. 1, No. 5,
pp. 311-320. <http://mct.aacrjournals.org/>. print.
ISSN: 1535-7163.
DOCUMENT TYPE: Article
LANGUAGE: English

L8 ANSWER 11 OF 355 MEDLINE DUPLICATE 7
ACCESSION NUMBER: 2002004306 MEDLINE
DOCUMENT NUMBER: 21624839 PubMed ID: 11752319
TITLE: SYSTERS, GeneNest, SpliceNest: exploring sequence space from genome to protein.
AUTHOR: Krause Antje; Haas Stefan A; Coward Eivind; Vingron Martin
CORPORATE SOURCE: Max-Planck-Institute for Molecular Genetics, Computational Molecular Biology, Ihnestrasse 73, 14195 Berlin, Germany.. krause_a@molgen.mpg.de
SOURCE: NUCLEIC ACIDS RESEARCH, (2002 Jan 1) 30 (1) 299-300.
Journal code: 0411011. ISSN: 1362-4962.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals

ENTRY MONTH: 200201
ENTRY DATE: Entered STN: 20020102
Last Updated on STN: 20020125
Entered Medline: 20020121

L8 ANSWER 12 OF 355 MEDLINE DUPLICATE 8
ACCESSION NUMBER: 2002104309 MEDLINE
DOCUMENT NUMBER: 21644001 PubMed ID: 11784322
TITLE: Cloning and expression of sterol Delta 14-reductase from bovine liver.
AUTHOR: Roberti Rita; Bennati Anna Maria; Galli Giovanni; Caruso Donatella; Maras Bruno; Aisa Cristina; Beccari Tommaso; Della Fazia Maria Agnese; Servillo Giuseppe
CORPORATE SOURCE: Department of Internal Medicine, University of Perugia, Italy.. roberti@unipg.it
SOURCE: EUROPEAN JOURNAL OF BIOCHEMISTRY, (2002 Jan) 269 (1) 283-90.
Journal code: 0107600. ISSN: 0014-2956.
PUB. COUNTRY: Germany: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20020212
Last Updated on STN: 20020222
Entered Medline: 20020221

L8 ANSWER 13 OF 355 MEDLINE DUPLICATE 9
ACCESSION NUMBER: 2002261138 IN-PROCESS
DOCUMENT NUMBER: 21996090 PubMed ID: 12000644
TITLE: cDNA cloning of two different serine protease inhibitor precursors in the migratory locust, Locusta migratoria.
AUTHOR: Simonet G; Claeys I; Vanderperren H; November T; De Loof A;
Vanden Broeck J
CORPORATE SOURCE: Laboratory for Developmental Physiology and Molecular Biology, Zoological Institute, K.U.Leuven, Belgium.
SOURCE: INSECT MOLECULAR BIOLOGY, (2002 Jun) 11 (3) 249-56.
Journal code: 9303579. ISSN: 0962-1075.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020510
Last Updated on STN: 20020510

L8 ANSWER 14 OF 355 MEDLINE DUPLICATE 10
ACCESSION NUMBER: 2002050047 MEDLINE
DOCUMENT NUMBER: 21634684 PubMed ID: 11774267
TITLE: Identification and characterization of 9D7, a novel human protein overexpressed in renal cell carcinoma.
COMMENT: Erratum in: Int J Cancer 2002 Apr 20;98(6):956
AUTHOR: Klade Christoph S; Dohnal Alexander; Furst Walter; Sommergruber Wolfgang; Heider Karl-Heinz; Gharwan Helen; Ratschek Manfred; Adolf Gunther R
CORPORATE SOURCE: Boehringer Ingelheim Austria GmbH, Research and Development, Vienna, Austria.. cklade@intercell.co.at
SOURCE: INTERNATIONAL JOURNAL OF CANCER, (2002 Jan 10) 97 (2) 217-24.
Journal code: 0042124. ISSN: 0020-7136.
PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200201
ENTRY DATE: Entered STN: 20020125
Last Updated on STN: 20020502
Entered Medline: 20020117

L8 ANSWER 15 OF 355 MEDLINE
ACCESSION NUMBER: 2002279888 IN-PROCESS
DOCUMENT NUMBER: 22014945 PubMed ID: 12020895
TITLE: Expressed sequence tag (EST) analysis of a Schistosoma japonicum cercariae cDNA library.
AUTHOR: Fung Ming Chiu; Lau Man Tat; Chen Xiao Guang
CORPORATE SOURCE: Department of Biology, The Chinese University of Hong Kong,
SOURCE: N.T., Shatin, Hong Kong.
ACTA TROPICA, (2002 May) 82 (2) 215-24.
Journal code: 0370374. ISSN: 0001-706X.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020522
Last Updated on STN: 20020522

L8 ANSWER 16 OF 355 MEDLINE DUPLICATE 11
ACCESSION NUMBER: 2002176222 IN-PROCESS
DOCUMENT NUMBER: 21905346 PubMed ID: 11908663
TITLE: Novel genes are enriched in normalized cDNA libraries from drought-stressed seedlings of rice (Oryza sativa L. subsp. indica cv. Nagina 22).
AUTHOR: Reddy Arjula R; Ramakrishna W; Sekhar A Chandra; Ithal Nagabhushana; Babu P Ravindra; Bonaldo M F; Soares M B; Bennetzen Jeffrey L
CORPORATE SOURCE: Department of Plant Sciences, School of Life Sciences, University of Hyderabad, India.. arjuls1@uohyd.ernet.in
SOURCE: GENOME, (2002 Feb) 45 (1) 204-11.
Journal code: 8704544. ISSN: 0831-2796.
PUB. COUNTRY: Canada
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020324
Last Updated on STN: 20020324

L8 ANSWER 17 OF 355 MEDLINE DUPLICATE 12
ACCESSION NUMBER: 2002122628 MEDLINE
DOCUMENT NUMBER: 21678990 PubMed ID: 11820815
TITLE: Gene expression profiles in tadpole larvae of Ciona intestinalis.
AUTHOR: Kusakabe Takehiro; Yoshida Reiko; Kawakami Isao; Kusakabe Rie; Mochizuki Yasuaki; Yamada Lixy; Shin-i Tadasu; Kohara Yuji; Satoh Nori; Tsuda Motoyuki; Satou Yutaka
CORPORATE SOURCE: Department of Life Science, Himeji Institute of Technology,
3-2-1 Kouto, Hyogo, 678-1297, Japan.. tgk@sci.himeji-tech.ac.jp
SOURCE: DEVELOPMENTAL BIOLOGY, (2002 Feb 15) 242 (2) 188-203.
Journal code: 0372762. ISSN: 0012-1606.
PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200203
ENTRY DATE: Entered STN: 20020223
Last Updated on STN: 20020313
Entered Medline: 20020312

L8 ANSWER 18 OF 355 MEDLINE DUPLICATE 13
ACCESSION NUMBER: 2002127103 MEDLINE
DOCUMENT NUMBER: 21829509 PubMed ID: 11840564
TITLE: The characterisation of novel secreted Ly-6 proteins from
rat urine by the combined use of two-dimensional gel
electrophoresis, microbore high performance liquid
chromatography and expressed sequence tag data.
AUTHOR: Southan Christopher; Cutler Paul; Birrell Helen; Connell
John; Fantom Kenneth G M; Sims Matthew; Shaikh Narjis;
Schneider Klaus
CORPORATE SOURCE: Department of Bioinformatics, Glaxo SmithKline
Pharmaceuticals, Harlow, UK.. chris.southan@ogs.co.uk
SOURCE: Proteomics, (2002 Feb) 2 (2) 187-96.
Journal code: 101092707. ISSN: 1615-9853.
PUB. COUNTRY: Germany: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: SWISSPROT-P81827; SWISSPROT-P81828; SWISSPROT-Q9QXN2
ENTRY MONTH: 200205
ENTRY DATE: Entered STN: 20020227
Last Updated on STN: 20020522
Entered Medline: 20020520

L8 ANSWER 19 OF 355 MEDLINE
ACCESSION NUMBER: 2002271428 IN-PROCESS
DOCUMENT NUMBER: 22006440 PubMed ID: 12012232
TITLE: Gene expression profiles in young adult Ciona
intestinalis.
AUTHOR: Ogasawara Michio; Sasaki Akane; Metoki Hito; Shin-I
Tadasu; Kohara Yuji; Satoh Nori; Satou Yutaka
CORPORATE SOURCE: Department of Zoology, Graduate School of Science, Kyoto
University, Sakyo-ku, Kyoto 606-8502, Japan.
SOURCE: DEVELOPMENT GENES AND EVOLUTION, (2002 May) 212 (4)
173-85.
Journal code: 9613264. ISSN: 0949-944X.
PUB. COUNTRY: Germany: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020516
Last Updated on STN: 20020516

L8 ANSWER 20 OF 355 MEDLINE
ACCESSION NUMBER: 2002284645 IN-PROCESS
DOCUMENT NUMBER: 22022787 PubMed ID: 12027216
TITLE: Large-scale analysis of gene expression: methods and
application to the kidney.
AUTHOR: Cheval Lydie; Virlon Berangere; Billon Emmanuelle; Aude
Jean-Christophe; Elalouf Jean-Marc; Doucet Alain
CORPORATE SOURCE: CEA Saclay, Laboratoire de Biologie Integree des Cellules
Renales, Gif sur Yvette, France.
SOURCE: JOURNAL OF NEPHROLOGY, (2002 Mar-Apr) 15 Suppl 5 S170-83.

JOURNAL code: 9012268. ISSN: 1120-3625.
PUB. COUNTRY: Italy
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020528
Last Updated on STN: 20020528

L8 ANSWER 21 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:323202 BIOSIS
DOCUMENT NUMBER: PREV200200323202
TITLE: A human testis-specific homolog of the very long-chain
acyl-CoA synthetase "bubblegum" (lipidosin).
AUTHOR(S): Pei, Zhengtong (1); Watkins, Paul A. (1)
CORPORATE SOURCE: (1) Neurology, Kennedy Krieger Inst. and Johns Hopkins
Univ. Sch. Med., 707 N. Broadway, Baltimore, MD, 21205 USA
SOURCE: FASEB Journal, (March 20, 2002) Vol. 16, No. 4, pp. A158.
<http://www.fasebj.org/>. print.
Meeting Info.: Annual Meeting of the Professional Research
Scientists on Experimental Biology New Orleans, Louisiana,
USA April 20-24, 2002
ISSN: 0892-6638.
DOCUMENT TYPE: Conference
LANGUAGE: English

L8 ANSWER 22 OF 355 MEDLINE
ACCESSION NUMBER: 2002090551 IN-PROCESS
DOCUMENT NUMBER: 21676815 PubMed ID: 11818518
TITLE: A set of 1542 mouse blastocyst and pre-blastocyst genes
with well-matched human homologues.
AUTHOR: Stanton J L; Green D P L
CORPORATE SOURCE: Department of Anatomy and Structural Biology, University
of
Otago Medical School, P.O. Box 913, Dunedin, New Zealand.
SOURCE: MOLECULAR HUMAN REPRODUCTION, (2002 Feb) 8 (2) 149-66.
Journal code: 9513710. ISSN: 1360-9947.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020131
Last Updated on STN: 20020131

L8 ANSWER 23 OF 355 MEDLINE DUPLICATE 14
ACCESSION NUMBER: 2002193348 IN-PROCESS
DOCUMENT NUMBER: 21923213 PubMed ID: 11926267
TITLE: Identification of transcripts expressed under functional
differentiation in primary culture of cerebral cortical
neurons.
AUTHOR: Li Qiang; Li Zhi; Sun Chun-Xiao; Yu Albert Cheung-Hoi
CORPORATE SOURCE: Shanghai Brain Research Institute, Shanghai Research
Center
of Life Sciences, Chinese Academy of Sciences.
SOURCE: NEUROCHEMICAL RESEARCH, (2002 Feb) 27 (1-2) 147-54.
Journal code: 7613461. ISSN: 0364-3190.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020404
Last Updated on STN: 20020404

L8 ANSWER 24 OF 355 MEDLINE DUPLICATE 15

ACCESSION NUMBER: 2002204350 MEDLINE

DOCUMENT NUMBER: 21932900 PubMed ID: 11910074

TITLE: Functional annotation of a full-length Arabidopsis cDNA collection.

AUTHOR: Seki Motoaki; Narusaka Mari; Kamiya Asako; Ishida Junko; Satou Masakazu; Sakurai Tetsuya; Nakajima Maiko; Enju Akiko; Akiyama Kenji; Oono Youko; Muramatsu Masami; Hayashizaki Yoshihide; Kawai Jun; Carninci Piero; Itoh Masayoshi; Ishii Yoshiyuki; Arakawa Takahiro; Shibata Kazuhiro; Shinagawa Akira; Shinozaki Kazuo

CORPORATE SOURCE: Plant Mutation Exploration Team, Plant Functional Genomics Research Group, RIKEN Genomic Sciences Center (GSC), 3-1-1 Koyadai, Tsukuba 305-0074, Japan.

SOURCE: SCIENCE, (2002 Apr 5) 296 (5565) 141-5.
Journal code: 0404511. ISSN: 1095-9203.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200204

ENTRY DATE: Entered STN: 20020409
Last Updated on STN: 20020424
Entered Medline: 20020423

L8 ANSWER 25 OF 355 MEDLINE DUPLICATE 16

ACCESSION NUMBER: 2002141330 MEDLINE

DOCUMENT NUMBER: 21838665 PubMed ID: 11848675

TITLE: Comparative analysis of sequences expressed during the liquid-cultured mycelia and fruit body stages of *Pleurotus ostreatus*.

AUTHOR: Lee Seung-Ho; Kim Beom-Gi; Kim Kyung-Jin; Lee Jin-Sung; Yun Doh-Won; Hahn Jang-Ho; Kim Gyu-Hyun; Lee Kang-Hyo; Suh Dong-Sang; Kwon Suk-Tae; Lee Chang-Soo; Yoo Young-Bok

CORPORATE SOURCE: Applied Microbiology Division, Cytogenetics Division, National Institute of Agricultural Science and Technology, 249 Seodun-dong, Suwon, 441-707, South Korea.

SOURCE: FUNGAL GENETICS AND BIOLOGY, (2002 Mar) 35 (2) 115-34.
Journal code: 9607601. ISSN: 1087-1845.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200204

ENTRY DATE: Entered STN: 20020307
Last Updated on STN: 20020426
Entered Medline: 20020425

L8 ANSWER 26 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC. DUPLICATE 17

ACCESSION NUMBER: 2002:175188 BIOSIS

DOCUMENT NUMBER: PREV200200175188

TITLE: EST analysis in barley defines a unigene set comprising 4,000 genes.

AUTHOR(S): Michalek, W. (1); Weschke, W.; Pleissner, K.-P.; Graner, A.

CORPORATE SOURCE: (1) PLANTA GmbH, Grimsehlstr. 31, 37555, Einbeck: w.michalek@kws.de Germany

SOURCE: Theoretical and Applied Genetics, (January, 2002) Vol. 104,

No. 1, pp. 97-103.
<http://link.springer.de/link/service/journals/00122/.print>.
ISSN: 0040-5752.

DOCUMENT TYPE: Article
LANGUAGE: English

L8 ANSWER 27 OF 355 MEDLINE

ACCESSION NUMBER: 2002314679 IN-PROCESS
DOCUMENT NUMBER: 22051175 PubMed ID: 12056416
TITLE: Structural analysis of a *Lotus japonicus* genome. II. Sequence features and mapping of sixty-five TAC clones which cover the 6.5-mb regions of the genome.
AUTHOR: Nakamura Yasukazu; Kaneko Takakazu; Asamizu Erika; Kato Tomohiko; Sato Shusei; Tabata Satoshi
CORPORATE SOURCE: Kazusa DNA Research Institute, Kisarazu, Chiba, Japan.
SOURCE: DNA RESEARCH, (2002 Apr 30) 9 (2) 63-70.
Journal code: 9423827. ISSN: 1340-2838.
PUB. COUNTRY: Japan
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020612
Last Updated on STN: 20020612

L8 ANSWER 28 OF 355 MEDLINE

DUPLICATE 18

ACCESSION NUMBER: 2002148542 MEDLINE
DOCUMENT NUMBER: 21843467 PubMed ID: 11854097
TITLE: Expression profile of active genes in the human pituitary gland.
AUTHOR: Tanaka S; Tatsumi K; Okubo K; Itoh K; Kawamoto S; Matsubara K; Amino N
CORPORATE SOURCE: Department of Laboratory Medicine, Graduate School of Medicine, Osaka University, Osaka 565-0871, Japan.
SOURCE: JOURNAL OF MOLECULAR ENDOCRINOLOGY, (2002 Feb) 28 (1) 33-44.
Journal code: 8902617. ISSN: 0952-5041.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200204
ENTRY DATE: Entered STN: 20020308
Last Updated on STN: 20020413
Entered Medline: 20020412

L8 ANSWER 29 OF 355 MEDLINE

DUPLICATE 19

ACCESSION NUMBER: 2002104551 MEDLINE
DOCUMENT NUMBER: 21686149 PubMed ID: 11827452
TITLE: Gene expression profile of human bone marrow stromal cells: high-throughput expressed sequence tag sequencing analysis.
AUTHOR: Jia Libin; Young Marian F; Powell John; Yang Liming; Ho Nicola C; Hotchkiss Robert; Robey Pamela Gehron; Francomano Clair A
CORPORATE SOURCE: Medical Genetics Branch, National Human Genome Research Institute, National Institutes of Health, Bethesda, MD 20892, USA.

SOURCE: GENOMICS, (2002 Jan) 79 (1) 7-17.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200205
ENTRY DATE: Entered STN: 20020212
Last Updated on STN: 20020522
Entered Medline: 20020520

L8 ANSWER 30 OF 355 MEDLINE DUPLICATE 20
ACCESSION NUMBER: 2002258011 IN-PROCESS
DOCUMENT NUMBER: 21993152 PubMed ID: 11997173
TITLE: Reexamining the polyadenylation signal: were we wrong
about

AAUAAA?.
AUTHOR: MacDonald Clinton C; Redondo Jose Luis
CORPORATE SOURCE: Department of Cell Biology & Biochemistry and Southwest
Cancer Center at University Medical Center, Texas Tech
University Health Sciences Center, 3601 4th Street, 79430,
Lubbock, TX, USA.
SOURCE: MOLECULAR AND CELLULAR ENDOCRINOLOGY, (2002 Apr 25) 190
(1-2) 1-8.
Journal code: 7500844. ISSN: 0303-7207.
PUB. COUNTRY: Ireland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020509
Last Updated on STN: 20020509

L8 ANSWER 31 OF 355 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI
ACCESSION NUMBER: 2002-04744 BIOTECHDS
TITLE: Novel nuclear receptor, retinaX receptor polypeptide, useful
for identifying modulators of the receptor which are used
for
treating diabetes, obesity, age-related macular
degeneration,
gout, conjunctivitis;
vector-mediated gene transfer and expression in host
cell,
expressed sequence tag, antibody, cDNA library for
diagnosis and gene therapy
AUTHOR: Moore J T
PATENT ASSIGNEE: Glaxo
LOCATION: Greenford, UK.
PATENT INFO: WO 2001083556 8 Nov 2001
APPLICATION INFO: WO 2001-US14601 4 May 2001
PRIORITY INFO: US 2000-201874 4 May 2000
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2002-049337 [06]

L8 ANSWER 32 OF 355 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI
ACCESSION NUMBER: 2002-02445 BIOTECHDS
TITLE: New polypeptides and nucleic acids, useful for diagnosis,
treatment of inflammatory, autoimmune, neurological, myeloid
or lymphoid cell, bone degenerative disorders, cancer and
promoting wound healing;
vector-mediated gene transfer and expression in host
cell,

array, hybridoma cell culture for antibody production, DNA
protein array and expressed sequence tag for gene therapy
AUTHOR: Tang Y T; Asundi V; Zhou P; Xue A J; Ren F; Zhang J; Wang J
R; Xi C; Yang Y; Zaho Q A; Chen R H; Wang D; Goodrich R W;
Liu C; Drmanac R T
PATENT ASSIGNEE: Hyseq
LOCATION: Sunnyvale, CA, USA.
PATENT INFO: WO 2001075093 11 Oct 2001
APPLICATION INFO: WO 2001-US10484 30 Mar 2001
PRIORITY INFO: US 2001-728711 14 Mar 2001; US 2000-540217 31 Mar 2000
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2001-626432 [72]

L8 ANSWER 33 OF 355 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI
ACCESSION NUMBER: 2002-01640 BIOTECHDS
TITLE: Novel polypeptides and nucleic acids obtained from cDNA
libraries from various human tissues, for diagnosis,
treatment of cancer, neurological, inflammatory disorders

and
for use in arrays for detection;
vector-mediated gene transfer and expression in host
cell,

antisense, DNA probe, DNA primer, antibody and DNA array
for disease, disorder diagnosis and gene therapy
AUTHOR: Tang Y T; Liu C; Zhou P; Asundi V; Zhang J; Zhao Q A; Ren F;
Xue A J; Yang Y; Wehrman T; Wang J R; Ma Y; Wang D; Chen R
H;

Xu C; Drmanac R
PATENT ASSIGNEE: Hyseq
LOCATION: Sunnyvale, CA, USA.
PATENT INFO: WO 2001064834 7 Sep 2001
APPLICATION INFO: WO 2001-US4926 26 Feb 2001
PRIORITY INFO: US 2000-664641 19 Sep 2000; US 2000-515126 28 Feb 2000
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2001-589862 [66]

L8 ANSWER 34 OF 355 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI
ACCESSION NUMBER: 2002-02306 BIOTECHDS
TITLE: New oligonucleotide of transcription factor specific for
central serotonergic neurons, useful in screening methods
for

identifying and testing agonists and antagonists of
serotonergic activity, comprises DNA sequence from Rattus
norvegicus;
vector-mediated expression, database comparison,
polymerase chain reaction and DNA primer for drug
screening

AUTHOR: Deneris E S; Fyodorov D V; Hendricks T J
PATENT ASSIGNEE: Univ.Case-Western-Reserve
LOCATION: Cleveland, OH, USA.
PATENT INFO: US 6268216 31 Jul 2001
APPLICATION INFO: US 1999-360779 26 Jul 1999
PRIORITY INFO: US 1999-360779 26 Jul 1999
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 2001-610396 [70]

ACCESSION NUMBER: 2002147096 MEDLINE
 DOCUMENT NUMBER: 21396555 PubMed ID: 11493695
 TITLE: Exploring the transcriptome of the malaria sporozoite stage.
 AUTHOR: Kappe S H; Gardner M J; Brown S M; Ross J; Matuschewski K; Ribeiro J M; Adams J H; Quackenbush J; Cho J; Carucci D J; Hoffman S L; Nussenzweig V
 CORPORATE SOURCE: Michael Heidelberger Division, Department of Pathology, Kaplan Cancer Center, New York University School of Medicine, New York, NY 10016, USA..
 SOURCE: kappes01@popmail.med.nyu.edu
 PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (2001 Aug 14) 98 (17) 9895-900.

PUB. COUNTRY: Journal code: 7505876. ISSN: 0027-8424.
 United States

LANGUAGE: Journal; Article; (JOURNAL ARTICLE)

FILE SEGMENT: English

OTHER SOURCE: Priority Journals

GENBANK-AF390551; GENBANK-AF390552; GENBANK-AF390553;
 GENBANK-BG601070; GENBANK-BG601071; GENBANK-BG601072;
 GENBANK-BG601073; GENBANK-BG601074; GENBANK-BG601075;
 GENBANK-BG601076; GENBANK-BG601077; GENBANK-BG601078;
 GENBANK-BG601079; GENBANK-BG601080; GENBANK-BG601081;
 GENBANK-BG601082; GENBANK-BG601083; GENBANK-BG601084;
 GENBANK-BG601085; GENBANK-BG601086; GENBANK-BG601087;
 GENBANK-BG601088; GENBANK-BG601089; GENBANK-BG601090;
 GENBANK-BG601091; GENBANK-BG601092; GENBANK-BG601093;
 GENBANK-BG601094; GENBANK-BG601095; GENBANK-BG601096;
 GENBANK-BG601097; GENBANK-BG601098; GENBANK-BG601099;
 GENBANK-BG601100; GENBANK-BG601101; GENBANK-BG601102;
 GENBANK-BG601103; GENBANK-BG601104; GENBANK-BG601105;
 GENBANK-BG601106; GENBANK-BG601107; GENBANK-BG601108;
 GENBANK-BG601109; GENBANK-BG601110; GENBANK-BG601111;
 GENBANK-BG601112; GENBANK-BG601113; GENBANK-BG601114;
 GENBANK-BG601115; GENBANK-BG601116; GENBANK-BG601117;
 GENBANK-BG601118; GENBANK-BG601119; GENBANK-BG601120;
 GENBANK-BG601121; GENBANK-BG601122; GENBANK-BG601123;
 GENBANK-BG601124; GENBANK-BG601125; GENBANK-BG601126;
 GENBANK-BG601127; GENBANK-BG601128; GENBANK-BG601129;
 GENBANK-BG601130; GENBANK-BG601131; GENBANK-BG601132;
 GENBANK-BG601133; GENBANK-BG601134; GENBANK-BG601135;
 GENBANK-BG601136; GENBANK-BG601137; GENBANK-BG601138;
 GENBANK-BG601139; GENBANK-BG601140; GENBANK-BG601141;
 GENBANK-BG601142; GENBANK-BG601143; GENBANK-BG601144;
 GENBANK-BG601145; GENBANK-BG601146; GENBANK-BG601147;
 GENBANK-BG601148; GENBANK-BG601149; GENBANK-BG601150;
 GENBANK-BG601151; GENBANK-BG601152; GENBANK-BG601153;
 GENBANK-BG601154; GENBANK-BG601155; GENBANK-BG601156;
 GENBANK-BG601157; GENBANK-BG601158; GENBANK-BG601159;
 GENBANK-BG601160; GENBANK-BG601161; GENBANK-BG601162;
 GENBANK-BG601163; GENBANK-BG601164; GENBANK-BG601165;
 GENBANK-BG601166; GENBANK-BG601167; GENBANK-BG601168;
 GENBANK-BG601169; GENBANK-BG601170; GENBANK-BG601171;
 GENBANK-BG601172; GENBANK-BG601173; GENBANK-BG601174;
 GENBANK-BG601175; GENBANK-BG601176; GENBANK-BG601177;
 GENBANK-BG601178; GENBANK-BG601179; GENBANK-BG601180;
 GENBANK-BG601181; GENBANK-BG601182; GENBANK-BG601183;
 GENBANK-BG601184; GENBANK-BG601185; GENBANK-BG601186;
 GENBANK-BG601187; GENBANK-BG601188; GENBANK-BG601189;
 GENBANK-BG601190; GENBANK-BG601191; GENBANK-BG601192;

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

GENBANK-BG602108; GENBANK-BG602109; GENBANK-BG602110;
 GENBANK-BG602111; GENBANK-BG602112; GENBANK-BG602113;
 GENBANK-BG602114; GENBANK-BG602115; GENBANK-BG602116;
 GENBANK-BG602117; GENBANK-BG602118; GENBANK-BG602119;
 GENBANK-BG602120; GENBANK-BG602121; GENBANK-BG602122;
 GENBANK-BG602123; GENBANK-BG602124; GENBANK-BG602125;
 GENBANK-BG602126; GENBANK-BG602127; GENBANK-BG602128;
 GENBANK-BG602129; GENBANK-BG602130; GENBANK-BG602131;
 GENBANK-BG602132; GENBANK-BG602133; GENBANK-BG602134;
 GENBANK-BG602135; GENBANK-BG602136; GENBANK-BG602137;
 GENBANK-BG602138; GENBANK-BG602139; GENBANK-BG602140;
 GENBANK-BG602141; GENBANK-BG602142; GENBANK-BG602143;
 GENBANK-BG602144; GENBANK-BG602145; GENBANK-BG602146;
 GENBANK-BG602147; GENBANK-BG602148; GENBANK-BG602149;
 GENBANK-BG602150; GENBANK-BG602151; GENBANK-BG602152

ENTRY MONTH:

200109

ENTRY DATE:

Entered STN: 20020308

Last Updated on STN: 20020308

Entered Medline: 20010920

L8 ANSWER 36 OF 355

MEDLINE

DUPLICATE 22

ACCESSION NUMBER: 2001352750 MEDLINE

DOCUMENT NUMBER: 21310014 PubMed ID: 11416224

TITLE: Identification of urocortin III, an additional member of the corticotropin-releasing factor (CRF) family with high affinity for the CRF2 receptor.

AUTHOR: Lewis K; Li C; Perrin M H; Blount A; Kunitake K; Donaldson C; Vaughan J; Reyes T M; Gulyas J; Fischer W; Bilezikjian L; Rivier J; Sawchenko P E; Vale W W

CORPORATE SOURCE: Clayton Foundation Laboratories for Peptide Biology and Laboratory of Neuronal Structure and Function, Salk Institute for Biological Studies, La Jolla, CA 92037,

USA.

CONTRACT NUMBER:

DK-26741 (NIDDK)

SOURCE:

PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (2001 Jun 19) 98 (13) 7570-5. Journal code: 7505876. ISSN: 0027-8424.

PUB. COUNTRY:

United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

OTHER SOURCE:

GENBANK-AF361943; GENBANK-AF361944

ENTRY MONTH:

200107

ENTRY DATE:

Entered STN: 20010730

Last Updated on STN: 20010730

Entered Medline: 20010726

L8 ANSWER 37 OF 355

MEDLINE

DUPLICATE 23

ACCESSION NUMBER: 2001676947 MEDLINE

DOCUMENT NUMBER: 21579733 PubMed ID: 11722583

TITLE: The interferon alpha induced protein ISG12 is localized to the nuclear membrane.

AUTHOR: Martensen P M; Sogaard T M; Gjermansen I M; Buttenschon H N; Rossing A B; Bonnevie-Nielsen V; Rosada C; Simonsen J

L;

Justesen J

CORPORATE SOURCE: University

Department of. Molecular and Structural Biology,

of Aarhus, Aarhus, Denmark.. pips@biobase.dk

SOURCE:

EUROPEAN JOURNAL OF BIOCHEMISTRY, (2001 Nov) 268 (22) 5947-54.

Journal code: 0107600. ISSN: 0014-2956.
 PUB. COUNTRY: Germany; Germany, Federal Republic of
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200112
 ENTRY DATE: Entered STN: 20011128
 Last Updated on STN: 20020124
 Entered Medline: 20011231

L8 ANSWER 38 OF 355 MEDLINE DUPLICATE 24
 ACCESSION NUMBER: 2002090100 MEDLINE
 DOCUMENT NUMBER: 21671825 PubMed ID: 11812828
 TITLE: Gene expression in the developing mouse retina by EST
 sequencing and microarray analysis.
 AUTHOR: Mu X; Zhao S; Pershad R; Hsieh T F; Scarpa A; Wang S W;
 White R A; Beremand P D; Thomas T L; Gan L; Klein W H
 CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, The
 University of Texas M. D. Anderson Cancer Center, Houston,
 TX 77030, USA.
 CONTRACT NUMBER: CA16672 (NCI)
 EY11930 (NEI)
 EY13523 (NEI)
 SOURCE: NUCLEIC ACIDS RESEARCH, (2001 Dec 15) 29 (24) 4983-93.
 Journal code: 0411011. ISSN: 1362-4962.
 PUB. COUNTRY: England; United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200204
 ENTRY DATE: Entered STN: 20020131
 Last Updated on STN: 20020420
 Entered Medline: 20020419

L8 ANSWER 39 OF 355 MEDLINE DUPLICATE 25
 ACCESSION NUMBER: 2001213322 MEDLINE
 DOCUMENT NUMBER: 21103328 PubMed ID: 11160356
 TITLE: Isolation of a new melanoma antigen, MART-2, containing a
 mutated epitope recognized by autologous
 tumor-infiltrating
 T lymphocytes.
 AUTHOR: Kawakami Y; Wang X; Shofuda T; Sumimoto H; Tupesis J;
 Fitzgerald E; Rosenberg S
 CORPORATE SOURCE: Division of Cellular Signaling, Institute for Advanced
 Medical Research, Keio University School of Medicine,
 Tokyo, Japan.. yutakawa@med.keio.ac.jp
 SOURCE: JOURNAL OF IMMUNOLOGY, (2001 Feb 15) 166 (4) 2871-7.
 Journal code: 2985117R. ISSN: 0022-1767.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
 ENTRY MONTH: 200104
 ENTRY DATE: Entered STN: 20010425
 Last Updated on STN: 20010425
 Entered Medline: 20010419

L8 ANSWER 40 OF 355 MEDLINE DUPLICATE 26
 ACCESSION NUMBER: 2002036073 MEDLINE
 DOCUMENT NUMBER: 21604065 PubMed ID: 11763134
 TITLE: Analysis of genes expressed during rice-Magnaporthe grisea

interactions.
 AUTHOR: Kim S; Ahn I P; Lee Y H
 CORPORATE SOURCE: School of Agricultural Biotechnology and Research Center
 for New Bio-Materials in Agriculture, Seoul National
 University, Suwon, Korea.
 SOURCE: MOLECULAR PLANT-MICROBE INTERACTIONS, (2001 Nov) 14 (11)
 1340-6.
 Journal code: 9107902. ISSN: 0894-0282.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200206
 ENTRY DATE: Entered STN: 20020124
 Last Updated on STN: 20020604
 Entered Medline: 20020603

L8 ANSWER 41 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 2001:547066 BIOSIS
 DOCUMENT NUMBER: PREV200100547066
 TITLE: Functional characterization of gene expression profiles in
 an animal model of Batten's disease.
 AUTHOR(S): Brooks, A. I. (1); Chattopadhyay, S.; Curran, T. M.;
 Consaul, S. E.; Pearce, D. A. (1)
 CORPORATE SOURCE: (1) Functional Genomics Center, Univ Rochester Medical
 Center, Rochester, NY USA
 SOURCE: Society for Neuroscience Abstracts, (2001) Vol. 27, No. 1,
 pp. 1206. print.
 Meeting Info.: 31st Annual Meeting of the Society for
 Neuroscience San Diego, California, USA November 10-15,
 2001
 ISSN: 0190-5295.
 DOCUMENT TYPE: Conference
 LANGUAGE: English
 SUMMARY LANGUAGE: English

L8 ANSWER 42 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 2002:98066 BIOSIS
 DOCUMENT NUMBER: PREV200200098066
 TITLE: Temporal and spatial expression analyses of TrEnod40,
 TrEnod5 and a novel early nodulin in white clover roots
 and
 nodules.
 AUTHOR(S): Crockard, Martin A. (1); Bjourson, Anthony J.; Pulvirenti,
 Maria Gabriella; Cooper, James E.
 CORPORATE SOURCE: (1) Applied Plant Science Division, Department of
 Agriculture and Rural Development (NI), Newforge Lane,
 Belfast, BT9 5PX: martin.crockard@dardni.gov.uk UK
 SOURCE: Plant Science (Shannon), (November, 2001) Vol. 161, No. 6,
 pp. 1161-1170. print.
 ISSN: 0168-9452.
 DOCUMENT TYPE: Article
 LANGUAGE: English

L8 ANSWER 43 OF 355 MEDLINE DUPLICATE 27
 ACCESSION NUMBER: 2001648583 MEDLINE
 DOCUMENT NUMBER: 21557683 PubMed ID: 11700951
 TITLE: Cloning and identification of differentially expressed
 transcripts in primary culture of GABAergic neurons.
 AUTHOR: Li Z; Li Q; Sun C X; Hertz L; Yu A C
 CORPORATE SOURCE: Brain Research Institute, Shanghai Research Center of Life

SOURCE: Sciences, Chinese Academy of Sciences.
NEUROCHEMICAL RESEARCH, (2001 Oct) 26 (10) 1101-5.
Journal code: 7613461. ISSN: 0364-3190.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200205
ENTRY DATE: Entered STN: 20011112
Last Updated on STN: 20020503
Entered Medline: 20020502

L8 ANSWER 44 OF 355 MEDLINE DUPLICATE 28
ACCESSION NUMBER: 2001301641 MEDLINE
DOCUMENT NUMBER: 21141967 PubMed ID: 11207211
TITLE: Identification, cloning, and initial characterization of a
novel mouse testicular germ cell-specific antigen.
AUTHOR: Kurita A; Takizawa T; Takayama T; Totsukawa K; Matsubara
S;
Shibahara H; Orgebin-Crist M C; Sendo F; Shinkai Y; Araki
Y
CORPORATE SOURCE: Department of Immunology & Parasitology, Yamagata
University School of Medicine, Yamagata 990-9585, Japan.
SOURCE: BIOLOGY OF REPRODUCTION, (2001 Mar) 64 (3) 935-45.
Journal code: 0207224. ISSN: 0006-3363.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB022914
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010604
Last Updated on STN: 20010604
Entered Medline: 20010531

L8 ANSWER 45 OF 355 MEDLINE DUPLICATE 29
ACCESSION NUMBER: 2001566832 MEDLINE
DOCUMENT NUMBER: 21526457 PubMed ID: 11673235
TITLE: DIANA-EST: a statistical analysis.
AUTHOR: Hatzigeorgiou A G; Fiziev P; Reczko M
CORPORATE SOURCE: Metagen GmbH, Ihnestr.63, 14195 Berlin, Germany..
artemis@pcbi.upenn.edu
SOURCE: BIOINFORMATICS, (2001 Oct) 17 (10) 913-9.
Journal code: 9808944. ISSN: 1367-4803.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20011024
Last Updated on STN: 20020209
Entered Medline: 20020208

L8 ANSWER 46 OF 355 MEDLINE DUPLICATE 30
ACCESSION NUMBER: 2001485446 MEDLINE
DOCUMENT NUMBER: 21418781 PubMed ID: 11527381
TITLE: Analysis of the mammalian talin2 gene TLN2.
AUTHOR: Monkley S J; Pritchard C A; Critchley D R
CORPORATE SOURCE: Department of Biochemistry, University of Leicester,
University Road, Leicester, LE1 7RH, United Kingdom.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2001

Sep 7) 286 (5) 880-5.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200110
ENTRY DATE: Entered STN: 20010903
Last Updated on STN: 20011015
Entered Medline: 20011011

L8 ANSWER 47 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:245085 BIOSIS
DOCUMENT NUMBER: PREV200100245085
TITLE: Identification and characterisation of ACEH, a human
homolog of angiotensin-converting enzyme.
AUTHOR(S): Tipnis, Sarah R. (1); Hooper, Nigel M. (1); Christie,
Gary;
Turner, Anthony J. (1)
CORPORATE SOURCE: (1) School of Biochemistry and Molecular Biology,
University of Leeds, Leeds, West Yorkshire, LS2 9JT UK
SOURCE: FASEB Journal, (March 8, 2001) Vol. 15, No. 5, pp. A875.
print.
Meeting Info.: Annual Meeting of the Federation of
American
Societies for Experimental Biology on Experimental Biology
2001 Orlando, Florida, USA March 31-April 04, 2001
ISSN: 0892-6638.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L8 ANSWER 48 OF 355 MEDLINE
ACCESSION NUMBER: 2001209051 MEDLINE
DOCUMENT NUMBER: 21193750 PubMed ID: 11300479
TITLE: Genetic approach to insight into the immunobiology of
human
dendritic cells and identification of CD84-H1, a novel
CD84
homologue.
AUTHOR: Zhang W; Wan T; Li N; Yuan Z; He L; Zhu X; Yu M; Cao X
CORPORATE SOURCE: Department of Immunology, Second Military Medical
University, Shanghai, People's Republic of China.
SOURCE: CLINICAL CANCER RESEARCH, (2001 Mar) 7 (3 Suppl)
822s-829s.
Journal code: 9502500. ISSN: 1078-0432.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010827
Last Updated on STN: 20010827
Entered Medline: 20010823

L8 ANSWER 49 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:492683 BIOSIS
DOCUMENT NUMBER: PREV200100492683
TITLE: Cloning of a novel mouse Gabarapl2 cDNA and its
characterization.
AUTHOR(S): Chen, Zheng (1); Xin, Yu-Rong; Jiang, Ying; Jiang,
Ju-Xiang

CORPORATE SOURCE: (1) School of Life Science, Suzhou University, Suzhou,
215006: zhengchen_99@yahoo.com, xinyu@umdnj.edu China
SOURCE: Acta Pharmacologica Sinica, (August, 2001) Vol. 22, No. 8,
pp. 751-755. print.
ISSN: 0253-9756.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: Chinese; English

L8 ANSWER 50 OF 355 MEDLINE DUPLICATE 31
ACCESSION NUMBER: 2001221832 MEDLINE
DOCUMENT NUMBER: 21210945 PubMed ID: 11311134
TITLE: Cloning, expression and localization of human BM88 shows
that it maps to chromosome 11p15.5, a region implicated in
Beckwith-Wiedemann syndrome and tumorigenesis.
AUTHOR: Gaitanou M; Buanne P; Pappa C; Georgopoulou N; Mamalaki A;
Tirone F; Matsas R
CORPORATE SOURCE: Department of Biochemistry, Hellenic Pasteur Institute,
127
Vassilissis Sofias Avenue, 115 21 Athens, Greece.
SOURCE: BIOCHEMICAL JOURNAL, (2001 May 1) 355 (Pt 3) 715-24.
Journal code: 2984726R. ISSN: 0264-6021.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF235030; GENBANK-AF243130
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010604
Last Updated on STN: 20010604
Entered Medline: 20010531

L8 ANSWER 51 OF 355 MEDLINE DUPLICATE 32
ACCESSION NUMBER: 2001261706 MEDLINE
DOCUMENT NUMBER: 21201248 PubMed ID: 11304808
TITLE: Identification of genes differentially expressed in benign
prostatic hyperplasia.
AUTHOR: DiLella A G; Toner T J; Austin C P; Connolly B M
CORPORATE SOURCE: Departments of Pharmacology, Merck Research Laboratories,
P.O. Box 4, West Point, PA 19486.. tony_dilella@merck.com
SOURCE: JOURNAL OF HISTOCHEMISTRY AND CYTOCHEMISTRY, (2001 May) 49
(5) 669-70.
Journal code: 9815334. ISSN: 0022-1554.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010521
Last Updated on STN: 20010521
Entered Medline: 20010517

L8 ANSWER 52 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:492398 BIOSIS
DOCUMENT NUMBER: PREV200100492398
TITLE: Identification of genes induced after peripheral nerve
injury: Expression profiling and novel gene discovery.
AUTHOR(S): Araki, T. (1); Nagarajan, R. (1); Milbrandt, J. (1)
CORPORATE SOURCE: (1) Dept Pathol, Washington Univ Sch Med, Saint Louis, MO
USA
SOURCE: Society for Neuroscience Abstracts, (2001) Vol. 27, No. 1,

pp. 667. print.
Meeting Info.: 31st Annual Meeting of the Society for
Neuroscience San Diego, California, USA November 10-15,
2001
ISSN: 0190-5295.

DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L8 ANSWER 53 OF 355 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI
ACCESSION NUMBER: 2001-12435 BIOTECHDS
TITLE: Polymorphism of human alpha class glutathione-transferases;
plasmid-mediated glutathione-transferase gene transfer,
expression in Escherichia coli, DNA primer, polymerase
chain reaction and restriction fragment length
polymorphism for pharmacogenetics
AUTHOR: Tetlow N; Liu D; *Board P
CORPORATE SOURCE: Univ.Australian-Nat.
LOCATION: Division of Molecular Medicine, John Curtin School of
Medical
Research, P.O. Box 334, Canberra, Australian Capital
Territory 2601, Australia.
Email: philip.board@anu.edu.au
SOURCE: Pharmacogenetics; (2001) 11, 7, 609-17
CODEN: PHMCE
ISSN: 0960-314X
DOCUMENT TYPE: Journal
LANGUAGE: English

L8 ANSWER 54 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:526231 BIOSIS
DOCUMENT NUMBER: PREV200100526231
TITLE: Random sequencing of cDNAs and identification of mRNAs.
AUTHOR(S): Anderson, James V. (1); Horvath, David P.
CORPORATE SOURCE: (1) Biosciences Research Laboratory, Plant Science
Research, U.S. Department of Agriculture, Agricultural
Research Service, 1605 Albrecht Boulevard, Fargo, ND,
58105: andersjv@fargo.ars.usda.gov USA
SOURCE: Weed Science, (September October, 2001) Vol. 49, No. 5,
pp.
590-597. print.
ISSN: 0043-1745.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

L8 ANSWER 55 OF 355 MEDLINE DUPLICATE 33
ACCESSION NUMBER: 2001653629 MEDLINE
DOCUMENT NUMBER: 21560218 PubMed ID: 11703281
TITLE: Keratin K6irs is specific to the inner root sheath of hair
follicles in mice and humans.
AUTHOR: Porter R M; Corden L D; Lunny D P; Smith F J; Lane E B;
McLean W H
CORPORATE SOURCE: CRC Cell Structure Research Group, School of Life
Sciences,
University of Dundee, Dundee DD1 4HN, UK.
SOURCE: BRITISH JOURNAL OF DERMATOLOGY, (2001 Oct) 145 (4) 558-68.
Journal code: 0004041. ISSN: 0007-0963.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English

FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AA354256
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20011115
Last Updated on STN: 20020123
Entered Medline: 20011210

L8 ANSWER 56 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2002:199005 BIOSIS

DOCUMENT NUMBER: PREV200200199005

TITLE: The transcriptome of bone marrow cells in chronic leukemias.

AUTHOR(S): Silva, Wilson A., Jr. (1); Alberto, Fernando L.; Uliana, Ronie M. (1); Simpson, Andrew J.; Costa, Fernando F.;

Zago,

Marco A. (1)

CORPORATE SOURCE: (1) Center for Cell Therapy, Regional Blood Center, Ribeirao Preto Brazil

SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 1, pp. 550a-551a. <http://www.bloodjournal.org/>. print.
Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 1 Orlando, Florida, USA December

07-11,

2001

ISSN: 0006-4971.

DOCUMENT TYPE: Conference

LANGUAGE: English

L8 ANSWER 57 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:290301 BIOSIS

DOCUMENT NUMBER: PREV200100290301

TITLE: Characterization of gene transcripts expressed in the individual identified neuron.

AUTHOR(S): Sadreyev, Ruslan I. (1); Meleshkevich, Ella A. (1); Matz, Mikhail V. (1); Moroz, Leonid L. (1)

CORPORATE SOURCE: (1) University of Florida, 9505 Ocean Shore Blvd, St Augustine, FL, 32080 USA

SOURCE: FASEB Journal, (March 7, 2001) Vol. 15, No. 4, pp. A541. print.

Meeting Info.: Annual Meeting of the Federation of

American

Societies for Experimental Biology on Experimental Biology 2001 Orlando, Florida, USA March 31-April 04, 2001

ISSN: 0892-6638.

DOCUMENT TYPE: Conference

LANGUAGE: English

SUMMARY LANGUAGE: English

L8 ANSWER 58 OF 355 MEDLINE

DUPLICATE 34

ACCESSION NUMBER: 2002054749 MEDLINE

DOCUMENT NUMBER: 21639644 PubMed ID: 11780420

TITLE: Molecular cloning and characterization of NAG-7: a novel gene downregulated in human nasopharyngeal carcinoma.

AUTHOR: Xie Y; Bin L; Yang J; Li Z; Yu Y; Zhang X; Cao L; Li G

CORPORATE SOURCE: Laboratory of Cellular/Molecular Genetics, Cancer Research Institute, Hunan Medical University, Changsha 410078, China.

SOURCE: CHINESE MEDICAL JOURNAL, (2001 May) 114 (5) 530-4.

Journal code: 7513795. ISSN: 0366-6999.

PUB. COUNTRY: China

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20020125
Last Updated on STN: 20020222
Entered Medline: 20020221

L8 ANSWER 59 OF 355 MEDLINE
ACCESSION NUMBER: 2001312137 MEDLINE
DOCUMENT NUMBER: 21278998 PubMed ID: 11385108
TITLE: A set of 840 mouse oocyte genes with well-matched human homologues.
AUTHOR: Stanton J L; Green D P
CORPORATE SOURCE: Department of Anatomy and Structural Biology, University of Otago, Medical School, P.O.Box 913, Dunedin, New Zealand.
SOURCE: MOLECULAR HUMAN REPRODUCTION, (2001 Jun) 7 (6) 521-43.
Journal code: 9513710. ISSN: 1360-9947.
PUB. COUNTRY: England; United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010903
Last Updated on STN: 20010903
Entered Medline: 20010830

L8 ANSWER 60 OF 355 MEDLINE DUPLICATE 35
ACCESSION NUMBER: 2001543308 MEDLINE
DOCUMENT NUMBER: 21475973 PubMed ID: 11591886
TITLE: MRP8, a new member of ABC transporter superfamily, identified by EST database mining and gene prediction program, is highly expressed in breast cancer.
AUTHOR: Bera T K; Lee S; Salvatore G; Lee B; Pastan I
CORPORATE SOURCE: Laboratory of Molecular Biology, Division of Basic Sciences, National Cancer Institute, National Institutes of Health, Bethesda, Maryland 20892-4255, USA.
SOURCE: MOLECULAR MEDICINE, (2001 Aug) 7 (8) 509-16.
Journal code: 9501023. ISSN: 1076-1551.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20011010
Last Updated on STN: 20020215
Entered Medline: 20020214

L8 ANSWER 61 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:181371 BIOSIS
DOCUMENT NUMBER: PREV200200181371
TITLE: Expressed sequence tags from cold-acclimatized barley can identify novel plant genes.
AUTHOR(S): Faccioli, P. (1); Pecchioni, N. (1); Cattivelli, L. (1); Stanca, A. M. (1); Terzi, V. (1)
CORPORATE SOURCE: (1) Sezione di Fiorenzuola d'Arda, Istituto Sperimentale per la Cerealicoltura, Via S. Protaso, 302, I-29017, Fiorenzuola d'Arda: p.faccioli@iol.it Italy
SOURCE: Plant Breeding, (December, 2001) Vol. 120, No. 6, pp. 497-502. print.
ISSN: 0179-9541.

DOCUMENT TYPE: Article
LANGUAGE: English

L8 ANSWER 62 OF 355 MEDLINE DUPLICATE 36
ACCESSION NUMBER: 2001528350 MEDLINE
DOCUMENT NUMBER: 21458702 PubMed ID: 11574066
TITLE: A novel human metalloprotease synthesized in the liver and secreted into the blood: possibly, the von Willebrand factor-cleaving protease?.
COMMENT: Erratum in: J Biochem (Tokyo) 2001 Nov;130(5):719
AUTHOR: Soejima K; Mimura N; Hirashima M; Maeda H; Hamamoto T; Nakagaki T; Nozaki C
CORPORATE SOURCE: First Research Departmen, The Chemo-Sero-Therapeutic Research Institute, Kumamoto 869-1298, Japan.. soejima@kaketsuken.or.jp
SOURCE: JOURNAL OF BIOCHEMISTRY, (2001 Oct) 130 (4) 475-80. Journal code: 0376600. ISSN: 0021-924X.
PUB. COUNTRY: Japan
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB069698
ENTRY MONTH: 200201
ENTRY DATE: Entered STN: 20011001
Last Updated on STN: 20020226
Entered Medline: 20020130

L8 ANSWER 63 OF 355 MEDLINE DUPLICATE 37
ACCESSION NUMBER: 2001448437 MEDLINE
DOCUMENT NUMBER: 21227151 PubMed ID: 11329013
TITLE: Creation of genome-wide protein expression libraries using random activation of gene expression.
AUTHOR: Harrington J J; Sherf B; Rundlett S; Jackson P D; Perry R; Cain S; Leventhal C; Thornton M; Ramachandran R; Whittington J; Lerner L; Costanzo D; McElligott K; Boozer S; Mays R; Smith E; Veloso N; Klika A; Hess J; Cothren K; Lo K; Offenbacher J; Danzig J; Ducar M
CORPORATE SOURCE: Athersys, Inc., 3201 Carnegie Ave., Cleveland, OH 44115, USA.. jharrington@athersys.com
SOURCE: NATURE BIOTECHNOLOGY, (2001 May) 19 (5) 440-5. Journal code: 9604648. ISSN: 1087-0156.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010813
Last Updated on STN: 20010813
Entered Medline: 20010809

L8 ANSWER 64 OF 355 MEDLINE DUPLICATE 38
ACCESSION NUMBER: 2001155138 MEDLINE
DOCUMENT NUMBER: 21092618 PubMed ID: 11162530
TITLE: Molecular cloning of a novel human gene on chromosome 4p11 by immunoscreening of an ovarian carcinoma cDNA library.
AUTHOR: Luo L Y; Soosaipillai A; Diamandis E P
CORPORATE SOURCE: Department of Pathology and Laboratory Medicine, Mount Sinai Hospital, Toronto, Ontario, M5G 1X5, Canada.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2001 Jan 12) 280 (1) 401-6. Journal code: 0372516. ISSN: 0006-291X.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200103
ENTRY DATE: Entered STN: 20010404
Last Updated on STN: 20010404
Entered Medline: 20010322

L8 ANSWER 65 OF 355 MEDLINE DUPLICATE 39
ACCESSION NUMBER: 2001332502 MEDLINE
DOCUMENT NUMBER: 21294745 PubMed ID: 11401471
TITLE: Generation and analysis of canine retinal ESTs: isolation
and expression of retina-specific gene transcripts.
AUTHOR: Lin C T; Sargan D R
CORPORATE SOURCE: Department of Veterinary Medicine, National Taiwan
University, Taipei, Taiwan.. ctlin@ccms.ntu.edu.tw
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2001
Mar 30) 282 (2) 394-403.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200106
ENTRY DATE: Entered STN: 20010702
Last Updated on STN: 20010702
Entered Medline: 20010628

L8 ANSWER 66 OF 355 MEDLINE DUPLICATE 40
ACCESSION NUMBER: 2001351997 MEDLINE
DOCUMENT NUMBER: 21309072 PubMed ID: 11414766
TITLE: Cloning and characterization of the human retina-specific
gene MPP4, a novel member of the p55 subfamily of MAGUK
proteins.
AUTHOR: Stohr H; Weber B H
CORPORATE SOURCE: Institut fur Humangenetik, Biozentrum, Universitat
Wurzburg, Wurzburg, D-97074, Germany.
SOURCE: GENOMICS, (2001 Jun 15) 74 (3) 377-84.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF316032
ENTRY MONTH: 200109
ENTRY DATE: Entered STN: 20010917
Last Updated on STN: 20010917
Entered Medline: 20010913

L8 ANSWER 67 OF 355 MEDLINE DUPLICATE 41
ACCESSION NUMBER: 2002013892 MEDLINE
DOCUMENT NUMBER: 21310278 PubMed ID: 11417722
TITLE: The analysis of expressed genes in the kidney of Japanese
flounder, Paralichthys olivaceus, injected with the
immunostimulant peptidoglycan.
AUTHOR: Kono T; Sakai M
CORPORATE SOURCE: United Graduate School of Agricultural Sciences, Kagoshima
University, Japan.
SOURCE: FISH & SHELLFISH IMMUNOLOGY, (2001 May) 11 (4) 357-66.
Journal code: 9505220. ISSN: 1050-4648.

PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20020121
Last Updated on STN: 20020121
Entered Medline: 20011204

L8 ANSWER 68 OF 355 MEDLINE DUPLICATE 42
ACCESSION NUMBER: 2001354670 MEDLINE
DOCUMENT NUMBER: 21154910 PubMed ID: 11230159
TITLE: Identification of human epidermal differentiation complex
(EDC)-encoded genes by subtractive hybridization of entire
YACs to a gridded keratinocyte cDNA library.
AUTHOR: Marenholz I; Zirra M; Fischer D F; Backendorf C; Ziegler
A;
Mischke D
CORPORATE SOURCE: Institut fur Immungenetik, Universitatsklinikum Charite
der
Humboldt-Universitat zu Berlin, 14050 Berlin, Germany.
SOURCE: GENOME RESEARCH, (2001 Mar) 11 (3) 341-55.
Journal code: 9518021. ISSN: 1088-9051.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AJ243659; GENBANK-AJ243660; GENBANK-AJ243661;
GENBANK-AJ243662; GENBANK-AJ243663; GENBANK-AJ243664;
GENBANK-AJ243665; GENBANK-AJ243666; GENBANK-AJ243667;
GENBANK-AJ243668; GENBANK-AJ243669; GENBANK-AJ243670;
GENBANK-AJ243671; GENBANK-AJ243672; GENBANK-AJ243673
ENTRY MONTH: 200106
ENTRY DATE: Entered STN: 20010625
Last Updated on STN: 20010625
Entered Medline: 20010621

L8 ANSWER 69 OF 355 MEDLINE DUPLICATE 43
ACCESSION NUMBER: 2002057146 MEDLINE
DOCUMENT NUMBER: 21643859 PubMed ID: 11784013
TITLE: Profiles of maternally expressed genes in fertilized eggs
of Ciona intestinalis.
AUTHOR: Nishikata T; Yamada L; Mochizuki Y; Satou Y; Shin-i T;
Kohara Y; Satoh N
CORPORATE SOURCE: Department of Biology, Konan University, Kobe, Okamoto,
658-8501, Japan.. nisikata@konan-u.ac.jp
SOURCE: DEVELOPMENTAL BIOLOGY, (2001 Oct 15) 238 (2) 315-31.
Journal code: 0372762. ISSN: 0012-1606.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200201
ENTRY DATE: Entered STN: 20020125
Last Updated on STN: 20020128
Entered Medline: 20020123

L8 ANSWER 70 OF 355 MEDLINE
ACCESSION NUMBER: 2002119421 IN-PROCESS
DOCUMENT NUMBER: 21842141 PubMed ID: 11853318
TITLE: Structural analysis of a Lotus japonicus genome. I.

which Sequence features and mapping of fifty-six TAC clones
cover the 5.4 mb regions of the genome.
AUTHOR: Sato S; Kaneko T; Nakamura Y; Asamizu E; Kato T; Tabata S
CORPORATE SOURCE: Kazusa DNA Research Institute, Kisarazu, Japan.
SOURCE: DNA RESEARCH, (2001 Dec 31) 8 (6) 311-8.
Journal code: 9423827. ISSN: 1340-2838.
PUB. COUNTRY: Japan
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020221
Last Updated on STN: 20020221

L8 ANSWER 71 OF 355 MEDLINE DUPLICATE 44
ACCESSION NUMBER: 2001325836 MEDLINE
DOCUMENT NUMBER: 21226134 PubMed ID: 11327696
TITLE: Cloning, mapping, genomic organization, and expression of
mouse M-LP, a new member of the peroxisomal membrane
protein Mpv17 domain family.
AUTHOR: Iida R; Yasuda T; Tsubota E; Matsuki T; Kishi K
CORPORATE SOURCE: Department of Forensic Medicine, Fukui Medical University,
Matsuoka-cho, Fukui, 910-1193, Japan..
ireiko@fmsrsa.fukui-
med.ac.jp
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2001
May 4) 283 (2) 292-6.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AI482564
ENTRY MONTH: 200106
ENTRY DATE: Entered STN: 20010611
Last Updated on STN: 20010611
Entered Medline: 20010607

L8 ANSWER 72 OF 355 MEDLINE DUPLICATE 45
ACCESSION NUMBER: 2002158014 MEDLINE
DOCUMENT NUMBER: 21888117 PubMed ID: 11891679
TITLE: Comprehensive resource: Skeletal gene database.
AUTHOR: Jia L; Ho N C; Park S S; Powell J; Francomano C A
CORPORATE SOURCE: MGB/NHGRI/NIH Rockville, MD 20892, USA..
libinj2@mail.nih.gov
SOURCE: AMERICAN JOURNAL OF MEDICAL GENETICS, (2001 Winter) 106
(4)
275-81.
Journal code: 7708900. ISSN: 0148-7299.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200206
ENTRY DATE: Entered STN: 20020314
Last Updated on STN: 20020606
Entered Medline: 20020605

L8 ANSWER 73 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:290628 BIOSIS
DOCUMENT NUMBER: PREV200100290628

TITLE: Using lab on-line to clone and identify the esophageal cancer related gene 4.
 AUTHOR(S): Bi Mei-Xia; Han Wei-Dong; Lu Shi-Xin (1)
 CORPORATE SOURCE: (1) Cancer Institute (Hospital), Chinese Academy of Medical Sciences, Peking Union Medical College, Beijing, 100021: shlu@public.bta.net.cn China
 SOURCE: Shengwu Huaxue yu Shengwu Wuli Xuebao, (May, 2001) Vol. 33, No. 3, pp. 257-261. print.
 ISSN: 0582-9879.
 DOCUMENT TYPE: Article
 LANGUAGE: Chinese
 SUMMARY LANGUAGE: Chinese; English

L8 ANSWER 74 OF 355 MEDLINE DUPLICATE 46
 ACCESSION NUMBER: 2001360421 MEDLINE
 DOCUMENT NUMBER: 21317063 PubMed ID: 11424210
 TITLE: In silico mining of EST databases for novel pre-implantation embryo-specific zinc finger protein genes.
 AUTHOR: Choo K B; Chen H H; Cheng W T; Chang H S; Wang M
 CORPORATE SOURCE: Recombinant DNA Laboratory, Department of Medical Research and Education, Veterans General Hospital-Taipei, Shih-Pai, Taipei, Taiwan.. kcbhu@vghtpe.gov.tw
 SOURCE: MOLECULAR REPRODUCTION AND DEVELOPMENT, (2001 Jul) 59 (3) 249-55.
 Journal code: 8903333. ISSN: 1040-452X.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AA422810; GENBANK-AA549412; GENBANK-AA666887
 ENTRY MONTH: 200110
 ENTRY DATE: Entered STN: 20011029
 Last Updated on STN: 20011029
 Entered Medline: 20011025

L8 ANSWER 75 OF 355 MEDLINE DUPLICATE 47
 ACCESSION NUMBER: 2001493705 MEDLINE
 DOCUMENT NUMBER: 21427669 PubMed ID: 11536302
 TITLE: GDEP, a new gene differentially expressed in normal prostate and prostate cancer.
 AUTHOR: Olsson P; Bera T K; Essand M; Kumar V; Duray P; Vincent J; Lee B; Pastan I
 CORPORATE SOURCE: Laboratory of Molecular Biology, Division of Basic Sciences, National Cancer Institute, National Institutes of Health, Bethesda, Maryland 20892-4255, USA.
 SOURCE: PROSTATE, (2001 Sep 15) 48 (4) 231-41.
 Journal code: 8101368. ISSN: 0270-4137.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200110
 ENTRY DATE: Entered STN: 20010906
 Last Updated on STN: 20011008
 Entered Medline: 20011004

L8 ANSWER 76 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

DUPLICATE 48
 ACCESSION NUMBER: 2001:463029 BIOSIS
 DOCUMENT NUMBER: PREV200100463029
 TITLE: SAND, a new protein family: From nucleic acid to protein structure and function prediction.
 AUTHOR(S): Cottage, Amanda; Edwards, Yvonne J. K.; Elgar, Greg (1)
 CORPORATE SOURCE: (1) UK Human Genome Mapping Project Resource Centre, Hinxton, Wellcome Trust Genome Campus, Cambridge, CB10
 LSB:
 SOURCE: gelgar@hgmp.mrc.ac.uk UK
 Comparative and Functional Genomics, (August, 2001) Vol. 2,
 No. 4, pp. 226-235. print.
 ISSN: 1531-6912.
 DOCUMENT TYPE: Article
 LANGUAGE: English
 SUMMARY LANGUAGE: English

L8 ANSWER 77 OF 355 MEDLINE DUPLICATE 49
 ACCESSION NUMBER: 2002023163 MEDLINE
 DOCUMENT NUMBER: 21362234 PubMed ID: 11469587
 TITLE: A putative plant homolog of the yeast beta-1,3-glucan synthase subunit FKS1 from cotton (*Gossypium hirsutum* L.) fibers.
 AUTHOR: Cui X; Shin H; Song C; Laosinchai W; Amano Y; Brown R M Jr
 CORPORATE SOURCE: Section of Molecular Genetics and Microbiology, School of Biological Sciences, The University of Texas at Austin, 78712, USA.
 SOURCE: PLANTA, (2001 Jun) 213 (2) 223-30.
 Journal code: 1250576. ISSN: 0032-0935.
 PUB. COUNTRY: Germany: Germany, Federal Republic of
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200202
 ENTRY DATE: Entered STN: 20020121
 Last Updated on STN: 20020206
 Entered Medline: 20020205

L8 ANSWER 78 OF 355 MEDLINE DUPLICATE 50
 ACCESSION NUMBER: 2001381449 MEDLINE
 DOCUMENT NUMBER: 21100894 PubMed ID: 11161815
 TITLE: The MEIS1 oncogene is highly expressed in neuroblastoma and amplified in cell line IMR32.
 AUTHOR: Spieker N; van Sluis P; Beitsma M; Boon K; van Schaik B D; van Kampen A H; Caron H; Versteeg R
 CORPORATE SOURCE: Department of Human Genetics, University of Amsterdam, Amsterdam, 1100DE, The Netherlands.
 SOURCE: GENOMICS, (2001 Jan 15) 71 (2) 214-21.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AZ081511
 ENTRY MONTH: 200107
 ENTRY DATE: Entered STN: 20010709
 Last Updated on STN: 20010709
 Entered Medline: 20010705

L8 ANSWER 79 OF 355 MEDLINE DUPLICATE 51

ACCESSION NUMBER: 2001314104 MEDLINE

DOCUMENT NUMBER: 21280915 PubMed ID: 11386757

TITLE: Central nervous system, uterus, heart, and leukocyte expression of the LOXL3 gene, encoding a novel lysyl oxidase-like protein.

AUTHOR: Jourdan-Le Saux C; Tomsche A; Ujfalusi A; Jia L; Csiszar K

CORPORATE SOURCE: Pacific Biomedical Research Center, University of Hawaii, 1993 East-West Road, Honolulu, Hawaii, 96822.

CONTRACT NUMBER: CA76580 (NCI)
RR03061 (NCRR)

SOURCE: GENOMICS, (2001 Jun 1) 74 (2) 211-8.
Journal code: 8800135. ISSN: 0888-7543.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AA852888; GENBANK-AF311313; GENBANK-AI752772;
GENBANK-R55706

ENTRY MONTH: 200110

ENTRY DATE: Entered STN: 20011008
Last Updated on STN: 20011008
Entered Medline: 20011004

L8 ANSWER 80 OF 355 MEDLINE DUPLICATE 52

ACCESSION NUMBER: 2001494209 MEDLINE

DOCUMENT NUMBER: 21202219 PubMed ID: 11308019

TITLE: Cloning and expression of Drosophila melanogaster UDP-GlcNAc:alpha-3-D-mannoside beta1,2-N-acetylglucosaminyltransferase I.

AUTHOR: Sarkar M; Schachter H

CORPORATE SOURCE: The Research Institute, Hospital for Sick Children, Toronto, Ontario, Canada.

SOURCE: BIOLOGICAL CHEMISTRY, (2001 Feb) 382 (2) 209-17.
Journal code: 9700112. ISSN: 1431-6730.

PUB. COUNTRY: Germany: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AF251495

ENTRY MONTH: 200109

ENTRY DATE: Entered STN: 20010910
Last Updated on STN: 20010910
Entered Medline: 20010906

L8 ANSWER 81 OF 355 MEDLINE DUPLICATE 53

ACCESSION NUMBER: 2001696575 MEDLINE

DOCUMENT NUMBER: 21610571 PubMed ID: 11746756

TITLE: ERCC1: a comparative genomic perspective.

AUTHOR: Wilson M D; Ruttan C C; Koop B F; Glickman B W

CORPORATE SOURCE: Centre for Environmental Health, Department of Biology, University of Victoria, Victoria, British Columbia, Canada.

SOURCE: ENVIRONMENTAL AND MOLECULAR MUTAGENESIS, (2001) 38 (2-3) 209-15.
Journal code: 8800109. ISSN: 0893-6692.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AC073787

ENTRY MONTH: 200201
ENTRY DATE: Entered STN: 20011218
Last Updated on STN: 20020125
Entered Medline: 20020109

L8 ANSWER 82 OF 355 MEDLINE DUPLICATE 54
ACCESSION NUMBER: 2001692422 MEDLINE
DOCUMENT NUMBER: 21602807 PubMed ID: 11738710
TITLE: Profiling the malaria genome: a gene survey of three species of malaria parasite with comparison to other apicomplexan species.
AUTHOR: Carlton J M; Muller R; Yowell C A; Fluegge M R; Sturrock K A; Pritt J R; Vargas-Serrato E; Galinski M R; Barnwell J W;
CORPORATE SOURCE: Mulder N; Kanapin A; Cawley S E; Hide W A; Dame J B
Computational Biology Branch, National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, MD 20892, USA.. carlton@tigr.org
CONTRACT NUMBER: N01-A1-65315
SOURCE: MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (2001 Dec) 118 (2) 201-10.
Journal code: 8006324. ISSN: 0166-6851.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AZ521913; GENBANK-AZ521914; GENBANK-AZ521915;
GENBANK-AZ521916; GENBANK-AZ521917; GENBANK-AZ521918;
GENBANK-AZ521919; GENBANK-AZ521920; GENBANK-AZ521921;
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[illegible]

[illegible]

[illegible]

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GENBANK-AZ522906; GENBANK-AZ522907; GENBANK-AZ522908;
GENBANK-AZ522909; GENBANK-AZ522910; GENBANK-AZ522911;
GENBANK-AZ522912

ENTRY MONTH:

ENTRY DATE:

200202

Entered STN: 20011213

Last Updated on STN: 20020228

Entered Medline: 20020227

L8 ANSWER 83 OF 355 MEDLINE DUPLICATE 55
 ACCESSION NUMBER: 2001257285 MEDLINE
 DOCUMENT NUMBER: 21097016 PubMed ID: 11169194
 TITLE: Identification of symbiosis-regulated genes in Eucalyptus
 globulus-Pisolithus tinctorius ectomycorrhiza by
 differential hybridization of arrayed cDNAs.
 AUTHOR: Voiblet C; Duplessis S; Encelot N; Martin F
 CORPORATE SOURCE: Equipe de Microbiologie Forestiere, Institut National de
 la
 Recherche Agronomique, Centre de Recherches de Nancy,
 54280
 Champenoux, France.
 SOURCE: PLANT JOURNAL, (2001 Jan) 25 (2) 181-91.
 Journal code: 9207397. ISSN: 0960-7412.
 PUB. COUNTRY: England: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AW600807; GENBANK-AW600808; GENBANK-AW600809;
 GENBANK-AW600810; GENBANK-AW600811; GENBANK-AW600812;
 GENBANK-AW600813; GENBANK-AW600814; GENBANK-AW600815;
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 GENBANK-AW731605; GENBANK-AW731606; GENBANK-AW731607;
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 GENBANK-AW731617; GENBANK-BE704426; GENBANK-BE704427;
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GENBANK-BE704446; GENBANK-BE704447; GENBANK-BE704448;
GENBANK-BE704449

ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010521
Last Updated on STN: 20010521
Entered Medline: 20010517

L8 ANSWER 84 OF 355 MEDLINE DUPLICATE 56
ACCESSION NUMBER: 2001322373 MEDLINE
DOCUMENT NUMBER: 21113412 PubMed ID: 11160995
TITLE: Identification and characterization of a novel human
vanilloid receptor-like protein, VRL-2.
AUTHOR: Delany N S; Hurle M; Facer P; Alnadaf T; Plumpton C;
Kinghorn I; See C G; Costigan M; Anand P; Woolf C J;
Crowther D; Sanseau P; Tate S N
CORPORATE SOURCE: Genome Informatics and Analysis, Virology and Vaccine
Systems, Ion Channel Section, Molecular Recognition,
Molecular Genetics, Glaxo Wellcome Research and
Development, Medicines Research Centre, Stevenage,
Hertfordshire SG1 2NY, United Kingdom.
SOURCE: PHYSIOLOGICAL GENOMICS, (2001 Jan 19) 4 (3) 165-74.
Journal code: 100894125. ISSN: 1094-8341.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200106
ENTRY DATE: Entered STN: 20010611
Last Updated on STN: 20010611
Entered Medline: 20010607

L8 ANSWER 85 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:497385 BIOSIS
DOCUMENT NUMBER: PREV200100497385
TITLE: Identification and tissue distribution of an odorant
receptor in the honey bee (*Apis mellifera*).
AUTHOR(S): Velarde, R. A. (1); Patch, H. M. (1); Robertson, H. M.
(1);
Robinson, G. E. (1); Fahrbach, S. E. (1)
CORPORATE SOURCE: (1) Department of Entomology, University of Illinois at
Urbana-Champaign, Urbana, IL USA
SOURCE: Society for Neuroscience Abstracts, (2001) Vol. 27, No. 1,
pp. 161. print.
Meeting Info.: 31st Annual Meeting of the Society for
Neuroscience San Diego, California, USA November 10-15,
2001
ISSN: 0190-5295.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L8 ANSWER 86 OF 355 MEDLINE DUPLICATE 57
ACCESSION NUMBER: 2002018578 MEDLINE
DOCUMENT NUMBER: 21335421 PubMed ID: 11441502
TITLE: Expressed sequence tags (ESTs) analysis of *Acanthamoeba*
healyi.
AUTHOR: Kong H H; Hwang M Y; Kim H K; Chung D I
CORPORATE SOURCE: Department of Parasitology, Kyungpook National University
School of Medicine, Taeyu 700-422, Korea.

SOURCE: KOREAN JOURNAL OF PARASITOLOGY, (2001 Jun) 39 (2) 151-60.
Journal code: 9435800. ISSN: 0023-4001.
PUB. COUNTRY: Korea (South)
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20020121
Last Updated on STN: 20020121
Entered Medline: 20011207

L8 ANSWER 87 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:151965 BIOSIS
DOCUMENT NUMBER: PREV200200151965
TITLE: Defining the Dexter-type human bone marrow culture system
using cDNA microarray analysis.
AUTHOR(S): Seshi, Beerelli (1); Kumar, Sanjay (1); King, Debra (1)
CORPORATE SOURCE: (1) Interdisciplinary Oncology Program, H. Lee Moffitt
Cancer Center, USF, Tampa, FL USA
SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 2, pp.
146b. <http://www.bloodjournal.org/>. print.
Meeting Info.: 43rd Annual Meeting of the American Society
of Hematology, Part 2 Orlando, Florida, USA December
07-11,
2001
ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English

L8 ANSWER 88 OF 355 MEDLINE DUPLICATE 58
ACCESSION NUMBER: 2001497494 MEDLINE
DOCUMENT NUMBER: 21428165 PubMed ID: 11545437
TITLE: Analysis of expressed sequence tags (ESTs) from the scaly
green flagellate *Scherffelia dubia* Pascher emend.
Melkonian
et Preisig.
AUTHOR: Becker B; Feja N; Melkonian M
CORPORATE SOURCE: Botanisches Institut, Universitat zu Koln, Germany..
b.becker@uni-koeln.de
SOURCE: PROTIST, (2001 Jul) 152 (2) 139-47.
Journal code: 9806488. ISSN: 1434-4610.
PUB. COUNTRY: Germany: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200201
ENTRY DATE: Entered STN: 20010910
Last Updated on STN: 20020130
Entered Medline: 20020129

L8 ANSWER 89 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:151910 BIOSIS
DOCUMENT NUMBER: PREV200200151910
TITLE: Cloning and characterization of zebrafish gp130.
AUTHOR(S): Layton, Judith E. (1); Hall, Nathan E. (1); Connell, Fiona
(1); Varma, Sony (1); Fujiki, Kazuhiro; Lieschke, Graham
J.
(1)
CORPORATE SOURCE: (1) Melbourne Tumour Biology Branch, Ludwig Institute for
Cancer Research, Parkville, VIC Australia

SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 2, pp. 134b. <http://www.bloodjournal.org/>. print.
Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 2 Orlando, Florida, USA December 07-11, 2001
ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English

L8 ANSWER 90 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:151895 BIOSIS
DOCUMENT NUMBER: PREV200200151895
TITLE: The transcriptome of bone marrow cells in chronic leukemia.
AUTHOR(S): Silva-Junior, Wilson A. (1); Alberto, Fernando L.; Uliana, Ronie M. (1); Simpson, Andrew J.; Costa, Fernando F.; Zago, Marco A.
CORPORATE SOURCE: (1) Center for Cell Therapy, Regional Blood Center, Ribeirao Preto Brazil
SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 2, pp. 131b. <http://www.bloodjournal.org/>. print.
Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 2 Orlando, Florida, USA December 07-11, 2001
ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English

L8 ANSWER 91 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:151892 BIOSIS
DOCUMENT NUMBER: PREV200200151892
TITLE: Novel transcription factors in CD34+ cells.
AUTHOR(S): Sharma, Tiffany T. (1); Gomes, Ignatius (1); Edassery, Seby (1); Mar, Brenton (1); Westbrook, Carol A. (1)
CORPORATE SOURCE: (1) Dept of Medicine, Section of Hem/Onc, University of Illinois at Chicago, Chicago, IL USA
SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 2, pp. 130b. <http://www.bloodjournal.org/>. print.
Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 2 Orlando, Florida, USA December 07-11, 2001
ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English

L8 ANSWER 92 OF 355 MEDLINE DUPLICATE 59
ACCESSION NUMBER: 2001272086 MEDLINE
DOCUMENT NUMBER: 21238674 PubMed ID: 11340635
TITLE: PRAC: A novel small nuclear protein that is specifically expressed in human prostate and colon.
AUTHOR: Liu X F; Olsson P; Wolfgang C D; Bera T K; Duray P; Lee B; Pastan I
CORPORATE SOURCE: Laboratory of Molecular Biology, Division of Basic Sciences, National Cancer Institute, National Institutes of Health, Bethesda, Maryland, USA.

SOURCE: PROSTATE, (2001 May 1) 47 (2) 125-31.
Journal code: 8101368. ISSN: 0270-4137.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010529
Last Updated on STN: 20010529
Entered Medline: 20010521

L8 ANSWER 93 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:350919 BIOSIS
DOCUMENT NUMBER: PREV200200350919
TITLE: Base excision repair in sugarcane.
AUTHOR(S): Agnez-Lima, Lucymara F. (1); Batistuzzo de Medeiros,
Silvia
CORPORATE SOURCE: R.; Maggi, Bruno S.; Quaresma, Giovanna A. S.
(1) Departamento de Biologia Celular e Genetica, Centro de
Biociencias, Universidade Federal do Rio Grande do Norte,
59072-970, Natal, RN: lfagnez@ufrnet.br Brazil
SOURCE: Genetics and Molecular Biology, (March, 2001) Vol. 24, No.
1-4, pp. 123-129. print.
ISSN: 1415-4757.
DOCUMENT TYPE: Article
LANGUAGE: English

L8 ANSWER 94 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:462511 BIOSIS
DOCUMENT NUMBER: PREV200100462511
TITLE: Molecular cloning and expression of cDNAs encoding
testis-specific and non-specific ATPase inhibitor-like
proteins in Bombyx mori.
AUTHOR(S): Ogura, Ichiro; Kusakabe, Takahiro (1); Kawaguchi, Yutaka;
Maeda, Takuji; Koga, Katsumi
CORPORATE SOURCE: (1) Laboratory of Silkworm Science, Kyushu University
Graduate School of Bioresource and Bioenvironmental
Sciences, Hakozaki 6-10-1, Fukuoka, 812-8581:
kusakabe@agr.kyushu-u.ac.jp Japan
SOURCE: Journal of Insect Biotechnology and Sericology, (June,
2001) Vol. 70, No. 2, pp. 121-128. print.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

L8 ANSWER 95 OF 355 MEDLINE DUPLICATE 60
ACCESSION NUMBER: 2001292584 MEDLINE
DOCUMENT NUMBER: 21269186 PubMed ID: 11374908
TITLE: Isolation of novel heart-specific genes using the BodyMap
database.
AUTHOR: Soejima H; Kawamoto S; Akai J; Miyoshi O; Arai Y; Morohka
T; Matsuo S; Niikawa N; Kimura A; Okubo K; Mukai T
CORPORATE SOURCE: Department of Biochemistry, Saga Medical School, 5-1-1
Nabeshima, Saga, 849-8501, Japan.. soejimah@post.saga-
med.ac.jp
SOURCE: GENOMICS, (2001 May 15) 74 (1) 115-20.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AB042554; GENBANK-AB042555; GENBANK-AB042556;
GENBANK-AB042557; GENBANK-AB042558; GENBANK-AB044805;
GENBANK-AB044806; GENBANK-AB044807

ENTRY MONTH: 200108

ENTRY DATE: Entered STN: 20010827

Last Updated on STN: 20010827

Entered Medline: 20010823

L8 ANSWER 96 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2002:350917 BIOSIS

DOCUMENT NUMBER: PREV200200350917

TITLE: In silico differential display of defense-related
expressed

sequence tags from sugarcane tissues infected with
diazotrophic endophytes.

AUTHOR(S): Lambais, Marcio R. (1)

CORPORATE SOURCE: (1) Departamento de Solos e Nutricao de Plantas, ESALQ,
Universidade de Sao Paulo, Av. Padua Dias, 11, 13418-900,
Piracicaba, SP: mlambais@carpa.ciaagri.usp.br Brazil

SOURCE: Genetics and Molecular Biology, (March, 2001) Vol. 24, No.
1-4, pp. 103-111. print.

ISSN: 1415-4757.

DOCUMENT TYPE: Article

LANGUAGE: English

L8 ANSWER 97 OF 355 MEDLINE

DUPLICATE 61

ACCESSION NUMBER: 2001443642 MEDLINE

DOCUMENT NUMBER: 21382160 PubMed ID: 11488641

TITLE: Genomic analysis of differentially expressed genes in
liver

and biliary epithelial cells of patients with primary
biliary cirrhosis.

AUTHOR: Tanaka A; Leung P S; Kenny T P; Au-Young J; Prindiville T;
Coppel R L; Ansari A A; Gershwin M E

CORPORATE SOURCE: Division of Rheumatology, Allergy and Clinical Immunology,
Department of Internal Medicine, University of California
at Davis, CA 95616, USA.

CONTRACT NUMBER: DK39588 (NIDDK)

SOURCE: JOURNAL OF AUTOIMMUNITY, (2001 Aug) 17 (1) 89-98.
Journal code: 8812164. ISSN: 0896-8411.

PUB. COUNTRY: England: United Kingdom

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200112

ENTRY DATE: Entered STN: 20010813

Last Updated on STN: 20020121

Entered Medline: 20011204

L8 ANSWER 98 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2002:129805 BIOSIS

DOCUMENT NUMBER: PREV200200129805

TITLE: Notch signaling pathway modifier Lunatic Fringe gene is
upregulated by retinoic acid during granulocytic
differentiation in APL.

AUTHOR(S): Park, Dorothy J. (1); Vuong, Peter T. (1); Koeffler, H.
Phillip (1)

CORPORATE SOURCE: (1) Hematology/Oncology, Cedars-Sinai Medical Center, Los
Angeles, CA USA

SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 1, pp.
89a.

<http://www.bloodjournal.org/>. print.
Meeting Info.: 43rd Annual Meeting of the American Society
of Hematology, Part 1 Orlando, Florida, USA December

07-11,

2001
ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English

L8 ANSWER 99 OF 355 MEDLINE DUPLICATE 62
ACCESSION NUMBER: 2001274672 MEDLINE
DOCUMENT NUMBER: 21262822 PubMed ID: 11370684
TITLE: Characterization of expressed sequence tags generated from
skin cDNA clones of Equus caballus by single pass
sequencing.
AUTHOR: Lieto L D; Cothran E G
CORPORATE SOURCE: University of Kentucky, Dept. of Veterinary Science,
Lexington 40546, USA.
SOURCE: ANIMAL BIOTECHNOLOGY, (2001 May) 12 (1) 87-97.
Journal code: 9011409. ISSN: 1049-5398.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200109
ENTRY DATE: Entered STN: 20010924
Last Updated on STN: 20010924
Entered Medline: 20010920

L8 ANSWER 100 OF 355 MEDLINE DUPLICATE 63
ACCESSION NUMBER: 2001528245 MEDLINE
DOCUMENT NUMBER: 21458557 PubMed ID: 11574155
TITLE: Discovery and mapping of ten novel G protein-coupled
receptor genes.
AUTHOR: Lee D K; Nguyen T; Lynch K R; Cheng R; Vanti W B; Arkhitko
O; Lewis T; Evans J F; George S R; O'Dowd B F
CORPORATE SOURCE: Department of Pharmacology, University of Toronto,
Toronto,
Ontario, M5S 1A8, Canada.
SOURCE: GENE, (2001 Sep 5) 275 (1) 83-91.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF411107; GENBANK-AF411108; GENBANK-AF411109;
GENBANK-AF411110; GENBANK-AF411111; GENBANK-AF411112;
GENBANK-AF411113; GENBANK-AF411114; GENBANK-AF411115;
GENBANK-AF411116; GENBANK-AF411117
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20011001
Last Updated on STN: 20020122
Entered Medline: 20011213

L8 ANSWER 101 OF 355 MEDLINE DUPLICATE 64
ACCESSION NUMBER: 2002031515 MEDLINE
DOCUMENT NUMBER: 21593328 PubMed ID: 11757806
TITLE: DAPIT, a novel protein down-regulated in insulin-sensitive
tissues in streptozotocin-induced diabetes.
AUTHOR: Paivarinne H; Kainulainen H
CORPORATE SOURCE: Institute of Medical Technology, University of Tampere,

Finland.
 SOURCE: ACTA DIABETOLOGICA, (2001) 38 (2) 83-6.
 Journal code: 9200299. ISSN: 0940-5429.
 PUB. COUNTRY: Germany: Germany, Federal Republic of
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200204
 ENTRY DATE: Entered STN: 20020124
 Last Updated on STN: 20020501
 Entered Medline: 20020430

L8 ANSWER 102 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 2002:350911 BIOSIS
 DOCUMENT NUMBER: PREV200200350911
 TITLE: Dissecting the Sugarcane Expressed Sequence Tag (SUCEST)
 database: Unraveling flower-specific genes.
 AUTHOR(S): Figueiredo, R. C.; Brito, M. S.; Figueiredo, L. H. M.;
 Quiapin, A. C.; Vitorelli, P. M.; Silva, L. R.; Santos, R.
 V.; Molfetta, J. B.; Goldman, G. H.; Goldman, M. H. S. (1)
 CORPORATE SOURCE: (1) Depto. Biologia FFCLRP, Universidade de Sao Paulo, Av.
 Bandeirantes 3900, 14040-901, Ribeirao Preto, SP:
 mgoldman@ffclrp.usp.br Brazil
 SOURCE: Genetics and Molecular Biology, (March, 2001) Vol. 24, No.
 1-4, pp. 77-84. print.
 ISSN: 1415-4757.
 DOCUMENT TYPE: Article
 LANGUAGE: English

L8 ANSWER 103 OF 355 MEDLINE DUPLICATE 65
 ACCESSION NUMBER: 2001691666 MEDLINE
 DOCUMENT NUMBER: 21601106 PubMed ID: 11738820
 TITLE: Application of differential display RT-PCR to identify
 porcine liver ESTs.
 AUTHOR: Ponsuksili S; Wimmers K; Schellander K
 CORPORATE SOURCE: Institute of Animal Breeding Science, University of Bonn,
 Endenicher Allee 15, 53115 Bonn, Germany..
 spon@itz.uni-bonn.de
 SOURCE: GENE, (2001 Dec 12) 280 (1-2) 75-85.
 Journal code: 7706761. ISSN: 0378-1119.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200202
 ENTRY DATE: Entered STN: 20011213
 Last Updated on STN: 20020301
 Entered Medline: 20020228

L8 ANSWER 104 OF 355 MEDLINE DUPLICATE 66
 ACCESSION NUMBER: 2001222169 MEDLINE
 DOCUMENT NUMBER: 21211403 PubMed ID: 11311557
 TITLE: The NIEHS Xenopus maternal EST project: interim analysis
 of
 the first 13,879 ESTs from unfertilized eggs.
 AUTHOR: Blackshear P J; Lai W S; Thorn J M; Kennington E A; Staffa
 N G; Moore D T; Bouffard G G; Beckstrom-Sternberg S M;
 Touchman J W; Bonaldo M F; Soares M B
 CORPORATE SOURCE: Office of Clinical Research and Laboratory of Signal
 Transduction, National Institute of Environmental Health
 Sciences, 111 Alexander Drive, Research Triangle Park, NC

SOURCE: 27709, USA.. black009@niehs.nih.gov
GENE, (2001 Apr 4) 267 (1) 71-87.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200106
ENTRY DATE: Entered STN: 20010611
Last Updated on STN: 20010611
Entered Medline: 20010607

L8 ANSWER 105 OF 355 MEDLINE DUPLICATE 67
ACCESSION NUMBER: 2001342930 MEDLINE
DOCUMENT NUMBER: 21299051 PubMed ID: 11406272
TITLE: FebA: a gene for eukaryotic translation initiation factor
4E-binding protein (4E-BP) in Dictyostelium discoideum.
AUTHOR: Morio T; Yasukawa H; Urushihara H; Saito T; Ochiai H;
Takeuchi I; Maeda M; Tanaka Y
CORPORATE SOURCE: Institute of Biological Sciences, University of Tsukuba,
Ibaraki, Japan.. morio@sakura.cc.tsukuba.ac.hjp
SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (2001 May 28) 1519 (1-2)
65-9.
Journal code: 0217513. ISSN: 0006-3002.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010806
Last Updated on STN: 20010806
Entered Medline: 20010802

L8 ANSWER 106 OF 355 MEDLINE DUPLICATE 68
ACCESSION NUMBER: 2001190983 MEDLINE
DOCUMENT NUMBER: 21024389 PubMed ID: 11149669
TITLE: Blood-brain barrier genomics.
AUTHOR: Li J Y; Boado R J; Pardridge W M
CORPORATE SOURCE: Department of Medicine, UCLA School of Medicine, Los
Angeles, California 90095-1682, USA.
CONTRACT NUMBER: NS-38894 (NINDS)
SOURCE: JOURNAL OF CEREBRAL BLOOD FLOW AND METABOLISM, (2001 Jan)
21 (1) 61-8.
Journal code: 8112566. ISSN: 0271-678X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF306546
ENTRY MONTH: 200104
ENTRY DATE: Entered STN: 20010410
Last Updated on STN: 20010410
Entered Medline: 20010405

L8 ANSWER 107 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:248884 BIOSIS
DOCUMENT NUMBER: PREV200100248884
TITLE: Molecular cloning and functional expression of a human
intestinal lactoferrin receptor.
AUTHOR(S): Suzuki, Yasushi A. (1); Shin, Kouichirou (1); Lonnerdal,
Bo

(1)
CORPORATE SOURCE: (1) University of California Davis, One Shields Ave,
Davis,
CA, 95616 USA
SOURCE: FASEB Journal, (March 7, 2001) Vol. 15, No. 4, pp. A60.
print.
Meeting Info.: Annual Meeting of the Federation of
American
Societies for Experimental Biology on Experimental Biology
2001 Orlando, Florida, USA March 31-April 04, 2001
ISSN: 0892-6638.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L8 ANSWER 108 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:350902 BIOSIS
DOCUMENT NUMBER: PREV200200350902
TITLE: In silico characterization and expression analyses of
sugarcane putative sucrose non-fermenting-1 (SNF1) related
kinases.
AUTHOR(S): Carraro, Dirce Maria (1); Lambais, Marcio R.; Carrer,
Helaine
CORPORATE SOURCE: (1) Ludwig Institute for Cancer Research, Rua Prof.
Antonio
Prudente, 109, 01509-010, Sao Paulo, SP:
dcarraro@ludwig.org.br Brazil
SOURCE: Genetics and Molecular Biology, (March, 2001) Vol. 24, No.
1-4, pp. 35-41. print.
ISSN: 1415-4757.
DOCUMENT TYPE: Article
LANGUAGE: English

L8 ANSWER 109 OF 355 MEDLINE
ACCESSION NUMBER: 2001471934 MEDLINE
DOCUMENT NUMBER: 21407917 PubMed ID: 11516336
TITLE: Gene trapping identifies transiently induced survival
genes
during programmed cell death.
AUTHOR: Wempe F; Yang J Y; Hammann J; von Melchner H
CORPORATE SOURCE: Laboratory for Molecular Hematology, University of
Frankfurt Medical School, 60590 Frankfurt am Main,
Germany.
SOURCE: GENOMEBIOLOGY.COM, (2001) 2 (7) RESEARCH0023.
Journal code: 100960660. ISSN: 1465-6914.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200205
ENTRY DATE: Entered STN: 20010823
Last Updated on STN: 20020505
Entered Medline: 20020503

L8 ANSWER 110 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:288231 BIOSIS
DOCUMENT NUMBER: PREV200100288231
TITLE: Molecular cloning of NELIN, a putative human cytoskeleton
regulation gene.
AUTHOR(S): Zhao Yong; Wei Ying-Jie; Cao Hui-Qing; Ding Jin-Feng (1)
CORPORATE SOURCE: (1) Molecular Medicine Center for Cardiovascular Diseases,

SOURCE: Fu Wai Heart Hospital and Cardiovascular Institute, Peking Union Medical College and Chinese Academy of Medical Sciences, Beijing, 100037: jinfengd@yahoo.com China
Shengwu Huaxue yu Shengwu Wuli Xuebao, (2001) Vol. 33, No. 1, pp. 19-24. print.
ISSN: 0582-9879.

DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: Chinese; English

L8 ANSWER 111 OF 355 MEDLINE DUPLICATE 69
ACCESSION NUMBER: 2001654635 MEDLINE
DOCUMENT NUMBER: 21564197 PubMed ID: 11707067
TITLE: Identification, genomic organization, and mRNA expression of LACTB, encoding a serine beta-lactamase-like protein with an amino-terminal transmembrane domain.
AUTHOR: Smith T S; Southan C; Ellington K; Campbell D; Tew D G; Debouck C
CORPORATE SOURCE: Department of Genetics Research, GlaxoSmithKline Pharmaceuticals, King of Prussia, Pennsylvania 19406, USA.
SOURCE: GENOMICS, (2001 Nov) 78 (1-2) 12-4.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF317901
ENTRY MONTH: 200201
ENTRY DATE: Entered STN: 20011115
Last Updated on STN: 20020125
Entered Medline: 20020107

L8 ANSWER 112 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:129475 BIOSIS
DOCUMENT NUMBER: PREV200200129475
TITLE: Identification of a new human gene that codes for a potential cytoskeletal protein belonging to a new
sudfamily
of Rho-GAP proteins.
AUTHOR(S): Basseres, Daniela S. (1); Tizzei, Edna R. V. (1); Costa, Fernando F. (1); Saad, Sara T. O. (1)
CORPORATE SOURCE: (1) Hematology and Hemotherapy Center, State University of Campinas, Campinas, SP Brazil
SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 1, pp. 11a-12a. <http://www.bloodjournal.org/>. print.
Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 1 Orlando, Florida, USA December 07-11,
2001
ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English

L8 ANSWER 113 OF 355 MEDLINE DUPLICATE 70
ACCESSION NUMBER: 2001542518 MEDLINE
DOCUMENT NUMBER: 21473253 PubMed ID: 11589565
TITLE: Tagged Transcriptome Display (TTD) in indica rice using Ac transposition.
AUTHOR: Kohli A; Xiong J; Greco R; Christou P; Pereira A
CORPORATE SOURCE: Molecular Biotechnology Unit, John Innes Centre, Norwich

SOURCE: Research Park, UK.
Mol Genet Genomics, (2001 Sep) 266 (1) 1-11.
Journal code: 101093320. ISSN: 1617-4615.
PUB. COUNTRY: Germany: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200110
ENTRY DATE: Entered STN: 20011009
Last Updated on STN: 20011029
Entered Medline: 20011025

L8 ANSWER 114 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:350898 BIOSIS
DOCUMENT NUMBER: PREV200200350898
TITLE: The libraries that made SUCEST.
AUTHOR(S): Vettore, Andre L.; da Silva, Felipe R.; Kemper, Edson L.;
Arruda, Paulo (1)
CORPORATE SOURCE: (1) Centro de Biologia Molecular e Engenharia Genetica,
Universidade Estadual de Campinas, 13083-970, Campinas,
SP:
parruda@unicamp.br Brazil
SOURCE: Genetics and Molecular Biology, (March, 2001) Vol. 24, No.
1-4, pp. 1-7. print.
ISSN: 1415-4757.
DOCUMENT TYPE: Article
LANGUAGE: English

L8 ANSWER 115 OF 355 MEDLINE DUPLICATE 71
ACCESSION NUMBER: 2001027226 MEDLINE
DOCUMENT NUMBER: 20490576 PubMed ID: 11035752
TITLE: Identification of tgh-2, a filarial nematode homolog of
Caenorhabditis elegans daf-7 and human transforming growth
factor beta, expressed in microfilarial and adult stages
of
Brugia malayi.
AUTHOR: Gomez-Escobar N; Gregory W F; Maizels R M
CORPORATE SOURCE: Institute of Cell, Animal and Population Biology,
University of Edinburgh, Edinburgh EH9 3JT, United
Kingdom.
SOURCE: INFECTION AND IMMUNITY, (2000 Nov) 68 (11) 6402-10.
Journal code: 0246127. ISSN: 0019-9567.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF104016
ENTRY MONTH: 200011
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001115

L8 ANSWER 116 OF 355 MEDLINE DUPLICATE 72
ACCESSION NUMBER: 2000410298 MEDLINE
DOCUMENT NUMBER: 20399702 PubMed ID: 10945605
TITLE: Cancer gene discovery using digital differential display.
AUTHOR: Scheurle D; DeYoung M P; Binniger D M; Page H; Jahanzeb
M;
Narayanan R
CORPORATE SOURCE: Department of Biology, Florida Atlantic University, Boca
Raton 33431, USA.

SOURCE: CANCER RESEARCH, (2000 Aug 1) 60 (15) 4037-43.
Journal code: 2984705R. ISSN: 0008-5472.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200008
ENTRY DATE: Entered STN: 20000907
Last Updated on STN: 20000907
Entered Medline: 20000831

L8 ANSWER 117 OF 355 MEDLINE DUPLICATE 73
ACCESSION NUMBER: 2001025016 MEDLINE
DOCUMENT NUMBER: 20507688 PubMed ID: 11053263
TITLE: Characterization of gene expression in human trabecular
meshwork using single-pass sequencing of 1060 clones.
AUTHOR: Gonzalez P; Epstein D L; Borrás T
CORPORATE SOURCE: Department of Ophthalmology, Duke University Medical
Center, Durham, North Carolina, USA.
CONTRACT NUMBER: EY01894 (NEI)
EY11906 (NEI)
SOURCE: INVESTIGATIVE OPHTHALMOLOGY AND VISUAL SCIENCE, (2000 Nov)
41 (12) 3678-93.
Journal code: 7703701. ISSN: 0146-0404.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-BE439390; GENBANK-BE440238
ENTRY MONTH: 200011
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001114

L8 ANSWER 118 OF 355 MEDLINE DUPLICATE 74
ACCESSION NUMBER: 2000456856 MEDLINE
DOCUMENT NUMBER: 20440414 PubMed ID: 10982890
TITLE: Human RNA lariat debranching enzyme cDNA complements the
phenotypes of *Saccharomyces cerevisiae* dbr1 and
Schizosaccharomyces pombe dbr1 mutants.
AUTHOR: Kim J W; Kim H C; Kim G M; Yang J M; Boeke J D; Nam K
CORPORATE SOURCE: Department of Biochemistry, Inha University College of
Medicine, Incheon, Republic of Korea, Clinical Research
Center, Samsung Biomedical Research Institute, 50 Ilwon
Dong, Kangnam Ku, Seoul 135-230, Republic of Korea.
SOURCE: NUCLEIC ACIDS RESEARCH, (2000 Sep 15) 28 (18) 3666-73.
Journal code: 0411011. ISSN: 1362-4962.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF180919
ENTRY MONTH: 200009
ENTRY DATE: Entered STN: 20001005
Last Updated on STN: 20010521
Entered Medline: 20000925

L8 ANSWER 119 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
DUPLICATE 75
ACCESSION NUMBER: 2001:151465 BIOSIS
DOCUMENT NUMBER: PREV200100151465

TITLE: Preliminary analysis of expressed sequence tags for sugarcane.
 AUTHOR(S): Carson, Deborah L.; Botha, Frederik C. (1)
 CORPORATE SOURCE: (1) Institute for Plant Biotechnology, Univ. of Stellenbosch, Matieland, 7602: xtecdc@sugar.org.za, FCB@land.sun.ac.za South Africa
 SOURCE: Crop Science, (November December, 2000) Vol. 40, No. 6, PP. 1769-1779. print.
 ISSN: 0011-183X.
 DOCUMENT TYPE: Article
 LANGUAGE: English
 SUMMARY LANGUAGE: English

L8 ANSWER 120 OF 355 MEDLINE DUPLICATE 76
 ACCESSION NUMBER: 2001084101 MEDLINE
 DOCUMENT NUMBER: 20499367 PubMed ID: 11042152
 TITLE: Cloning and functional analysis of cDNAs with open reading frames for 300 previously undefined genes expressed in CD34+ hematopoietic stem/progenitor cells.
 AUTHOR: Zhang Q H; Ye M; Wu X Y; Ren S X; Zhao M; Zhao C J; Fu G; Shen Y; Fan H Y; Lu G; Zhong M; Xu X R; Han Z G; Zhang J W;
 CORPORATE SOURCE: Tao J; Huang Q H; Zhou J; Hu G X; Gu J; Chen S J; Chen Z Shanghai Institute of Hematology (SIH), Rui Jin Hospital affiliated with Shanghai Second Medical University, Shanghai 200025, China.
 SOURCE: GENOME RESEARCH, (2000 Oct) 10 (10) 1546-60.
 Journal code: 9518021. ISSN: 1088-9051.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF038950; GENBANK-AF038952; GENBANK-AF038953; GENBANK-AF038954; GENBANK-AF038955; GENBANK-AF038956; GENBANK-AF038957; GENBANK-AF038958; GENBANK-AF038959; GENBANK-AF038960; GENBANK-AF038961; GENBANK-AF038962; GENBANK-AF038965; GENBANK-AF038966; GENBANK-AF047432; GENBANK-AF047433; GENBANK-AF047434; GENBANK-AF047435; GENBANK-AF047436; GENBANK-AF047437; GENBANK-AF047438; GENBANK-AF047439; GENBANK-AF047440; GENBANK-AF047441; GENBANK-AF047442; GENBANK-AF054174; GENBANK-AF054175; GENBANK-AF054176; GENBANK-AF054177; GENBANK-AF054178
 ENTRY MONTH: 200101
 ENTRY DATE: Entered STN: 20010322
 Last Updated on STN: 20010322
 Entered Medline: 20010118

L8 ANSWER 121 OF 355 MEDLINE DUPLICATE 77
 ACCESSION NUMBER: 2001105929 MEDLINE
 DOCUMENT NUMBER: 21022034 PubMed ID: 11142426
 TITLE: Searching expressed sequence tag databases: discovery and confirmation of a common polymorphism in the thymidylate synthase gene.
 AUTHOR: Ulrich C M; Bigler J; Velicer C M; Greene E A; Farin F M; Potter J D
 CORPORATE SOURCE: Cancer Prevention Research Program, Fred Hutchinson Cancer Research Center, Seattle, Washington 98109, USA..
 nulrich@fhcrc.org
 CONTRACT NUMBER: P30 ES-07033 (NIEHS)
 SOURCE: CANCER EPIDEMIOLOGY, BIOMARKERS AND PREVENTION, (2000 Dec)

9 (12) 1381-5.
 Journal code: 9200608. ISSN: 1055-9965.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-X02308
 ENTRY MONTH: 200102
 ENTRY DATE: Entered STN: 20010322
 Last Updated on STN: 20010322
 Entered Medline: 20010208

L8 ANSWER 122 OF 355 MEDLINE DUPLICATE 78
 ACCESSION NUMBER: 2000505301 MEDLINE
 DOCUMENT NUMBER: 20508574 PubMed ID: 11054275
 TITLE: cDNA cloning of biologically active chicken
 interleukin-18.
 AUTHOR: Schneider K; Puehler F; Baeuerle D; Elvers S; Staeheli P;
 Kaspers B; Weining K C
 CORPORATE SOURCE: Abteilung Virologie, Institut fur Medizinische
 Mikrobiologie und Hygiene, University of Freiburg, 79008
 Freiburg, Germany.
 SOURCE: JOURNAL OF INTERFERON AND CYTOKINE RESEARCH, (2000 Oct) 20
 (10) 879-83.
 Journal code: 9507088. ISSN: 1079-9907.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AJ277865
 ENTRY MONTH: 200011
 ENTRY DATE: Entered STN: 20010322
 Last Updated on STN: 20010322
 Entered Medline: 20001113

L8 ANSWER 123 OF 355 MEDLINE DUPLICATE 79
 ACCESSION NUMBER: 2000233676 MEDLINE
 DOCUMENT NUMBER: 20233676 PubMed ID: 10769175
 TITLE: cDNA cloning and characterization of human
 Delta5-desaturase involved in the biosynthesis of
 arachidonic acid.
 AUTHOR: Leonard A E; Kelder B; Bobik E G; Chuang L T;
 Parker-Barnes
 J M; Thurmond J M; Kroeger P E; Kopchick J J; Huang Y S;
 Mukerji P
 CORPORATE SOURCE: Department of Strategic Discovery Research, Ross Products
 Division, Abbott Laboratories, 3300 Stelzer Road,
 Columbus,
 OH 43219, USA.
 SOURCE: BIOCHEMICAL JOURNAL, (2000 May 1) 347 Pt 3 719-24.
 Journal code: 2984726R. ISSN: 0264-6021.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF226273
 ENTRY MONTH: 200006
 ENTRY DATE: Entered STN: 20000622
 Last Updated on STN: 20000622
 Entered Medline: 20000615

L8 ANSWER 124 OF 355 MEDLINE DUPLICATE 80
 ACCESSION NUMBER: 2000267003 MEDLINE
 DOCUMENT NUMBER: 20267003 PubMed ID: 10809006
 TITLE: In Arabidopsis thaliana, 1% of the genome codes for a novel protein family unique to plants.
 AUTHOR: Aubourg S; Boudet N; Kreis M; Lecharny A
 CORPORATE SOURCE: Institut de Biotechnologie des Plantes, UMR CNRS 8618, Laboratoire de Biologie du Developpement des Plantes, Universite de Paris-Sud, Orsay, France.
 SOURCE: PLANT MOLECULAR BIOLOGY, (2000 Mar) 42 (4) 603-13.
 Journal code: 9106343. ISSN: 0167-4412.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AJ006040; GENBANK-AJ006041; GENBANK-AJ006042; GENBANK-AJ006043
 ENTRY MONTH: 200005
 ENTRY DATE: Entered STN: 20000606
 Last Updated on STN: 20000606
 Entered Medline: 20000525

L8 ANSWER 125 OF 355 MEDLINE DUPLICATE 81
 ACCESSION NUMBER: 2000404486 MEDLINE
 DOCUMENT NUMBER: 20334634 PubMed ID: 10874211
 TITLE: Isolation and characterization of human NBL4, a gene involved in the beta-catenin/tcf signaling pathway.
 AUTHOR: Ishiguro H; Furukawa Y; Daigo Y; Miyoshi Y; Nagasawa Y; Nishiwaki T; Kawasoe T; Fujita M; Satoh S; Miwa N; Fujii Y;
 Nakamura Y
 CORPORATE SOURCE: Laboratory of Molecular Medicine, Human Genome Center, Institute of Medical Science, The University of Tokyo, Minato-ku, Tokyo 108-8639, Japan.
 SOURCE: JAPANESE JOURNAL OF CANCER RESEARCH, (2000 Jun) 91 (6) 597-603.
 Journal code: 8509412. ISSN: 0910-5050.
 PUB. COUNTRY: Japan
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AB030240; GENBANK-D30788; GENBANK-U13673
 ENTRY MONTH: 200008
 ENTRY DATE: Entered STN: 20000901
 Last Updated on STN: 20000922
 Entered Medline: 20000818

L8 ANSWER 126 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 2001:302674 BIOSIS
 DOCUMENT NUMBER: PREV200100302674
 TITLE: CARD-10, a novel caspase-9 binding protein.
 AUTHOR(S): Pathan, Nuzhat I. (1); Torii, Seiji (1); Krajewski, Stanislaw (1); Xie, Zhihua (1); Godzik, Adam (1); Reed, John C. (1)
 CORPORATE SOURCE: (1) The Burnham Institute, La Jolla, CA USA
 SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 1, pp. 569a. print.
 Meeting Info.: 42nd Annual Meeting of the American Society of Hematology San Francisco, California, USA December 01-05, 2000 American Society of Hematology

. ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L8 ANSWER 127 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:312513 BIOSIS
DOCUMENT NUMBER: PREV200100312513
TITLE: Cloning and characterization of BAL2, a novel member of a
risk-related gene family in diffuse large B-cell
lymphomas.
AUTHOR(S): Aguiar, Ricardo C. T. (1); Kreinbrink, Katherine D. (1);
Shipp, Margaret A. (1)
CORPORATE SOURCE: (1) Adult Oncology, Dana Farber Cancer Institute, Harvard
Medical School, Boston, MA USA
SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 1, pp.
505a. print.
Meeting Info.: 42nd Annual Meeting of the American Society
of Hematology San Francisco, California, USA December
01-05, 2000 American Society of Hematology
. ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L8 ANSWER 128 OF 355 MEDLINE DUPLICATE 82
ACCESSION NUMBER: 2000503652 MEDLINE
DOCUMENT NUMBER: 20505383 PubMed ID: 11052202
TITLE: Characterisation of complementary DNAs from the expressed
sequence tag analysis of life cycle stages of *Laminaria*
digitata (Phaeophyceae).
AUTHOR: Crepineau F; Roscoe T; Kaas R; Kloareg B; Boyen C
CORPORATE SOURCE: UMR 1931, CNRS and Laboratoires Goemar, Observatoire
Océanologique de Roscoff, France.
SOURCE: PLANT MOLECULAR BIOLOGY, (2000 Jul) 43 (4) 503-13.
Journal code: 9106343. ISSN: 0167-4412.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AW400409; GENBANK-AW400410; GENBANK-AW400411;
GENBANK-AW400412; GENBANK-AW400413; GENBANK-AW400414;
GENBANK-AW400415; GENBANK-AW400416; GENBANK-AW400417;
GENBANK-AW400418; GENBANK-AW400419; GENBANK-AW400420;
GENBANK-AW400421; GENBANK-AW400422; GENBANK-AW400423;
GENBANK-AW400424; GENBANK-AW400425; GENBANK-AW400426;
GENBANK-AW400427; GENBANK-AW400428; GENBANK-AW400429;
GENBANK-AW400430; GENBANK-AW400431; GENBANK-AW400432;
GENBANK-AW400433; GENBANK-AW400434; GENBANK-AW400435;
GENBANK-AW400436; GENBANK-AW400437; GENBANK-AW400438; +
ENTRY MONTH: 200011
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001107

L8 ANSWER 129 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2000:266418 BIOSIS
DOCUMENT NUMBER: PREV200000266418
TITLE: Genes expressed in the latex of *Hevea brasiliensis*.
AUTHOR(S): Han, Kyung-Hwan (1); Shin, Dong Ho; Yang, Jaemo; Kim, In
Jeong; Oh, Soo Kyung; Chow, K. S.

CORPORATE SOURCE: (1) Department of Forestry, Michigan State University, 126
Natural Resources Building, East Lansing, MI, 48824-1222
USA

SOURCE: Tree Physiology, (April, 2000) Vol. 20, No. 8, pp.
503-510.

print..
ISSN: 0829-318X.

DOCUMENT TYPE: Article

LANGUAGE: English

SUMMARY LANGUAGE: English

L8 ANSWER 130 OF 355 MEDLINE DUPLICATE 83

ACCESSION NUMBER: 2000171380 MEDLINE

DOCUMENT NUMBER: 20171380 PubMed ID: 10704287

TITLE: Characterization, chromosomal assignment, and tissue
expression of a novel human gene belonging to the ARF GAP
family.

AUTHOR: Zhang C; Yu Y; Zhang S; Liu M; Xing G; Wei H; Bi J; Liu X;
Zhou G; Dong C; Hu Z; Zhang Y; Luo L; Wu C; Zhao S; He F

CORPORATE SOURCE: Department of Genomics and Proteomics, Beijing Institute
of

Radiation Medicine, Chinese National Human Genome Center
at

Beijing, 27 Taiping Road, Beijing, 100850, People's
Republic of China.

SOURCE: GENOMICS, (2000 Feb 1) 63 (3) 400-8.

Journal code: 8800135. ISSN: 0888-7543.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AF111847

ENTRY MONTH: 200007

ENTRY DATE: Entered STN: 20000810

Last Updated on STN: 20000810

Entered Medline: 20000727

L8 ANSWER 131 OF 355 MEDLINE DUPLICATE 84

ACCESSION NUMBER: 2000144006 MEDLINE

DOCUMENT NUMBER: 20144006 PubMed ID: 10677432

TITLE: Toward a functional catalog of the plant genome. A survey
of genes for lipid biosynthesis.

AUTHOR: Mekhedov S; de Ilarduya O M; Ohlrogge J

CORPORATE SOURCE: Department of Botany and Plant Pathology, Michigan State
University, East Lansing, Michigan 48824, USA.

SOURCE: PLANT PHYSIOLOGY, (2000 Feb) 122 (2) 389-402.

Journal code: 0401224. ISSN: 0032-0889.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200003

ENTRY DATE: Entered STN: 20000407

Last Updated on STN: 20000407

Entered Medline: 20000324

L8 ANSWER 132 OF 355 MEDLINE

ACCESSION NUMBER: 2001114022 MEDLINE

DOCUMENT NUMBER: 20421939 PubMed ID: 10968729

TITLE: Partial genome scale analysis of gene expression in human
adipose tissue using DNA array.

AUTHOR: Gabrielsson B L; Carlsson B; Carlsson L M
 CORPORATE SOURCE: Research Centre for Endocrinology & Metabolism, Department of Internal Medicine, Sahlgrenska University Hospital, Goteborg University, Sweden.
 SOURCE: OBESITY RESEARCH, (2000 Aug) 8 (5) 374-84.
 Journal code: 9305691. ISSN: 1071-7323.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200102
 ENTRY DATE: Entered STN: 20010322
 Last Updated on STN: 20010322
 Entered Medline: 20010215

L8 ANSWER 133 OF 355 MEDLINE DUPLICATE 85
 ACCESSION NUMBER: 2001182568 MEDLINE
 DOCUMENT NUMBER: 21100433 PubMed ID: 11167026
 TITLE: Transcriptome analysis of channel catfish (Ictalurus punctatus): genes and expression profile from the brain.
 AUTHOR: Ju Z; Karsi A; Kocabas A; Patterson A; Li P; Cao D; Dunham R; Liu Z
 CORPORATE SOURCE: The Fish Molecular Genetics and Biotechnology Laboratory, 203 Swingle Hall, Department of Fisheries and Allied Aquacultures and Program of Cell and Molecular Biosciences,
 Auburn University, AL, Auburn 36849, USA.
 SOURCE: GENE, (2000 Dec 31) 261 (2) 373-82.
 Journal code: 7706761. ISSN: 0378-1119.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200103
 ENTRY DATE: Entered STN: 20010404
 Last Updated on STN: 20010404
 Entered Medline: 20010329

L8 ANSWER 134 OF 355 MEDLINE DUPLICATE 86
 ACCESSION NUMBER: 2001058771 MEDLINE
 DOCUMENT NUMBER: 20472053 PubMed ID: 11018261
 TITLE: Isolation of a cDNA for a novel human RING finger protein gene, RNF18, by the virtual transcribed sequence (VTS) approach(1).
 AUTHOR: Yoshikawa T; Seki N; Azuma T; Masuho Y; Muramatsu M; Miyajima N; Saito T
 CORPORATE SOURCE: Biological Technology Laboratory, Helix Research Institute,
 Kisarazu, Chiba, Japan.
 SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (2000 Oct 2) 1493 (3) 349-55.
 Journal code: 0217513. ISSN: 0006-3002.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AB037682
 ENTRY MONTH: 200012
 ENTRY DATE: Entered STN: 20010322
 Last Updated on STN: 20010322
 Entered Medline: 20001222

L8 ANSWER 135 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 2001:302173 BIOSIS
 DOCUMENT NUMBER: PREV200100302173
 TITLE: Identification of RNA-splicing genes expressed as a result of p210 BCR/ABL in CD34+ cells using subtractive hybridization.
 AUTHOR(S): Salesse, Stephanie; Qi, Huilin; Verfaillie, Catherine M.
 SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 1, pp. 347a. print.
 Meeting Info.: 42nd Annual Meeting of the American Society of Hematology San Francisco, California, USA December 01-05, 2000 American Society of Hematology
 . ISSN: 0006-4971.
 DOCUMENT TYPE: Conference
 LANGUAGE: English
 SUMMARY LANGUAGE: English

L8 ANSWER 136 OF 355 MEDLINE DUPLICATE 87
 ACCESSION NUMBER: 2000171375 MEDLINE
 DOCUMENT NUMBER: 20171375 PubMed ID: 10704282
 TITLE: Expression profile viewer (ExProView): a software tool for transcriptome analysis.
 AUTHOR: Larsson M; Stahl S; Uhlen M; Wennborg A
 CORPORATE SOURCE: Department of Biotechnology, Royal Institute of Technology (KTH), Stockholm, S-100 44, Sweden.. magnus@biochem.kth.se
 SOURCE: GENOMICS, (2000 Feb 1) 63 (3) 341-53.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200007
 ENTRY DATE: Entered STN: 20000810
 Last Updated on STN: 20000810
 Entered Medline: 20000727

L8 ANSWER 137 OF 355 MEDLINE DUPLICATE 88
 ACCESSION NUMBER: 2000231760 MEDLINE
 DOCUMENT NUMBER: 20231760 PubMed ID: 10767556
 TITLE: cDNA cloning of acyl-CoA desaturase homologs in the silkworm, Bombyx mori.
 AUTHOR: Yoshiga T; Okano K; Mita K; Shimada T; Matsumoto S
 CORPORATE SOURCE: Laboratory of Molecular Entomology and Baculovirology, RIKEN, Hirosawa 2-1, Wako, Saitama, Japan.
 SOURCE: GENE, (2000 Apr 4) 246 (1-2) 339-45.
 Journal code: 7706761. ISSN: 0378-1119.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF157627; GENBANK-AF182405; GENBANK-AF182406
 ENTRY MONTH: 200005
 ENTRY DATE: Entered STN: 20000613
 Last Updated on STN: 20000613
 Entered Medline: 20000531

L8 ANSWER 138 OF 355 MEDLINE DUPLICATE 89
 ACCESSION NUMBER: 2001182562 MEDLINE
 DOCUMENT NUMBER: 21100427 PubMed ID: 11167020
 TITLE: Identification of a novel mammalian endoplasmic

motif reticulum-resident KDEL protein using an EST database
 search.
 AUTHOR: Kimata Y; Ooboki K; Nomura-Furuwatari C; Hosoda A; Tsuru
 A; Kohno K
 CORPORATE SOURCE: Research and Education Center for Genetic Information,
 Nara Institute of Science and Technology, 8916-5 Takayama,
 Ikoma, 630-0101, Nara, Japan.
 SOURCE: GENE, (2000 Dec 31) 261 (2) 321-7.
 Journal code: 7706761. ISSN: 0378-1119.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AJ404004
 ENTRY MONTH: 200103
 ENTRY DATE: Entered STN: 20010404
 Last Updated on STN: 20010404
 Entered Medline: 20010329

L8 ANSWER 139 OF 355 MEDLINE DUPLICATE 90
 ACCESSION NUMBER: 2000149852 MEDLINE
 DOCUMENT NUMBER: 20149852 PubMed ID: 10684976
 TITLE: Cloning and characterization of additional members of the
 G protein-coupled receptor family.
 AUTHOR: Lee D K; Lynch K R; Nguyen T; Im D S; Cheng R; Saldivia V
 B R; Liu Y; Liu I S; Heng H H; Seeman P; George S R; O'Dowd
 F; Marchese A
 CORPORATE SOURCE: Department of Pharmacology, University of Toronto, Medical
 Sciences Building, Toronto, Ont., Canada.
 CONTRACT NUMBER: R01 GM52722 (NIGMS)
 SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (2000 Feb 29) 1490 (3)
 311-23.
 Journal code: 0217513. ISSN: 0006-3002.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF112460; GENBANK-AF112462; GENBANK-AF208288
 ENTRY MONTH: 200006
 ENTRY DATE: Entered STN: 20000616
 Last Updated on STN: 20000616
 Entered Medline: 20000606

L8 ANSWER 140 OF 355 MEDLINE DUPLICATE 91
 ACCESSION NUMBER: 2001027156 MEDLINE
 DOCUMENT NUMBER: 20453189 PubMed ID: 10995571
 TITLE: Identification of BPESC1, a novel gene disrupted by a
 a balanced chromosomal translocation, t(3;4)(q23;p15.2), in
 patient with BPES.
 AUTHOR: De Baere E; Fukushima Y; Small K; Udar N; Van Camp G;
 Verhoeven K; Palotie A; De Paepe A; Messiaen L
 CORPORATE SOURCE: Department of Medical Genetics, Ghent University Hospital,
 Ghent, B-9000, Belgium.
 CONTRACT NUMBER: RO-1 EY11645 (NEI)
 SOURCE: GENOMICS, (2000 Sep 15) 68 (3) 296-304.

PUB. COUNTRY: Journal code: 8800135. ISSN: 0888-7543.
United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF196864; GENBANK-AF196865
ENTRY MONTH: 200011
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001116

L8 ANSWER 141 OF 355 MEDLINE DUPLICATE 92
ACCESSION NUMBER: 2001181863 MEDLINE
DOCUMENT NUMBER: 21098486 PubMed ID: 11173868
TITLE: EST mining of the UniGene dataset to identify
retina-specific genes.
AUTHOR: Stohr H; Mah N; Schulz H L; Gehrig A; Frohlich S; Weber B
H
CORPORATE SOURCE: Institut fur Humangenetik, Biozentrum, Universitat
Wurzburg, Wurzburg , Germany.
SOURCE: CYTOGENETICS AND CELL GENETICS, (2000) 91 (1-4) 267-77.
Journal code: 0367735. ISSN: 0301-0171.
PUB. COUNTRY: Switzerland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF295725; GENBANK-AF295730
ENTRY MONTH: 200103
ENTRY DATE: Entered STN: 20010404
Last Updated on STN: 20020125
Entered Medline: 20010329

L8 ANSWER 142 OF 355 MEDLINE DUPLICATE 93
ACCESSION NUMBER: 2001076993 MEDLINE
DOCUMENT NUMBER: 20510011 PubMed ID: 11054555
TITLE: Human allantoicase gene: cDNA cloning, genomic
organization
and chromosome localization.
AUTHOR: Vigetti D; Monetti C; Acquati F; Taramelli R; Bernardini G
CORPORATE SOURCE: Dipartimento di Biologia Strutturale e Funzionale,
Universita degli Studi dell'Insubria, Via J. H. Dunant 3,
I-21100, Varese, Italy.
SOURCE: GENE, (2000 Oct 3) 256 (1-2) 253-60.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF215924
ENTRY MONTH: 200101
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010111

L8 ANSWER 143 OF 355 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI
ACCESSION NUMBER: 2000-06347 BIOTECHDS
TITLE: Analysis of large gene databases for discovery of novel
therapeutic agents;
e.g. cathepsin-K, lipoprotein-associated phospholipase,
and G-protein coupled receptor
AUTHOR: Browne M J

CORPORATE SOURCE: SK-Beecham
LOCATION: SmithKline Beecham, New Frontiers Science Park, Third Avenue
Harlow, Essex CM19 5AW, UK.
SOURCE: J.Biotechnol.; (2000) 78, 3, 247-50
CODEN: JBITD4
ISSN: 0168-1656
DOCUMENT TYPE: Journal
LANGUAGE: English

L8 ANSWER 144 OF 355 MEDLINE DUPLICATE 94
ACCESSION NUMBER: 2000149846 MEDLINE
DOCUMENT NUMBER: 20149846 PubMed ID: 10684970
TITLE: Expression and characterization of the human mitochondrial
leucyl-tRNA synthetase.
AUTHOR: Bullard J M; Cai Y C; Spremulli L L
CORPORATE SOURCE: Department of Chemistry, University of North Carolina,
Chapel Hill, NC 27599-3290, USA.
CONTRACT NUMBER: GM19117 (NIGMS)
GM32734 (NIGMS)
SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (2000 Feb 29) 1490 (3)
245-58.
Journal code: 0217513. ISSN: 0006-3002.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200006
ENTRY DATE: Entered STN: 20000616
Last Updated on STN: 20000616
Entered Medline: 20000606

L8 ANSWER 145 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:311511 BIOSIS
DOCUMENT NUMBER: PREV200100311511
TITLE: Two unique genes cloned from differentially expressed ESTs
after induction of K562 cells with sodium butyrate.
AUTHOR(S): Mitchell, T. (1); Plonczynski, M.; Hardy, C. L.; Safaya,
S.; Steinberg, M. H.
CORPORATE SOURCE: (1) Pediatric Hematology/Oncology, University of
Mississippi Medical Center, Jackson, MS USA
SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 1, pp.
235a. print.
Meeting Info.: 42nd Annual Meeting of the American Society
of Hematology San Francisco, California, USA December
01-05, 2000 American Society of Hematology
. ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L8 ANSWER 146 OF 355 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI
ACCESSION NUMBER: 2000-06824 BIOTECHDS
TITLE: PPMdb: a plant plasma membrane database;
Arabidopsis thaliana proteome database; goals and
applications
AUTHOR: Sahnoun I; Dehais P; van Montagu M; Rossignol M; *Rouze P
CORPORATE SOURCE: Univ.Ghent; Flanders-Inst.Biotechnol.; INRA; CNRS; ENSA
LOCATION: Laboratoire Associe de l'Institut de la Recherche
Agronomique
(France), Department of Plant Genetics, University of Gent,
K.L. Ledeganckstraat 35, B-9000 Gent, Belgium.

SOURCE: Email: pirou@gengenp.rug.ac.be
J.Biotechnol.; (2000) 78, 3, 235-46
CODEN: JBITD4
ISSN: 0168-1656
DOCUMENT TYPE: Journal
LANGUAGE: English

L8 ANSWER 147 OF 355 MEDLINE DUPLICATE 95
ACCESSION NUMBER: 2000166975 MEDLINE
DOCUMENT NUMBER: 20166975 PubMed ID: 10700458
TITLE: A novel PCR-based technique using expressed sequence tags
and gene homology for murine genetic mapping: localization
of the complement genes.
AUTHOR: Lawson P R; Reid K B
CORPORATE SOURCE: MRC Immunochemistry Unit, Department of Biochemistry,
South
Parks Road, Oxford University, Oxford OX1 3QU, UK.
SOURCE: INTERNATIONAL IMMUNOLOGY, (2000 Mar) 12 (3) 231-40.
Journal code: 8916182. ISSN: 0953-8178.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200005
ENTRY DATE: Entered STN: 20000512
Last Updated on STN: 20000512
Entered Medline: 20000501

L8 ANSWER 148 OF 355 MEDLINE DUPLICATE 96
ACCESSION NUMBER: 2000456215 MEDLINE
DOCUMENT NUMBER: 20392318 PubMed ID: 10932001
TITLE: Molecular cloning of a novel gene located on chromosome
3p25.3 and an analysis of its expression in nasopharyngeal
carcinoma.
AUTHOR: Xie Y; Deng L; Jiang N; Zhan F; Cao L; Qiu Y; Tang X; Li G
CORPORATE SOURCE: Cancer Research Institute, Hunan Medical University,
Changsha, Hunan, P. R. China.
SOURCE: CHUNG-HUA I HSUEH I CHUAN HSUEH TSA CHIH, (2000 Aug) 17
(4)
225-8.
Journal code: 9425197. ISSN: 1003-9406.
PUB. COUNTRY: China
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: Chinese
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200009
ENTRY DATE: Entered STN: 20001005
Last Updated on STN: 20001005
Entered Medline: 20000925

L8 ANSWER 149 OF 355 MEDLINE
ACCESSION NUMBER: 2001095154 MEDLINE
DOCUMENT NUMBER: 20363098 PubMed ID: 10907852
TITLE: Analysis of expressed sequence tags of flower buds in
Lotus
japonicus.
AUTHOR: Endo M; Kokubun T; Takahata Y; Higashitani A; Tabata S;
Watanabe M
CORPORATE SOURCE: Laboratory of Plant Breeding, Faculty of Agriculture,
Iwate
University, Ueda, Morioka, Japan.

SOURCE: DNA RESEARCH, (2000 Jun 30) 7 (3) 213-6.
Journal code: 9423827. ISSN: 1340-2838.
PUB. COUNTRY: Japan
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200102
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010201

L8 ANSWER 150 OF 355 MEDLINE DUPLICATE 97
ACCESSION NUMBER: 2001040426 MEDLINE
DOCUMENT NUMBER: 20435298 PubMed ID: 10978524
TITLE: Murine cDNA encoding a novel type I HSP40/DNAJ homolog,
mmDjA4(1).
AUTHOR: Hata M; Ohtsuka K
CORPORATE SOURCE: Cell Stress Biology Research Group, Aichi Cancer Center
Research Institute, Chikusa-ku, 464-8681, Nagoya, Japan.
SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (2000 Sep 7) 1493 (1-2)
208-10.
Journal code: 0217513. ISSN: 0006-3002.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB032401
ENTRY MONTH: 200012
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001207

L8 ANSWER 151 OF 355 MEDLINE DUPLICATE 98
ACCESSION NUMBER: 2001012409 MEDLINE
DOCUMENT NUMBER: 20461778 PubMed ID: 10858550
TITLE: Cloning, expression and functional characterization of rat
napsin.
AUTHOR: Schauer-Vukasinovic V; Wright M B; Breu V; Giller T
CORPORATE SOURCE: F. Hoffmann-La Roche Ltd., Pharma Division, Preclinical
Research, Grenzacherstrasse 124, CH-4070 Basel,
Switzerland.
SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (2000 Jun 21) 1492 (1)
207-10.
Journal code: 0217513. ISSN: 0006-3002.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200010
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001031

L8 ANSWER 152 OF 355 MEDLINE DUPLICATE 99
ACCESSION NUMBER: 2000397938 MEDLINE
DOCUMENT NUMBER: 20299143 PubMed ID: 10837915
TITLE: Molecular cloning and characterisation of GPR74 a novel
G-protein coupled receptor closest related to the
Y-receptor family.
AUTHOR: Parker R M; Copeland N G; Eyre H J; Liu M; Gilbert D J;
Crawford J; Couzens M; Sutherland G R; Jenkins N A; Herzog

CORPORATE SOURCE: H
Garvan Institute of Medical Research, Neurobiology
Program,
St. Vincent's Hospital, 384 Victoria Street, Darlinghurst,
NSW 2010, Sydney, Australia.
SOURCE: BRAIN RESEARCH. MOLECULAR BRAIN RESEARCH, (2000 May 5) 77
(2) 199-208.
Journal code: 8908640. ISSN: 0169-328X.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200008
ENTRY DATE: Entered STN: 20000824
Last Updated on STN: 20000824
Entered Medline: 20000811

L8 ANSWER 153 OF 355 LIFESCI COPYRIGHT 2002 CSA
ACCESSION NUMBER: 2001:38412 LIFESCI
TITLE: Mass Spectrometry in Protein Studies from Genome to
Function
AUTHOR: Roepstorff, P.
CORPORATE SOURCE: Department of Molecular Biology, Odense University, DK
5230
Odense M, Denmark
SOURCE: Biotechnologia Aplicada [Biotechnol. Apl.], (20000900) vol.
17, no. 3, p. 194.
ISSN: 0864-4551.
DOCUMENT TYPE: Journal
FILE SEGMENT: W3
LANGUAGE: English

L8 ANSWER 154 OF 355 MEDLINE DUPLICATE 100
ACCESSION NUMBER: 2000184737 MEDLINE
DOCUMENT NUMBER: 20184737 PubMed ID: 10721712
TITLE: Cloning and characterization of a novel histone
acetyltransferase homologue from the protozoan parasite
Toxoplasma gondii reveals a distinct GCN5 family member.
AUTHOR: Sullivan W J Jr; Smith C K 2nd
CORPORATE SOURCE: Animal Science Discovery Research, Elanco Animal Health,
Greenfield, IN 46140, USA.. sullivan_william_j@lilly.com
SOURCE: GENE, (2000 Jan 25) 242 (1-2) 193-200.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF197953
ENTRY MONTH: 200004
ENTRY DATE: Entered STN: 20000413
Last Updated on STN: 20000413
Entered Medline: 20000403

L8 ANSWER 155 OF 355 MEDLINE DUPLICATE 101
ACCESSION NUMBER: 2000396058 MEDLINE
DOCUMENT NUMBER: 20318620 PubMed ID: 10860663
TITLE: Mouse RNA helicase II/Gu: cDNA and genomic sequences,
chromosomal localization, and regulation of expression.
AUTHOR: Valdez B C; Wang W
CORPORATE SOURCE: Department of Pharmacology, Baylor College of Medicine,
One

Baylor Plaza, Houston, Texas, 77030, USA..
bvaldez@bcm.tmc.edu
CONTRACT NUMBER: DK52341 (NIDDK)
SOURCE: GENOMICS, (2000 Jun 1) 66 (2) 184-94.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF159131; GENBANK-AF220365
ENTRY MONTH: 200008
ENTRY DATE: Entered STN: 20000824
Last Updated on STN: 20000824
Entered Medline: 20000811

L8 ANSWER 156 OF 355 MEDLINE DUPLICATE 102
ACCESSION NUMBER: 2000467360 MEDLINE
DOCUMENT NUMBER: 20473755 PubMed ID: 11015613
TITLE: Large-scale analysis of gene expression changes during
acute and chronic exposure to [Delta]9-THC in rats.
AUTHOR: Kittler J T; Grigorenko E V; Clayton C; Zhuang S Y; Bunday
S C; Trower M M; Wallace D; Hampson R; Deadwyler S
CORPORATE SOURCE: University College of London, WC1E6BT London, UK.
SOURCE: PHYSIOLOGICAL GENOMICS, (2000 Sep 8) 3 (3) 175-85.
Journal code: 100894125. ISSN: 1094-8341.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200103
ENTRY DATE: Entered STN: 20010404
Last Updated on STN: 20010404
Entered Medline: 20010308

L8 ANSWER 157 OF 355 MEDLINE
ACCESSION NUMBER: 2001095149 MEDLINE
DOCUMENT NUMBER: 20363093 PubMed ID: 10907847
TITLE: A large scale analysis of cDNA in Arabidopsis thaliana:
generation of 12,028 non-redundant expressed sequence tags
from normalized and size-selected cDNA libraries.
AUTHOR: Asamizu E; Nakamura Y; Sato S; Tabata S
CORPORATE SOURCE: Kazusa DNA Research Institute, Kisarazu, Chiba, Japan.
SOURCE: DNA RESEARCH, (2000 Jun 30) 7 (3) 175-80.
Journal code: 9423827. ISSN: 1340-2838.
PUB. COUNTRY: Japan
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB038710; GENBANK-AB038711; GENBANK-AB038712;
GENBANK-AB038713; GENBANK-AB038714; GENBANK-AB038715;
GENBANK-AB038716; GENBANK-AB038717; GENBANK-AB038718;
GENBANK-AB038719; GENBANK-AB038720; GENBANK-AB038721;
GENBANK-AB038722; GENBANK-AB038723; GENBANK-AB038724;
GENBANK-AB038725; GENBANK-AB038726; GENBANK-AV439465;
GENBANK-AV439466; GENBANK-AV439467; GENBANK-AV439468;
GENBANK-AV439469; GENBANK-AV439470; GENBANK-AV439471;
GENBANK-AV439472; GENBANK-AV439473; GENBANK-AV439474;
GENBANK-AV439475; GENBANK-AV439476; GENBANK-AV439477; +
ENTRY MONTH: 200102
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322

Entered Medline: 20010201

L8 ANSWER 158 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:37750 BIOSIS

DOCUMENT NUMBER: PREV200100037750

TITLE: Expressed sequence tags of young floral buds and characterization of a bud-preferential lectin-like cDNA from Pharbitis nil.

AUTHOR(S): Kim, Soo-Jin; Kim, Seong-Ryong (1)

CORPORATE SOURCE: (1) Department of Life Science, Sogang University, Seoul, 121-742: sungkim@ccs.sogang.ac.kr South Korea

SOURCE: Journal of Plant Biology, (September, 2000) Vol. 43, No. 3,

pp. 171-178. print.

ISSN: 1226-9239.

DOCUMENT TYPE: Article

LANGUAGE: English

SUMMARY LANGUAGE: English

L8 ANSWER 159 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:299307 BIOSIS

DOCUMENT NUMBER: PREV200100299307

TITLE: Overexpression of ribosomal proteins in chronic lymphocytic

leukemia identified by subtractive hybridization.

AUTHOR(S): Witzens, Mathias (1); Krackhardt, Angela M. (1); Harig, Sabine (1); Donovan, John W. (1); Gribben, John G. (1)

CORPORATE SOURCE: (1) Adult Oncology, Dana-Farber Cancer Institute, Boston, MA USA

SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 2, pp. 168b. print.

Meeting Info.: 42nd Annual Meeting of the American Society of Hematology San Francisco, California, USA December 01-05, 2000 American Society of Hematology . ISSN: 0006-4971.

DOCUMENT TYPE: Conference

LANGUAGE: English

SUMMARY LANGUAGE: English

L8 ANSWER 160 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:37441 BIOSIS

DOCUMENT NUMBER: PREV200100037441

TITLE: Arabidopsis thaliana cytidine deaminase 1 shows more similarity to prokaryotic enzymes than to eukaryotic enzymes.

AUTHOR(S): Kafer, Chris; Thornburg, Robert W. (1)

CORPORATE SOURCE: (1) Department of Biochemistry, Biophysics, and Molecular Biology, Iowa State University, 2212 Molecular Biology Building, Ames, IA, 50011: thorn@iastate.edu USA

SOURCE: Journal of Plant Biology, (September, 2000) Vol. 43, No. 3,

pp. 162-170. print.

ISSN: 1226-9239.

DOCUMENT TYPE: Article

LANGUAGE: English

SUMMARY LANGUAGE: English

L8 ANSWER 161 OF 355 MEDLINE

DUPLICATE 103

ACCESSION NUMBER: 2000069356 MEDLINE

DOCUMENT NUMBER: 20069356 PubMed ID: 10601861

TITLE: Characterization of a sulfurtransferase from Arabidopsis

thaliana.
 AUTHOR: Papenbrock J; Schmidt A
 CORPORATE SOURCE: Institute for Botany, University of Hannover, Germany..
 Jutta.Papenbrock@mbox.botanik.uni-hannover.de
 SOURCE: EUROPEAN JOURNAL OF BIOCHEMISTRY, (2000 Jan) 267 (1)
 145-54.
 Journal code: 0107600. ISSN: 0014-2956.
 PUB. COUNTRY: GERMANY: Germany, Federal Republic of
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AJ131404
 ENTRY MONTH: 200002
 ENTRY DATE: Entered STN: 20000229
 Last Updated on STN: 20000229
 Entered Medline: 20000215

L8 ANSWER 162 OF 355 MEDLINE DUPLICATE 104
 ACCESSION NUMBER: 2000400695 MEDLINE
 DOCUMENT NUMBER: 20371174 PubMed ID: 10908795
 TITLE: High-throughput protein expression of cDNA products as a
 tool in functional genomics.
 AUTHOR: Larsson M; Graslund S; Yuan L; Brundell E; Uhlen M; Hoog
 C;
 Stahl S
 CORPORATE SOURCE: Department of Biotechnology, Royal Institute of
 Technology,
 S-100 44, Stockholm, Sweden.
 SOURCE: JOURNAL OF BIOTECHNOLOGY, (2000 Jun 23) 80 (2) 143-57.
 Journal code: 8411927. ISSN: 0168-1656.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200008
 ENTRY DATE: Entered STN: 20000901
 Last Updated on STN: 20000901
 Entered Medline: 20000824

L8 ANSWER 163 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 2001:290176 BIOSIS
 DOCUMENT NUMBER: PREV200100290176
 TITLE: Specific expression of a novel cytokine-like gene in human
 CD34+ cells.
 AUTHOR(S): Ye, Zhaohui (1); Sung, Young Kwan (1); Cheng, Linzhao (1)
 CORPORATE SOURCE: (1) Johns Hopkins Oncology Center, Baltimore, MD USA
 SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 2, pp.
 142b. print.
 Meeting Info.: 42nd Annual Meeting of the American Society
 of Hematology San Francisco, California, USA December
 01-05, 2000 American Society of Hematology
 . ISSN: 0006-4971.
 DOCUMENT TYPE: Conference
 LANGUAGE: English
 SUMMARY LANGUAGE: English

L8 ANSWER 164 OF 355 MEDLINE DUPLICATE 105
 ACCESSION NUMBER: 2000247253 MEDLINE
 DOCUMENT NUMBER: 20247253 PubMed ID: 10783261
 TITLE: Evidence for a Niemann-pick C (NPC) gene family:
 identification and characterization of NPC1L1.

AUTHOR: Davies J P; Levy B; Ioannou Y A
 CORPORATE SOURCE: Department of Human Genetics, Mount Sinai School of
 Medicine, New York, New York, 10029, USA.
 SOURCE: GENOMICS, (2000 Apr 15) 65 (2) 137-45.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF192522; GENBANK-AF192523
 ENTRY MONTH: 200007
 ENTRY DATE: Entered STN: 20000728
 Last Updated on STN: 20000728
 Entered Medline: 20000720

L8 ANSWER 165 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 2001:290157 BIOSIS
 DOCUMENT NUMBER: PREV200100290157
 TITLE: Cloning and functional analysis of cDNAs with entire open
 reading frame for 300 previously undefined genes expressed
 in CD34+ hematopoietic stem/progenitor cells.
 AUTHOR(S): Zhang, Q. H. (1); Ye, M. (1); Wu, X. Y. (1); Ren, S. X.
 (1); Chen, S. J. (1); Chen, Z. (1)
 CORPORATE SOURCE: (1) Shanghai Institute of Hematology, Rui Jin Hospital,
 Shanghai Second Medical University, Shanghai China
 SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 2, pp.
 130b. print.
 Meeting Info.: 42nd Annual Meeting of the American Society
 of Hematology San Francisco, California, USA December
 01-05, 2000 American Society of Hematology
 . ISSN: 0006-4971.
 DOCUMENT TYPE: Conference
 LANGUAGE: English
 SUMMARY LANGUAGE: English

L8 ANSWER 166 OF 355 MEDLINE
 ACCESSION NUMBER: 2000433820 MEDLINE
 DOCUMENT NUMBER: 20277479 PubMed ID: 10819328
 TITLE: Generation of 7137 non-redundant expressed sequence tags
 from a legume, Lotus japonicus.
 AUTHOR: Asamizu E; Nakamura Y; Sato S; Tabata S
 CORPORATE SOURCE: Kazusa DNA Research Institute, Kisarazu, Chiba, Japan.
 SOURCE: DNA RESEARCH, (2000 Apr 28) 7 (2) 127-30.
 Journal code: 9423827. ISSN: 1340-2838.
 PUB. COUNTRY: Japan
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AV406328; GENBANK-AV406329; GENBANK-AV406330;
 GENBANK-AV406331; GENBANK-AV406332; GENBANK-AV406333;
 GENBANK-AV406334; GENBANK-AV406335; GENBANK-AV406336;
 GENBANK-AV406337; GENBANK-AV406338; GENBANK-AV406339;
 GENBANK-AV406340; GENBANK-AV406341; GENBANK-AV406342;
 GENBANK-AV406343; GENBANK-AV406344; GENBANK-AV406345;
 GENBANK-AV406346; GENBANK-AV406347; GENBANK-AV406348;
 GENBANK-AV406349; GENBANK-AV406350; GENBANK-AV406351;
 GENBANK-AV406352; GENBANK-AV406353; GENBANK-AV406354;
 GENBANK-AV406355; GENBANK-AV406356; GENBANK-AV406357; +
 ENTRY MONTH: 200009
 ENTRY DATE: Entered STN: 20000928
 Last Updated on STN: 20000928

Entered Medline: 20000921

L8 ANSWER 167 OF 355 MEDLINE
ACCESSION NUMBER: 2000123885 MEDLINE
DOCUMENT NUMBER: 20123885 PubMed ID: 10631317
TITLE: Caveolin-1 isoforms are encoded by distinct mRNAs.
Identification Of mouse caveolin-1 mRNA variants caused by
alternative transcription initiation and splicing.
AUTHOR: Kogo H; Fujimoto T
CORPORATE SOURCE: Department of Anatomy and Molecular Cell Biology, Nagoya
University School of Medicine, Showa-ku, Nagoya, Japan..
hkogo@med.nagoya-u.ac.jp
SOURCE: FEBS LETTERS, (2000 Jan 14) 465 (2-3) 119-23.
Journal code: 0155157. ISSN: 0014-5793.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200002
ENTRY DATE: Entered STN: 20000309
Last Updated on STN: 20000309
Entered Medline: 20000218

L8 ANSWER 168 OF 355 MEDLINE DUPLICATE 106
ACCESSION NUMBER: 2000247250 MEDLINE
DOCUMENT NUMBER: 20247250 PubMed ID: 10783258
TITLE: Molecular cloning of a novel NF2/ERM/4.1 superfamily gene,
ehm2, that is expressed in high-metastatic K1735 murine
melanoma cells.
AUTHOR: Shimizu K; Nagamachi Y; Tani M; Kimura K; Shiroishi T;
Wakana S; Yokota J
CORPORATE SOURCE: Biology Division, National Cancer Center Research
Institute, 1-1, Tsukiji 5-chome, Chuo-ku, Tokyo, 104-0045,
Japan.
SOURCE: GENOMICS, (2000 Apr 15) 65 (2) 113-20.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB032179; GENBANK-AB032366
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 20000728
Last Updated on STN: 20000728
Entered Medline: 20000720

L8 ANSWER 169 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2000:376622 BIOSIS
DOCUMENT NUMBER: PREV200000376622
TITLE: Analyses of expressed sequence tags of anther and
anther-specific cDNA clones in Nicotiana tabacum.
AUTHOR(S): Choi, Goh; Hong, Choo Bong (1)
CORPORATE SOURCE: (1) Institute of Molecular Biology and Genetics, Seoul
National University, Seoul, 151-742 South Korea
SOURCE: Journal of Plant Biology, (June, 2000) Vol. 43, No. 2, pp.
107-113. print.
ISSN: 1226-9239.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

L8 ANSWER 170 OF 355 MEDLINE
 ACCESSION NUMBER: 2001123002 MEDLINE
 DOCUMENT NUMBER: 21023480 PubMed ID: 11147971
 TITLE: Mammalian HSP40/DNAJ homologs: cloning of novel cDNAs and
 a proposal for their classification and nomenclature.
 AUTHOR: Ohtsuka K; Hata M
 CORPORATE SOURCE: Laboratory of Experimental Radiology, Aichi Cancer Center
 Research Institute, Nagoya, Japan.. kohtsuka@aichi-
 cc.pref.aichi.jp
 SOURCE: CELL STRESS AND CHAPERONES, (2000 Apr) 5 (2) 98-112.
 Journal code: 9610925. ISSN: 1355-8145.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200102
 ENTRY DATE: Entered STN: 20010322
 Last Updated on STN: 20010322
 Entered Medline: 20010222

L8 ANSWER 171 OF 355 MEDLINE DUPLICATE 107
 ACCESSION NUMBER: 2001074203 MEDLINE
 DOCUMENT NUMBER: 20541714 PubMed ID: 11087666
 TITLE: Identification of KLF13 and KLF14 (SP6), novel members of
 the SP/XKLF transcription factor family.
 AUTHOR: Scohy S; Gabant P; Van Reeth T; Hertveldt V; Dreze P L;
 Van Vooren P; Riviere M; Szpirer J; Szpirer C
 CORPORATE SOURCE: Universite Libre de Bruxelles, IBMM, Rue Professeurs
 Jeener & Brachet, 12, Gosselies, B-6041, Belgium.
 SOURCE: GENOMICS, (2000 Nov 15) 70 (1) 93-101.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AJ275987; GENBANK-AJ275988; GENBANK-AJ275989
 ENTRY MONTH: 200101
 ENTRY DATE: Entered STN: 20010322
 Last Updated on STN: 20010322
 Entered Medline: 20010104

L8 ANSWER 172 OF 355 MEDLINE DUPLICATE 108
 ACCESSION NUMBER: 2000409153 MEDLINE
 DOCUMENT NUMBER: 20239719 PubMed ID: 10775800
 TITLE: Identification of human estrogen-inducible transcripts
 that potentially mediate the apoptotic response in breast
 cancer.
 AUTHOR: Szelei J; Soto A M; Geck P; Desronvil M; Prechtel N V;
 Weill B C; Sonnenschein C
 CORPORATE SOURCE: Department of Anatomy and Cell Biology, Tufts University
 School of Medicine, 136 Harrison Avenue, Boston, MA 02111,
 USA.
 CONTRACT NUMBER: AG13807 (NIA)
 CA13410 (NCI)
 CA55574 (NCI)
 +

SOURCE: JOURNAL OF STEROID BIOCHEMISTRY AND MOLECULAR BIOLOGY,
(2000 Mar) 72 (3-4) 89-102.
Journal code: 9015483. ISSN: 0960-0760.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200008
ENTRY DATE: Entered STN: 20000907
Last Updated on STN: 20000907
Entered Medline: 20000825

L8 ANSWER 173 OF 355 MEDLINE DUPLICATE 109
ACCESSION NUMBER: 2000334233 MEDLINE
DOCUMENT NUMBER: 20334233 PubMed ID: 10873568
TITLE: Characterization of novel and identified genes in guinea
pig organ of corti.
AUTHOR: Oshima T; Nakajima T; Wada H; Ikeda K; Takasaka T
CORPORATE SOURCE: Department of Otorhinolaryngology, Tohoku University
School
of Medicine, 1-1 Seiryō-machi, Aoba-ku, Sendai, 980-8574,
Japan.. oshima@orl.med.tohoku.ac.jp
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2000
Jun 24) 273 (1) 84-9.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AU081352; GENBANK-AU081353; GENBANK-AU081354;
GENBANK-AU081355; GENBANK-AU081356; GENBANK-AU081357;
GENBANK-AU081358; GENBANK-AU081359; GENBANK-AU081360;
GENBANK-AU081361; GENBANK-AU081362; GENBANK-AU081363;
GENBANK-AU081364; GENBANK-AU081365; GENBANK-AU081366;
GENBANK-AU081367; GENBANK-AU081368; GENBANK-AU081369;
GENBANK-AU081370; GENBANK-AU081371; GENBANK-AU081372;
GENBANK-AU081373; GENBANK-AU081374; GENBANK-AU081375;
GENBANK-AU081376; GENBANK-AU081377; GENBANK-AU081378;
GENBANK-AU081379; GENBANK-AU081380; GENBANK-AU081381; +
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 20000810
Last Updated on STN: 20000810
Entered Medline: 20000727

L8 ANSWER 174 OF 355 MEDLINE DUPLICATE 110
ACCESSION NUMBER: 2001012874 MEDLINE
DOCUMENT NUMBER: 20374017 PubMed ID: 10919377
TITLE: Classification of sequences expressed during the
primordial
and basidiome stages of the cultivated mushroom *Agaricus
bisporus*.
AUTHOR: Ospina-Giraldo M D; Collopy P D; Romaine C P; Royse D J
CORPORATE SOURCE: Department of Plant Pathology, The Pennsylvania State
University, University Park 16802, USA.
SOURCE: FUNGAL GENETICS AND BIOLOGY, (2000 Mar) 29 (2) 81-94.
Journal code: 9607601. ISSN: 1087-1845.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200010

ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001031

L8 ANSWER 175 OF 355 LIFESCI COPYRIGHT 2002 CSA
ACCESSION NUMBER: 2000:47805 LIFESCI
TITLE: Molecular characterization of human and murine C11orf5, a
new member of the FAUNA gene cluster
AUTHOR: Lemmens, I.H.; Farnebo, F.; Piehl, F.; Merregaert, J.; Van
de Ven, W.J.M.; Larsson, C.; Kas, K.
CORPORATE SOURCE: Laboratory for Molecular Oncology, Center for Human
Genetics, University of Leuven & Flanders Interuniversity
Institute for Biotechnology, Center for Human Genetics, KU
Leuven, Herestraat 49, B-3000 Leuven, Belgium
SOURCE: Mammalian Genome [Mamm. Genome], (20000100) vol. 11, no.
1,
pp. 78-80.
ISSN: 0938-8990.
DOCUMENT TYPE: Journal
FILE SEGMENT: G
LANGUAGE: English
SUMMARY LANGUAGE: English

L8 ANSWER 176 OF 355 MEDLINE
ACCESSION NUMBER: 2001418681 MEDLINE
DOCUMENT NUMBER: 21360613 PubMed ID: 11466975
TITLE: Searching the expressed sequence tag (EST) databases:
panning for genes.
AUTHOR: Jongeneel C V
CORPORATE SOURCE: Office of Information Technology, Ludwig Institute for
Cancer Research and Swiss Institute of Bioinformatics,
chemin des Boveresses 155, CH-1066 Epalinges,
Switzerland..
Victor.Jongeneel@licr.org
SOURCE: Brief Bioinform, (2000 Feb) 1 (1) 76-92.
Journal code: 100912837. ISSN: 1467-5463.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010827
Last Updated on STN: 20010827
Entered Medline: 20010823

L8 ANSWER 177 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:307604 BIOSIS
DOCUMENT NUMBER: PREV200100307604
TITLE: Identification of genes responsible for bone
differentiation from human bone marrow derived multipotent
adult stem cells (MASC.
AUTHOR(S): Qi, Huilin (1); Aguiar, Dean (1); Verfaillie, Catherine M.
(1)
CORPORATE SOURCE: (1) Stem Cell Institute, Univ. of Minnesota, Minneapolis,
MN USA
SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 1, pp.
70a-71a. print.
Meeting Info.: 42nd Annual Meeting of the American Society
of Hematology San Francisco, California, USA December
01-05, 2000 American Society of Hematology
. ISSN: 0006-4971.

DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L8 ANSWER 178 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:514713 BIOSIS
DOCUMENT NUMBER: PREV200100514713
TITLE: Analysis of the filarial parasite *Brugia malayi* adult male stage EST clusters for novel gene identification.
AUTHOR(S): Kamal, Ibrahim H. (1); Ganatra, Mehul B. (1); Foster, Jeremy M. (1); Moran, Laurie S. (1); Ware, Jennifer L. (1);

Guiliano, David; Blaxter, Mark L.; Helmy, Hanan; Slatk, Barton E. (1); Ramzy, Reda M.
CORPORATE SOURCE: (1) New England Biolabs, Inc., Beverly, MA USA
SOURCE: International Genome Sequencing and Analysis Conference, (2000) Vol. 12, pp. 70-71. print.

Meeting Info.: 12th International Genome Sequencing and Analysis Conference Miami Beach, Florida, USA September 12-15, 2000

DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L8 ANSWER 179 OF 355 MEDLINE DUPLICATE 111

ACCESSION NUMBER: 2000163500 MEDLINE
DOCUMENT NUMBER: 20163500 PubMed ID: 10701565
TITLE: Analysis of messages expressed by *Echinostoma paraense* miracidia and sporocysts, obtained by random EST sequencing.
AUTHOR: Adema C M; Leonard P M; DeJong R J; Day H L; Edwards D J; Burgett G; Hertel L A; Loker E S
CORPORATE SOURCE: Department of Biology, University of New Mexico, Albuquerque 87131, USA.
CONTRACT NUMBER: AI24340 (NIAID)
SOURCE: JOURNAL OF PARASITOLOGY, (2000 Feb) 86 (1) 60-5.
Journal code: 7803124. ISSN: 0022-3395.
PUB. COUNTRY: United States
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200003
ENTRY DATE: Entered STN: 20000327
Last Updated on STN: 20000327
Entered Medline: 20000313

L8 ANSWER 180 OF 355 MEDLINE DUPLICATE 112

ACCESSION NUMBER: 2000232467 MEDLINE
DOCUMENT NUMBER: 20232467 PubMed ID: 10769634
TITLE: Relevant genomics of neurotensin receptor in cancer.
AUTHOR: Elek J; Pinzon W; Park K H; Narayanan R
CORPORATE SOURCE: Center for Molecular Biology and Biotechnology, Florida Atlantic University, Boca Raton 33431, USA.
SOURCE: ANTICANCER RESEARCH, (2000 Jan-Feb) 20 (1A) 53-8.
Journal code: 8102988. ISSN: 0250-7005.
PUB. COUNTRY: Greece
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200005
ENTRY DATE: Entered STN: 20000518

Last Updated on STN: 20000518
Entered Medline: 20000511

L8 ANSWER 181 OF 355 MEDLINE DUPLICATE 113
ACCESSION NUMBER: 2000267847 MEDLINE
DOCUMENT NUMBER: 20267847 PubMed ID: 10806350
TITLE: Functional characterization of a gene encoding a fourth
ATP
sulfurylase isoform from Arabidopsis thaliana.
AUTHOR: Hatzfeld Y; Lee S; Lee M; Leustek T; Saito K
CORPORATE SOURCE: Chiba University, Faculty of Pharmaceutical Sciences,
Laboratory of Molecular Biology and Biotechnology,
Yayoi-cho 1-33, Inage-ku, Japan.
SOURCE: GENE, (2000 May 2) 248 (1-2) 51-8.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF110407; GENBANK-AF198964; GENBANK-AJ012586;
GENBANK-U59737; GENBANK-U59738
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 20000714
Last Updated on STN: 20000714
Entered Medline: 20000706

L8 ANSWER 182 OF 355 MEDLINE DUPLICATE 114
ACCESSION NUMBER: 2000130112 MEDLINE
DOCUMENT NUMBER: 20130112 PubMed ID: 10662543
TITLE: A novel family of bromodomain genes.
AUTHOR: Jones M H; Hamana N; Nezu J i; Shimane M
CORPORATE SOURCE: Chugai Research Institute for Molecular Medicine, 153-2
Nagai, Niihari, Ibaraki, 300-4101, Japan.. mike@cimmed.com
SOURCE: GENOMICS, (2000 Jan 1) 63 (1) 40-5.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB032252; GENBANK-AB032253; GENBANK-AB032254;
GENBANK-AB032255
ENTRY MONTH: 200004
ENTRY DATE: Entered STN: 20000421
Last Updated on STN: 20000421
Entered Medline: 20000411

L8 ANSWER 183 OF 355 MEDLINE DUPLICATE 115
ACCESSION NUMBER: 2000163069 MEDLINE
DOCUMENT NUMBER: 20163069 PubMed ID: 10697961
TITLE: cDNA cloning, expression profile, and genomic structure of
human and mouse RNF10/Rnf 10 genes, encoding a novel RING
finger protein.
AUTHOR: Seki N; Hattori A; Sugano S; Muramatsu M; Saito T
CORPORATE SOURCE: National Institute of Radiological Sciences, Chiba,
Japan.
SOURCE: JOURNAL OF HUMAN GENETICS, (2000) 45 (1) 38-42.
Journal code: 9808008. ISSN: 1434-5161.
PUB. COUNTRY: Japan
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AB026621; GENBANK-AB027196
ENTRY MONTH: 200004
ENTRY DATE: Entered STN: 20000427
Last Updated on STN: 20000427
Entered Medline: 20000418

L8 ANSWER 184 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:223870 BIOSIS
DOCUMENT NUMBER: PREV200200223870
TITLE: Cloning and nephron localization of a rabbit kidney KCl cotransporter, KCC4.
AUTHOR(S): Velazquez, Heino (1); Silva, Teresa C.; Andujar, Eleanor
CORPORATE SOURCE: (1) Research, VA Connecticut Healthcare System and Yale University, New Haven, CT USA
SOURCE: Journal of the American Society of Nephrology, (September, 2000) Vol. 11, No. Program and Abstract Issue, pp. 38A.
<http://www.jasn.org/>. print.
Meeting Info.: 33rd Annual Meeting of the American Society of Nephrology and the 2000 Renal Week Toronto, Ontario, Canada October 10-16, 2000
ISSN: 1046-6673.
DOCUMENT TYPE: Conference
LANGUAGE: English

L8 ANSWER 185 OF 355 MEDLINE DUPLICATE 116
ACCESSION NUMBER: 2000412228 MEDLINE
DOCUMENT NUMBER: 20314386 PubMed ID: 10854696
TITLE: Mouse receptor-activity-modifying proteins 1, -2 and -3: amino acid sequence, expression and function.
AUTHOR: Husmann K; Sexton P M; Fischer J A; Born W
CORPORATE SOURCE: Research Laboratory for Calcium Metabolism, Departments of Orthopaedic Surgery and Medicine, Zurich, Switzerland..
khusmann@balgrist.unizh.ch
SOURCE: MOLECULAR AND CELLULAR ENDOCRINOLOGY, (2000 Apr 25) 162 (1-2) 35-43.
Journal code: 7500844. ISSN: 0303-7207.
PUB. COUNTRY: Ireland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200008
ENTRY DATE: Entered STN: 20000907
Last Updated on STN: 20000907
Entered Medline: 20000828

L8 ANSWER 186 OF 355 MEDLINE DUPLICATE 117
ACCESSION NUMBER: 2000130111 MEDLINE
DOCUMENT NUMBER: 20130111 PubMed ID: 10662542
TITLE: Identification and characterization of BPTF, a novel bromodomain transcription factor.
AUTHOR: Jones M H; Hamana N; Shimane M
CORPORATE SOURCE: Chugai Research Institute for Molecular Medicine, 153-2 Nagai, Niihari, Ibaraki, 300-4101, Japan.
SOURCE: GENOMICS, (2000 Jan 1) 63 (1) 35-9.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB032251
ENTRY MONTH: 200004

ENTRY DATE: Entered STN: 20000421
Last Updated on STN: 20000421
Entered Medline: 20000411

L8 ANSWER 187 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
DUPLICATE 118

ACCESSION NUMBER: 2000:478547 BIOSIS
DOCUMENT NUMBER: PREV200000478547
TITLE: Molecular cloning and characterization of a plant
homologue of the origin recognition complex 1 (ORC1.
AUTHOR(S): Kimura, Seisuke; Ishibashi, Toyotaka; Hatanaka, Masami;
Sakakibara, Yoshikiyo; Hashimoto, Junji; Sakaguchi, Kengo
(1)
CORPORATE SOURCE: (1) Department of Applied Biological Science, Faculty of
Science and Technology, Science University of Tokyo, 2641
Yamazaki, Noda-shi, Chiba-ken, 278-8510 Japan
SOURCE: Plant Science (Shannon), (September 8, 2000) Vol. 158, No.
1-2, pp. 33-39. print.
ISSN: 0168-9452.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

L8 ANSWER 188 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2002:223827 BIOSIS
DOCUMENT NUMBER: PREV200200223827
TITLE: Cloning and functional characterization of a cation-Cl
cotransporter interacting protein.
AUTHOR(S): Isenring, Paul (1); Gagnon, Edith (1); Caron, Luc (1)
CORPORATE SOURCE: (1) Groupe de Nephrologie de L'Hotel-Dieu de Quebec,
Departement de Medecine, Faculte de Medecine, Universite
Laval, Quebec, PQ Canada
SOURCE: Journal of the American Society of Nephrology, (September,
2000) Vol. 11, No. Program and Abstract Issue, pp.
30A-31A.
<http://www.jasn.org/>. print.
Meeting Info.: 33rd Annual Meeting of the American Society
of Nephrology and the 2000 Renal Week Toronto, Ontario,
Canada October 10-16, 2000
ISSN: 1046-6673.
DOCUMENT TYPE: Conference
LANGUAGE: English

L8 ANSWER 189 OF 355 MEDLINE

ACCESSION NUMBER: 2001700700 MEDLINE
DOCUMENT NUMBER: 21616802 PubMed ID: 11741232
TITLE: Human proton/oligopeptide transporter (POT) genes:
identification of putative human genes using
bioinformatics.
AUTHOR: Botka C W; Wittig T W; Graul R C; Nielsen C U; Higaka K;
Amidon G L; Sadee W
CORPORATE SOURCE: Department of Biopharmaceutical Sciences, University of
California San Francisco, San Francisco CA 94143-0446,
USA.
SOURCE: AAPS PharmSci, (2000) 2 (2) E16.
Journal code: 100897065. ISSN: 1522-1059.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals

ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20011220
Last Updated on STN: 20020208
Entered Medline: 20020207

L8 ANSWER 190 OF 355 MEDLINE DUPLICATE 119
ACCESSION NUMBER: 2000183851 MEDLINE
DOCUMENT NUMBER: 20183851 PubMed ID: 10717299
TITLE: Preliminary profile of the *Cryptosporidium parvum* genome:
an expressed sequence tag and genome survey sequence
analysis.
AUTHOR: Strong W B; Nelson R G
CORPORATE SOURCE: Division of Infectious Diseases, San Francisco General
Hospital, San Francisco, CA, USA.
CONTRACT NUMBER: R0-1 AI42565 (NIAID)
U0-1 AI40319 (NIAID)
SOURCE: MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (2000 Mar 15) 107
(1) 1-32.
Journal code: 8006324. ISSN: 0166-6851.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AA167850; GENBANK-AA167851; GENBANK-AA167852;
GENBANK-AA167853; GENBANK-AA167854; GENBANK-AA167855;
GENBANK-AA167856; GENBANK-AA167857; GENBANK-AA167858;
GENBANK-AA167859; GENBANK-AA167860; GENBANK-AA167861;
GENBANK-AA167862; GENBANK-AA167863; GENBANK-AA167864;
GENBANK-AA167865; GENBANK-AA167866; GENBANK-AA167867;
GENBANK-AA167868; GENBANK-AA167869; GENBANK-AA167870;
GENBANK-AA167871; GENBANK-AA167872; GENBANK-AA167873;
GENBANK-AA167874; GENBANK-AA167875; GENBANK-AA167876;
GENBANK-AA167877; GENBANK-AA167878; GENBANK-AA167879; +
ENTRY MONTH: 200006
ENTRY DATE: Entered STN: 20000616
Last Updated on STN: 20000616
Entered Medline: 20000606

L8 ANSWER 191 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:88451 BIOSIS
DOCUMENT NUMBER: PREV200100088451
TITLE: Cloning and functional characterization of a novel
beta-adrenergic-like receptor from *Drosophila*
melanogaster.
AUTHOR(S): Yu, E. J.; Kennedy, K.; Chatwin, H. M.; Reale, V.; Evans,
P. D.
SOURCE: Society for Neuroscience Abstracts, (2000) Vol. 26, No.
1-2, pp. Abstract No.-343.7. print.
Meeting Info.: 30th Annual Meeting of the Society of
Neuroscience New Orleans, LA, USA November 04-09, 2000
Society for Neuroscience
. ISSN: 0190-5295.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L8 ANSWER 192 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:76253 BIOSIS
DOCUMENT NUMBER: PREV200100076253
TITLE: Characterization of a novel subgroup of putative seven
transmembrane receptors.

AUTHOR(S): Soderberg, C. (1); Lind, P.
CORPORATE SOURCE: (1) Pharmacia Corp., Uppsala Sweden
SOURCE: Society for Neuroscience Abstracts, (2000) Vol. 26, No. 1-2, pp. Abstract No.-140.2. print.
Meeting Info.: 30th Annual Meeting of the Society of Neuroscience New Orleans, LA, USA November 04-09, 2000
Society for Neuroscience
. ISSN: 0190-5295.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L8 ANSWER 193 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:80859 BIOSIS
DOCUMENT NUMBER: PREV200100080859
TITLE: Discovery of a novel small membrane protein, NID67, preferentially induced by NGF in PC12 cells.
AUTHOR(S): Vician, L. J. (1); Farias-Eisner, R.; Silver, A.; Herschman, H. R.
CORPORATE SOURCE: (1) UCLA, Los Angeles, CA USA
SOURCE: Society for Neuroscience Abstracts, (2000) Vol. 26, No. 1-2, pp. Abstract No.-208.7. print.
Meeting Info.: 30th Annual Meeting of the Society of Neuroscience New Orleans, LA, USA November 04-09, 2000
Society for Neuroscience
. ISSN: 0190-5295.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L8 ANSWER 194 OF 355 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI
ACCESSION NUMBER: 1999-12578 BIOTECHDS
TITLE: New collectin protein of human origin and DNA encoding it; for the treatment of bacterium and virus infection
AUTHOR: Wakamiya N
PATENT ASSIGNEE: Fuso-Pharm.
LOCATION: Osaka, Japan.
PATENT INFO: WO 9937767 29 Jul 1999
APPLICATION INFO: WO 1998-JP3328 24 Jul 1998
PRIORITY INFO: JP 1998-11281 23 Jan 1998
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 1999-458691 [38]

L8 ANSWER 195 OF 355 MEDLINE DUPLICATE 120
ACCESSION NUMBER: 1999415747 MEDLINE
DOCUMENT NUMBER: 99415747 PubMed ID: 10484776
TITLE: The gene encoding hydroxypyruvate reductase (GRHPR) is mutated in patients with primary hyperoxaluria type II.
COMMENT: Erratum in: Hum Mol Genet 1999 Dec;8(13):2574
AUTHOR: Cramer S D; Ferree P M; Lin K; Milliner D S; Holmes R P
CORPORATE SOURCE: Department of Cancer Biology, Wake Forest University School of Medicine, Winston-Salem, NC 27157, USA..
scramer@wfubmc.edu
CONTRACT NUMBER: R01-DK54468-01 (NIDDK)
SOURCE: HUMAN MOLECULAR GENETICS, (1999 Oct) 8 (11) 2063-9.
Journal code: 9208958. ISSN: 0964-6906.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English

FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF146018; GENBANK-AF146689; GENBANK-AL031180;
 GENBANK-D31857; GENBANK-D49432; GENBANK-P37666;
 GENBANK-T72836
 ENTRY MONTH: 199912
 ENTRY DATE: Entered STN: 20000113
 Last Updated on STN: 20000229
 Entered Medline: 19991216

L8 ANSWER 196 OF 355 MEDLINE DUPLICATE 121
 ACCESSION NUMBER: 2000428146 MEDLINE
 DOCUMENT NUMBER: 20416026 PubMed ID: 10961844
 TITLE: A survey of genes in Eimeria tenella merozoites by EST sequencing.
 AUTHOR: Wan K L; Chong S P; Ng S T; Shirley M W; Tomley F M; Jangi M S
 CORPORATE SOURCE: Centre for Gene Analysis and Technology, School of BioSciences and Biotechnology, Faculty of Science and Technology, Universiti Kebangsaan Malaysia, Selangor DE.. klwan@pkisc.cc.ukm.my
 SOURCE: INTERNATIONAL JOURNAL FOR PARASITOLOGY, (1999 Dec) 29 (12) 1885-92.
 Journal code: 0314024. ISSN: 0020-7519.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AI676260; GENBANK-AI676261; GENBANK-AI676262;
 GENBANK-AI676263; GENBANK-AI676264; GENBANK-AI676265;
 GENBANK-AI676266; GENBANK-AI676267; GENBANK-AI676268;
 GENBANK-AI676269; GENBANK-AI676270; GENBANK-AI676271;
 GENBANK-AI676272; GENBANK-AI676273; GENBANK-AI676274;
 GENBANK-AI676275; GENBANK-AI676276; GENBANK-AI676277;
 GENBANK-AI676278; GENBANK-AI676279; GENBANK-AI676280;
 GENBANK-AI676281; GENBANK-AI676282; GENBANK-AI676283;
 GENBANK-AI676284; GENBANK-AI676285; GENBANK-AI676286;
 GENBANK-AI676287; GENBANK-AI676288; GENBANK-AI676289; +
 ENTRY MONTH: 200009
 ENTRY DATE: Entered STN: 20000922
 Last Updated on STN: 20000922
 Entered Medline: 20000913

L8 ANSWER 197 OF 355 MEDLINE DUPLICATE 122
 ACCESSION NUMBER: 2000012750 MEDLINE
 DOCUMENT NUMBER: 20012750 PubMed ID: 10544010
 TITLE: Identification and gene structure of a novel human PLZF-related transcription factor gene, TZFP.
 AUTHOR: Lin W; Lai C H; Tang C J; Huang C J; Tang T K
 CORPORATE SOURCE: Institute of Biomedical Sciences, Academia Sinica, Taipei, 115, Taiwan.. wenlin@ibms.sinica.edu.tw
 SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1999 Nov 2) 264 (3) 789-95.
 Journal code: 0372516. ISSN: 0006-291X.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF130255
 ENTRY MONTH: 199912
 ENTRY DATE: Entered STN: 20000113
 Last Updated on STN: 20000113

Entered Medline: 19991222

L8 ANSWER 198 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
DUPLICATE 123

ACCESSION NUMBER: 2000:123037 BIOSIS
DOCUMENT NUMBER: PREV200000123037
TITLE: Transcript profiling in rice (*Oryza sativa* L.) seedlings
using serial analysis of gene expression (SAGE).
AUTHOR(S): Matsumura, Hideo (1); Nirasawa, Shizuko; Terauchi, Ryohei
CORPORATE SOURCE: (1) Iwate Biotechnology Research Center, Narita, Kitakami,
Iwate, 024-0003 Japan
SOURCE: Plant Journal, (Dec., 1999) Vol. 20, No. 6, pp. 719-726.
ISSN: 0960-7412.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

L8 ANSWER 199 OF 355 MEDLINE DUPLICATE 124

ACCESSION NUMBER: 1999262157 MEDLINE
DOCUMENT NUMBER: 99262157 PubMed ID: 10329445
TITLE: A family of mammalian proteins homologous to yeast
Sec24p.
AUTHOR: Tang B L; Kausalya J; Low D Y; Lock M L; Hong W
CORPORATE SOURCE: Membrane Biology Laboratory, Institute of Molecular and
Cell Biology, 30 Medical Drive, Singapore, 117609,
Republic
of Singapore.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1999
May 19) 258 (3) 679-84.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF130464
ENTRY MONTH: 199906
ENTRY DATE: Entered STN: 19990712
Last Updated on STN: 19990712
Entered Medline: 19990624

L8 ANSWER 200 OF 355 MEDLINE DUPLICATE 125

ACCESSION NUMBER: 1999360495 MEDLINE
DOCUMENT NUMBER: 99360495 PubMed ID: 10433113
TITLE: Recent advances on proteins of plant terminal membranes.
AUTHOR: Grignon C
CORPORATE SOURCE: Biochimie et Physiologie Moleculaire des Plantes,
Agro-M/Inra/CNRS-URA 2133/Universite Montpellier, France.
SOURCE: BIOCHIMIE, (1999 Jun) 81 (6) 577-96. Ref: 170
Journal code: 1264604. ISSN: 0300-9084.
PUB. COUNTRY: France
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, ACADEMIC)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199909
ENTRY DATE: Entered STN: 19991012
Last Updated on STN: 19991012
Entered Medline: 19990928

L8 ANSWER 201 OF 355 MEDLINE DUPLICATE 126

ACCESSION NUMBER: 1999264388 MEDLINE
 DOCUMENT NUMBER: 99264388 PubMed ID: 10329163
 TITLE: Expression and characterization of a human mitochondrial phenylalanyl-tRNA synthetase.
 AUTHOR: Bullard J M; Cai Y C; Demeler B; Spremulli L L
 CORPORATE SOURCE: Department of Chemistry, University of Texas Health Science Center, San Antonio, TX, USA.
 CONTRACT NUMBER: GM19117 (NIGMS)
 GM32734 (NIGMS)
 SOURCE: JOURNAL OF MOLECULAR BIOLOGY, (1999 May 14) 288 (4) 567-77.
 Journal code: 2985088R. ISSN: 0022-2836.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF097441
 ENTRY MONTH: 199906
 ENTRY DATE: Entered STN: 19990618
 Last Updated on STN: 19990618
 Entered Medline: 19990609

L8 ANSWER 202 OF 355 MEDLINE DUPLICATE 127
 ACCESSION NUMBER: 1999263238 MEDLINE
 DOCUMENT NUMBER: 99263238 PubMed ID: 10330131
 TITLE: Inventory of high-abundance mRNAs in skeletal muscle of normal men.
 AUTHOR: Welle S; Bhatt K; Thornton C A
 CORPORATE SOURCE: University of Rochester, Rochester, New York 14642 USA.. swelle@ican.net
 CONTRACT NUMBER: AG-10463 (NIA)
 AG-13070 (NIA)
 RR-00044 (NCRR)
 SOURCE: GENOME RESEARCH, (1999 May) 9 (5) 506-13.
 Journal code: 9518021. ISSN: 1088-9051.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199906
 ENTRY DATE: Entered STN: 19990712
 Last Updated on STN: 19990712
 Entered Medline: 19990624

L8 ANSWER 203 OF 355 MEDLINE DUPLICATE 128
 ACCESSION NUMBER: 2000055743 MEDLINE
 DOCUMENT NUMBER: 20055743 PubMed ID: 10589826
 TITLE: Defective expression of the mu3 subunit of the AP-3 adaptor complex in the Drosophila pigmentation mutant carmine.
 AUTHOR: Mullins C; Hartnell L M; Wassarman D A; Bonifacino J S
 CORPORATE SOURCE: Cell Biology and Metabolism Branch, National Institute of Child Health and Human Development, National Institutes of Health, Bethesda, MD 20892, USA.
 SOURCE: MOLECULAR AND GENERAL GENETICS, (1999 Oct) 262 (3) 401-12.
 Journal code: 0125036. ISSN: 0026-8925.
 PUB. COUNTRY: GERMANY: Germany, Federal Republic of
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AF110231; GENBANK-AF110232; GENBANK-AF110233;
GENBANK-AF110234
ENTRY MONTH: 199912
ENTRY DATE: Entered STN: 20000113
Last Updated on STN: 20000113
Entered Medline: 19991228

L8 ANSWER 204 OF 355 LIFESCI COPYRIGHT 2002 CSA
ACCESSION NUMBER: 1999:112402 LIFESCI
TITLE: Alternative splicing of human genes more the rule than the
exception?
AUTHOR: Hanke, J.; Brett, D.; Zastrow, I.; Aydin, A.; Delbrueck,
S.; Lehmann, G.; Luft, F.; Reich, J.; Bork, P.
CORPORATE SOURCE: Max-Delbrueck-Center (MDC) for Molecular Medicine,
Robert-Roessle-Strasse 10, Berlin-Buch, 13125, Germany;
E-mail: hanke@mdc-berlin.de
SOURCE: Trends in Genetics [Trends Genet.], (19991000) vol. 15,
no. 10, pp. 389-390.
ISSN: 0168-9525.
DOCUMENT TYPE: Journal
TREATMENT CODE: General Review
FILE SEGMENT: G
LANGUAGE: English

L8 ANSWER 205 OF 355 MEDLINE DUPLICATE 129
ACCESSION NUMBER: 1999453299 MEDLINE
DOCUMENT NUMBER: 99453299 PubMed ID: 10521662
TITLE: A complex population of RNAs exists in human ejaculate
spermatozoa: implications for understanding molecular
aspects of spermiogenesis.
AUTHOR: Miller D; Briggs D; Snowden H; Hamlington J; Rollinson S;
Lilford R; Krawetz S A
CORPORATE SOURCE: Centre for Reproduction Growth and Development, University
of Leeds' Division of Obstetrics and Gynaecology, Level D,
Clarendon Wing, Leeds General Infirmary, Belmont Grove,
Leeds, UK.. d.miller@leeds.ac.uk
CONTRACT NUMBER: HD36512 (NICHD)
SOURCE: GENE, (1999 Sep 17) 237 (2) 385-92.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199911
ENTRY DATE: Entered STN: 20000111
Last Updated on STN: 20000111
Entered Medline: 19991108

L8 ANSWER 206 OF 355 MEDLINE DUPLICATE 130
ACCESSION NUMBER: 1999453298 MEDLINE
DOCUMENT NUMBER: 99453298 PubMed ID: 10521661
TITLE: Developmental expression of specific genes detected in
high-quality cDNA libraries from single human
preimplantation embryos.
AUTHOR: Adjaye J; Bolton V; Monk M
CORPORATE SOURCE: Molecular Embryology Unit, Institute of Child Health, 30
Guilford Street, London, UK.. j.adjaye@ich.ucl.ac.uk
SOURCE: GENE, (1999 Sep 17) 237 (2) 373-83.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands

Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199911
ENTRY DATE: Entered STN: 20000111
Last Updated on STN: 20000111
Entered Medline: 19991108

L8 ANSWER 207 OF 355 MEDLINE DUPLICATE 131
ACCESSION NUMBER: 1999121000 MEDLINE
DOCUMENT NUMBER: 99121000 PubMed ID: 9922225
TITLE: Isolation of a gene product expressed by a subpopulation
of
human lung fibroblasts by differential display.
AUTHOR: Lurton J; Rose T M; Raghu G; Narayanan A S
CORPORATE SOURCE: Department of Medicine, School of Medicine, University of
Washington, Seattle 98195, USA.
CONTRACT NUMBER: DE39584 (NIDCR)
SOURCE: AMERICAN JOURNAL OF RESPIRATORY CELL AND MOLECULAR
BIOLOGY,
(1999 Feb) 20 (2) 327-31.
Journal code: 8917225. ISSN: 1044-1549.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF115384
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990324
Last Updated on STN: 20000303
Entered Medline: 19990311

L8 ANSWER 208 OF 355 MEDLINE DUPLICATE 132
ACCESSION NUMBER: 1999189239 MEDLINE
DOCUMENT NUMBER: 99189239 PubMed ID: 10087198
TITLE: Coding sequence, genomic organization, chromosomal
localization, and expression pattern of the signalosome
component Cops2: the mouse homologue of Drosophila alien.
AUTHOR: Schaefer L; Beermann M L; Miller J B
CORPORATE SOURCE: Myogenesis Research Laboratory, Massachusetts General
Hospital, 149 13th Street, Charlestown, Massachusetts
02129, USA.
SOURCE: GENOMICS, (1999 Mar 15) 56 (3) 310-6.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF087688; GENBANK-AF114236; GENBANK-AF114237;
GENBANK-AF114238; GENBANK-AF114239; GENBANK-AF114240;
GENBANK-AF114241; GENBANK-AF114242; GENBANK-AF114244;
GENBANK-AF114245; GENBANK-AF114246; GENBANK-AF114247;
GENBANK-AH007585
ENTRY MONTH: 199905
ENTRY DATE: Entered STN: 19990607
Last Updated on STN: 19990607
Entered Medline: 19990524

L8 ANSWER 209 OF 355 MEDLINE DUPLICATE 133
ACCESSION NUMBER: 1999137667 MEDLINE
DOCUMENT NUMBER: 99137667 PubMed ID: 9950961

TITLE: Cloning of the human kidney PAH transporter: narrow substrate specificity and regulation by protein kinase C.
 AUTHOR: Lu R; Chan B S; Schuster V L
 CORPORATE SOURCE: Departments of Medicine, Physiology and Biophysics, Albert Einstein College of Medicine, Bronx, New York 10461, USA.
 CONTRACT NUMBER: DK-49688 (NIDDK)
 SOURCE: AMERICAN JOURNAL OF PHYSIOLOGY, (1999 Feb) 276 (2 Pt 2) F295-303.
 Journal code: 0370511. ISSN: 0002-9513.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199903
 ENTRY DATE: Entered STN: 19990413
 Last Updated on STN: 19990413
 Entered Medline: 19990330

L8 ANSWER 210 OF 355 MEDLINE DUPLICATE 134
 ACCESSION NUMBER: 1999203529 MEDLINE
 DOCUMENT NUMBER: 99203529 PubMed ID: 10103062
 TITLE: Organization and alternate splice products of the gene encoding nuclear inhibitor of protein phosphatase-1 (NIPP-1).
 AUTHOR: Van Eynde A; Perez-Callejon E; Schoenmakers E; Jacquemin M;
 CORPORATE SOURCE: Stalmans W; Bollen M
 Afdeling Biochemie, Campus Gasthuisberg KULeuven, Herestraat 49, B-3000 Leuven, Belgium.
 SOURCE: EUROPEAN JOURNAL OF BIOCHEMISTRY, (1999 Apr) 261 (1) 291-300.
 Journal code: 0107600. ISSN: 0014-2956.
 PUB. COUNTRY: GERMANY: Germany, Federal Republic of
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF061958; GENBANK-AF061959; GENBANK-AF064751; GENBANK-AF064752; GENBANK-AF064753; GENBANK-AF064754; GENBANK-AF064755; GENBANK-AF064756; GENBANK-AF064757; GENBANK-AF064758
 ENTRY MONTH: 199905
 ENTRY DATE: Entered STN: 19990601
 Last Updated on STN: 19990601
 Entered Medline: 19990519

L8 ANSWER 211 OF 355 MEDLINE
 ACCESSION NUMBER: 2000039610 MEDLINE
 DOCUMENT NUMBER: 20039610 PubMed ID: 10574453
 TITLE: Systematic isolation of genes expressed at low levels in inflorescence apices of Arabidopsis thaliana.
 AUTHOR: Takemura M; Fujishige K; Hyodo H; Ohashi Y; Kami C; Nishii A; Ohyama K; Kohchi T
 CORPORATE SOURCE: Graduate School of Biological Sciences, Nara Institute of Science and Technology, Ikoma, Japan.
 SOURCE: DNA RESEARCH, (1999 Oct 29) 6 (5) 275-82.
 Journal code: 9423827. ISSN: 1340-2838.
 PUB. COUNTRY: Japan
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200001

ENTRY DATE: Entered STN: 20000209
Last Updated on STN: 20000209
Entered Medline: 20000131

L8 ANSWER 212 OF 355 MEDLINE DUPLICATE 135
ACCESSION NUMBER: 1999375318 MEDLINE
DOCUMENT NUMBER: 99375318 PubMed ID: 10444326
TITLE: Endogenous retroviruses provide the primary
polyadenylation
signal for two new human genes (HHLA2 and HHLA3).
AUTHOR: Mager D L; Hunter D G; Schertzer M; Freeman J D
CORPORATE SOURCE: British Columbia Cancer Agency and Department of Medical
Genetics, University of British Columbia, Vancouver,
British Columbia, Canada.. dixie@interchange.ubc.ca
SOURCE: GENOMICS, (1999 Aug 1) 59 (3) 255-63.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF126162; GENBANK-AF126163; GENBANK-AF126164
ENTRY MONTH: 199911
ENTRY DATE: Entered STN: 20000113
Last Updated on STN: 20000113
Entered Medline: 19991130

L8 ANSWER 213 OF 355 MEDLINE DUPLICATE 136
ACCESSION NUMBER: 1999160849 MEDLINE
DOCUMENT NUMBER: 99160849 PubMed ID: 10049694
TITLE: The fourth member of the FHL family of LIM proteins is
expressed exclusively in the testis.
AUTHOR: Morgan M J; Madgwick A J
CORPORATE SOURCE: Department of Orthodontics, Eastman Dental Institute for
Oral Health Care Sciences, University of London, United
Kingdom.. mmorgan@eastman.ucl.ac.uk
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1999
Feb 16) 255 (2) 251-5.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF053486
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990324
Last Updated on STN: 19990324
Entered Medline: 19990311

L8 ANSWER 214 OF 355 MEDLINE DUPLICATE 137
ACCESSION NUMBER: 2000058752 MEDLINE
DOCUMENT NUMBER: 20058752 PubMed ID: 10593179
TITLE: Gender-specific gene expression in Brugia malayi.
AUTHOR: Michalski M L; Weil G J
CORPORATE SOURCE: Department of Molecular Microbiology and Microbial
Pathogenesis, Washington University School of Medicine,
St.
Louis, MO 63110, USA.. mlmichal@artsci.wustl.edu
SOURCE: MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (1999 Nov 30) 104
(2) 247-57.
Journal code: 8006324. ISSN: 0166-6851.
PUB. COUNTRY: Netherlands

Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF118551; GENBANK-AF118552; GENBANK-AF118553;
GENBANK-AF118554; GENBANK-AF118555
ENTRY MONTH: 200002
ENTRY DATE: Entered STN: 20000229
Last Updated on STN: 20000229
Entered Medline: 20000214

L8 ANSWER 215 OF 355 MEDLINE DUPLICATE 138
ACCESSION NUMBER: 2000117084 MEDLINE
DOCUMENT NUMBER: 20117084 PubMed ID: 10653359
TITLE: A novel member of murine Polycomb-group proteins, Sex comb
on midleg homolog protein, is highly conserved, and
interacts with RAE28/mph1 in vitro.
AUTHOR: Tomotsune D; Takihara Y; Berger J; Duhl D; Joo S; Kyba M;
Shirai M; Ohta H; Matsuda Y; Honda B M; Simon J; Shimada
K;
CORPORATE SOURCE: Brock H W; Randazzo F
Department of Medical Genetics, Research Institute for
Microbial Diseases, Osaka University, Suita, Japan.
SOURCE: DIFFERENTIATION, (1999 Dec) 65 (4) 229-39.
Journal code: 0401650. ISSN: 0301-4681.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB030906
ENTRY MONTH: 200003
ENTRY DATE: Entered STN: 20000320
Last Updated on STN: 20000320
Entered Medline: 20000306

L8 ANSWER 216 OF 355 MEDLINE
ACCESSION NUMBER: 1999279264 MEDLINE
DOCUMENT NUMBER: 99279264 PubMed ID: 10349647
TITLE: Construction and analysis of arrayed cDNA libraries.
AUTHOR: Clark M D; Panopoulou G D; Cahill D J; Bussow K; Lehrach H
CORPORATE SOURCE: Max Planck Institut fur Molekulare Genetik, Berlin,
Dahlem,
Germany.
SOURCE: METHODS IN ENZYMOLOGY, (1999) 303 205-33.
Journal code: 0212271. ISSN: 0076-6879.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199907
ENTRY DATE: Entered STN: 19990730
Last Updated on STN: 19990730
Entered Medline: 19990722

L8 ANSWER 217 OF 355 MEDLINE DUPLICATE 139
ACCESSION NUMBER: 1999132385 MEDLINE
DOCUMENT NUMBER: 99132385 PubMed ID: 9931487
TITLE: Identification and cloning of three novel human G
protein-coupled receptor genes GPR52, PsiGPR53 and GPR55:
GPR55 is extensively expressed in human brain.
AUTHOR: Sawzdargo M; Nguyen T; Lee D K; Lynch K R; Cheng R; Heng H
H; George S R; O'Dowd B F

CORPORATE SOURCE: Department of Pharmacology, University of Toronto, Medical Sciences Building, Toronto, Ontario, Canada, USA.
 SOURCE: BRAIN RESEARCH. MOLECULAR BRAIN RESEARCH, (1999 Feb 5) 64 (2) 193-8.
 Journal code: 8908640. ISSN: 0169-328X.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF096784; GENBANK-AF096785; GENBANK-AF096786; GENBANK-AF100789
 ENTRY MONTH: 199903
 ENTRY DATE: Entered STN: 19990326
 Last Updated on STN: 20000303
 Entered Medline: 19990312

L8 ANSWER 218 OF 355 LIFESCI COPYRIGHT 2002 CSA
 ACCESSION NUMBER: 1999:110119 LIFESCI
 TITLE: Assignment of human proliferation associated p100 gene (C20orf1) to human chromosome band 20q11.2 by in situ hybridization
 AUTHOR: Zhang, Y.; Heidebrecht, H.-J.; Rott, A.; Schlegelberger, B.; Parwaresch, R.
 CORPORATE SOURCE: Department of Hematopathology, University of Kiel, Michaelisstr. 11, 24105 Kiel, Germany; E-mail: hheidebrecht@path.uni-kiel.de
 SOURCE: Cytogenetics and Cell Genetics [Cytogenet. Cell Genet.], (19990000) vol. 84, no. 3-4, pp. 182-183.
 ISSN: 0301-0171.
 DOCUMENT TYPE: Journal
 FILE SEGMENT: G
 LANGUAGE: English

L8 ANSWER 219 OF 355 MEDLINE DUPLICATE 140
 ACCESSION NUMBER: 1999339982 MEDLINE
 DOCUMENT NUMBER: 99339982 PubMed ID: 10409429
 TITLE: Prostate cancer expression profiling by cDNA sequencing analysis.
 AUTHOR: Huang G M; Ng W L; Farkas J; He L; Liang H A; Gordon D; Yu J; Hood L
 CORPORATE SOURCE: Department of Molecular Biotechnology, University of Washington, Seattle, Washington 98195, USA..
 huanggm@yahoo.com
 SOURCE: GENOMICS, (1999 Jul 15) 59 (2) 178-86.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AI524829; GENBANK-AI524830; GENBANK-AI524831; GENBANK-AI524832; GENBANK-AI524833; GENBANK-AI524834; GENBANK-AI524835; GENBANK-AI524836; GENBANK-AI524837; GENBANK-AI524838; GENBANK-AI524839; GENBANK-AI524840; GENBANK-AI524841; GENBANK-AI524842; GENBANK-AI524843; GENBANK-AI524844; GENBANK-AI524845; GENBANK-AI524846; GENBANK-AI524847; GENBANK-AI524848; GENBANK-AI524849; GENBANK-AI524850; GENBANK-AI524851; GENBANK-AI524852; GENBANK-AI524853; GENBANK-AI524854; GENBANK-AI524855; GENBANK-AI524856; GENBANK-AI524857; GENBANK-AI524858; +
 ENTRY MONTH: 199909
 ENTRY DATE: Entered STN: 19990921

Last Updated on STN: 19990921
Entered Medline: 19990908

L8 ANSWER 220 OF 355 MEDLINE DUPLICATE 141
ACCESSION NUMBER: 1999132027 MEDLINE
DOCUMENT NUMBER: 99132027 PubMed ID: 9931475
TITLE: Structure, expression profile and chromosomal location of
an isolog of DNA-PKcs interacting protein (KIP) gene.
AUTHOR: Seki N; Hattori A; Hayashi A; Kozuma S; Ohira M; Horii T;
Saito T
CORPORATE SOURCE: Genome Research Group, National Institute of Radiological
Sciences, 4-9-1 Anagawa, Inage-ku, Chiba 263-8555, Japan.
SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (1999 Jan 18) 1444 (1)
143-7.
Journal code: 0217513. ISSN: 0006-3002.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB012955
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990324
Last Updated on STN: 19990324
Entered Medline: 19990309

L8 ANSWER 221 OF 355 MEDLINE DUPLICATE 142
ACCESSION NUMBER: 1999430869 MEDLINE
DOCUMENT NUMBER: 99430869 PubMed ID: 10503544
TITLE: Homologs of animal eyes absent (eya) genes are found in
higher plants.
AUTHOR: Takeda Y; Hatano S; Sentoku N; Matsuoka M
CORPORATE SOURCE: Bio Science Center, Nagoya University, Aichi, Japan.
SOURCE: MOLECULAR AND GENERAL GENETICS, (1999 Aug) 262 (1) 131-8.
Journal code: 0125036. ISSN: 0026-8925.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB028887
ENTRY MONTH: 199910
ENTRY DATE: Entered STN: 19991101
Last Updated on STN: 19991101
Entered Medline: 19991018

L8 ANSWER 222 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2000:96075 BIOSIS
DOCUMENT NUMBER: PREV200000096075
TITLE: Caveolin-1 isoforms are encoded by distinct mRNAs:
Identification of mouse caveolin-1 mRNA variants caused by
alternative transcription initiation and splicing.
AUTHOR(S): Kogo, Hiroshi (1); Fujimoto, Toyoshi
CORPORATE SOURCE: (1) Department of Anatomy and Molecular Cell Biology,
Nagoya University School of Medicine, Showa-ku, Nagoya,
466-8550 Japan
SOURCE: FEBS Letters, (Jan. 14, 1999) Vol. 464, No. 2-3, pp.
119-123.
ISSN: 0014-5793.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

L8 ANSWER 223 OF 355 MEDLINE DUPLICATE 143
 ACCESSION NUMBER: 1999326706 MEDLINE
 DOCUMENT NUMBER: 99326706 PubMed ID: 10396028
 TITLE: A novel human GnRH receptor homolog gene: abundant and wide tissue distribution of the antisense transcript.
 AUTHOR: Millar R; Conklin D; Lofton-Day C; Hutchinson E; Troskie B; Illing N; Sealfon S C; Hapgood J
 CORPORATE SOURCE: MRC Molecular Reproductive Endocrinology Research Unit, University of Cape Town Medical School, Observatory 7925, South Africa.
 SOURCE: JOURNAL OF ENDOCRINOLOGY, (1999 Jul) 162 (1) 117-26. Journal code: 0375363. ISSN: 0022-0795.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199909
 ENTRY DATE: Entered STN: 19991005
 Last Updated on STN: 19991005
 Entered Medline: 19990920

L8 ANSWER 224 OF 355 MEDLINE
 ACCESSION NUMBER: 1999110237 MEDLINE
 DOCUMENT NUMBER: 99110237 PubMed ID: 9894946
 TITLE: Large-scale sequencing of the rabbit corneal endothelial cDNA library.
 AUTHOR: Fujimaki T; Hotta Y; Sakuma H; Fujiki K; Kanai A
 CORPORATE SOURCE: Department of Ophthalmology, Juntendo University School of Medicine, Tokyo, Japan.. fujimaki@med.juntendo.ac.jp
 SOURCE: CORNEA, (1999 Jan) 18 (1) 109-14. Journal code: 8216186. ISSN: 0277-3740.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-C82380; GENBANK-C82381; GENBANK-C82382; GENBANK-C82383; GENBANK-C82384; GENBANK-C82385; GENBANK-C82386; GENBANK-C82387; GENBANK-C82388; GENBANK-C82389; GENBANK-C82390; GENBANK-C82391; GENBANK-C82392; GENBANK-C82393; GENBANK-C82394; GENBANK-C82395; GENBANK-C82396; GENBANK-C82397; GENBANK-C82398; GENBANK-C82399; GENBANK-C82400; GENBANK-C82401; GENBANK-C82402; GENBANK-C82403; GENBANK-C82404; GENBANK-C82405; GENBANK-C82406; GENBANK-C82407; GENBANK-C82408; GENBANK-C82409
 ENTRY MONTH: 199903
 ENTRY DATE: Entered STN: 19990402
 Last Updated on STN: 19990402
 Entered Medline: 19990322

L8 ANSWER 225 OF 355 MEDLINE DUPLICATE 144
 ACCESSION NUMBER: 1999173874 MEDLINE
 DOCUMENT NUMBER: 99173874 PubMed ID: 10072763
 TITLE: Identification of two hERR2-related novel nuclear receptors utilizing bioinformatics and inverse PCR.
 AUTHOR: Chen F; Zhang Q; McDonald T; Davidoff M J; Bailey W; Bai C;

CORPORATE SOURCE: Liu Q; Caskey C T
 Department of Human Genetics, Merck Research Laboratories,
 West Point, PA 19486, USA.. fang_chen@merck.com
 SOURCE: GENE, (1999 Mar 4) 228 (1-2) 101-9.
 Journal code: 7706761. ISSN: 0378-1119.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF094517; GENBANK-AF094518
 ENTRY MONTH: 199904
 ENTRY DATE: Entered STN: 19990426
 Last Updated on STN: 19990426
 Entered Medline: 19990413

L8 ANSWER 226 OF 355 MEDLINE DUPLICATE 145
 ACCESSION NUMBER: 1999249819 MEDLINE
 DOCUMENT NUMBER: 99249819 PubMed ID: 10231560
 TITLE: PKCnu, a new member of the protein kinase C family,
 composes a fourth subfamily with PKCmu.
 AUTHOR: Hayashi A; Seki N; Hattori A; Kozuma S; Saito T
 CORPORATE SOURCE: Genome Research Group, National Institute of Radiological
 Sciences, Anagawa 4-9-1, Inage-ku, Chiba 263-8555, Japan.
 SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (1999 May 6) 1450 (1)
 99-106.
 Journal code: 0217513. ISSN: 0006-3002.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AB015982
 ENTRY MONTH: 199906
 ENTRY DATE: Entered STN: 19990618
 Last Updated on STN: 19990618
 Entered Medline: 19990610

L8 ANSWER 227 OF 355 MEDLINE DUPLICATE 146
 ACCESSION NUMBER: 2000056376 MEDLINE
 DOCUMENT NUMBER: 20056376 PubMed ID: 10587472
 TITLE: Initial assessment of gene diversity for the oomycete
 pathogen Phytophthora infestans based on expressed
 sequences.
 AUTHOR: Kamoun S; Hraber P; Sobral B; Nuss D; Govers F
 CORPORATE SOURCE: Department of Plant Pathology, The Ohio State University,
 Ohio Agricultural Research and Development Center, 1680
 Madison Avenue, Wooster, Ohio 44691, USA.
 SOURCE: FUNGAL GENETICS AND BIOLOGY, (1999 Nov) 28 (2) 94-106.
 Journal code: 9607601. ISSN: 1087-1845.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200002
 ENTRY DATE: Entered STN: 20000229
 Last Updated on STN: 20000229
 Entered Medline: 20000216

L8 ANSWER 228 OF 355 LIFESCI COPYRIGHT 2002 CSA
 ACCESSION NUMBER: 2000:61361 LIFESCI
 TITLE: A cDNA sequence of phosphopyruvate hydratase (enolase)
 from

AUTHOR: Black Tiger Prawn, *Penaeus monodon*
 Boonchuoy, C.; Boonyawan, B.; Panyim, S.; Sonthayanon, B.*
 CORPORATE SOURCE: Institute of Molecular Biology and Genetics, Mahidol
 University, Salaya Campus, Phutthamonthon 4 Rd.,
 Phutthamonthon District, Nakhon Pathom 73170, Thailand;
 E-mail: scbst@mahidol.ac.th
 SOURCE: Asia-Pacific Journal of Molecular Biology and
 Biotechnology
 [Asia-Pacific J. Mol. Biol. Biotechnol.], (19990600) vol.
 7, no. 1, pp. 89-94.
 ISSN: 0128-7451.
 DOCUMENT TYPE: Journal
 FILE SEGMENT: Q4
 LANGUAGE: English
 SUMMARY LANGUAGE: English

L8 ANSWER 229 OF 355 MEDLINE DUPLICATE 147
 ACCESSION NUMBER: 1999442241 MEDLINE
 DOCUMENT NUMBER: 99442241 PubMed ID: 10514083
 TITLE: Analysis of the gene expression profile of *Schistosoma*
mansoni cercariae using the expressed sequence tag
 approach.
 AUTHOR: Santos T M; Johnston D A; Azevedo V; Ridgers I L; Martinez
 M F; Marotta G B; Santos R L; Fonseca S J; Ortega J M;
 Rabelo E M; Saber M; Ahmed H M; Romeih M H; Franco G R;
 Rollinson D; Pena S D
 CORPORATE SOURCE: Departamento de Bioquimica e Imunologia, ICB-UFMG, Belo
 Horizonte, MG, Brazil.
 SOURCE: MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (1999 Sep 20) 103
 (1) 79-97.
 Journal code: 8006324. ISSN: 0166-6851.
 PUB. COUNTRY: Netherlands
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AA999208; GENBANK-AA999209; GENBANK-AA999210;
 GENBANK-AA999211; GENBANK-AA999212; GENBANK-AA999213;
 GENBANK-AA999214; GENBANK-AA999215; GENBANK-AA999216;
 GENBANK-AA999217; GENBANK-AA999218; GENBANK-AA999219;
 GENBANK-AA999220; GENBANK-AA999221; GENBANK-AA999222;
 GENBANK-AA999223; GENBANK-AA999224; GENBANK-AA999225;
 GENBANK-AA999226; GENBANK-AA999227; GENBANK-AA999228;
 GENBANK-AA999229; GENBANK-AA999230; GENBANK-AA999231;
 GENBANK-AA999232; GENBANK-AA999233; GENBANK-AA999234;
 GENBANK-AA999235; GENBANK-AA999236; GENBANK-AA999237; +
 ENTRY MONTH: 199911
 ENTRY DATE: Entered STN: 20000113
 Last Updated on STN: 20000113
 Entered Medline: 19991130

L8 ANSWER 230 OF 355 MEDLINE DUPLICATE 148
 ACCESSION NUMBER: 2000033546 MEDLINE
 DOCUMENT NUMBER: 20033546 PubMed ID: 10564810
 TITLE: Identification and characterization of a putative *C.*
elegans potassium channel gene (*Ce-slo-2*) distantly
 related
 to Ca^{2+} -activated K^{+} channels.
 AUTHOR: Lim H H; Park B J; Choi H S; Park C S; Eom S H; Ahnn J
 CORPORATE SOURCE: Department of Life Science, Kwangju Institute of Science
 and Technology (K-JIST), Kwangju, South Korea.
 SOURCE: GENE, (1999 Nov 15) 240 (1) 35-43.

PUB. COUNTRY: Journal code: 7706761. ISSN: 0378-1119.
Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF173828
ENTRY MONTH: 200001
ENTRY DATE: Entered STN: 20000124
Last Updated on STN: 20000124
Entered Medline: 20000111

L8 ANSWER 231 OF 355 MEDLINE DUPLICATE 149
ACCESSION NUMBER: 2000077667 MEDLINE
DOCUMENT NUMBER: 20077667 PubMed ID: 10612420
TITLE: Structure and distribution of rat menin mRNA.
AUTHOR: Maruyama K; Tsukada T; Hosono T; Ohkura N; Kishi M; Honda
M; Nara-Ashizawa N; Nagasaki K; Yamaguchi K
CORPORATE SOURCE: Growth Factor Division, National Cancer Center Research
Institute, Tokyo, Japan.. kmaruyam@gan2.res.ncc.go.jp
SOURCE: MOLECULAR AND CELLULAR ENDOCRINOLOGY, (1999 Oct 25) 156
(1-2) 25-33.
Journal code: 7500844. ISSN: 0303-7207.
PUB. COUNTRY: Ireland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB023400; GENBANK-AB023401
ENTRY MONTH: 200001
ENTRY DATE: Entered STN: 20000124
Last Updated on STN: 20000124
Entered Medline: 20000113

L8 ANSWER 232 OF 355 MEDLINE DUPLICATE 150
ACCESSION NUMBER: 1999389722 MEDLINE
DOCUMENT NUMBER: 99389722 PubMed ID: 10458907
TITLE: Novel human and mouse homologs of Saccharomyces cerevisiae
DNA polymerase eta.
AUTHOR: McDonald J P; Raptic-Otrin V; Epstein J A; Broughton B C;
Wang X; Lehmann A R; Wolgemuth D J; Woodgate R
CORPORATE SOURCE: Section on DNA Replication, Repair and Mutagenesis,
National Institute of Child Health and Human Development,
Bethesda, Maryland, 20892-2725, USA.
CONTRACT NUMBER: RO1HD34915 (NICHD)
SOURCE: GENOMICS, (1999 Aug 15) 60 (1) 20-30.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
OTHER SOURCE: GENBANK-AF140501; GENBANK-AF151691
ENTRY MONTH: 199909
ENTRY DATE: Entered STN: 19991012
Last Updated on STN: 20020124
Entered Medline: 19990930

L8 ANSWER 233 OF 355 MEDLINE DUPLICATE 151
ACCESSION NUMBER: 1999156852 MEDLINE
DOCUMENT NUMBER: 99156852 PubMed ID: 10036181
TITLE: Discovery of three novel orphan G-protein-coupled
receptors.
AUTHOR: Marchese A; Sawzdargo M; Nguyen T; Cheng R; Heng H H;
Nowak

CORPORATE SOURCE: T; Im D S; Lynch K R; George S R; O'dowd B F
 Department of Pharmacology, Department of Medicine,
 University of Toronto, Medical Sciences Building, Toronto,
 Ontario, M5S 1A8, Canada.

SOURCE: GENOMICS, (1999 Feb 15) 56 (1) 12-21.
 Journal code: 8800135. ISSN: 0888-7543.

PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AF118265; GENBANK-AF118266; GENBANK-AF118670

ENTRY MONTH: 199905

ENTRY DATE: Entered STN: 19990517
 Last Updated on STN: 20000303
 Entered Medline: 19990505

L8 ANSWER 234 OF 355 MEDLINE DUPLICATE 152

ACCESSION NUMBER: 199395627 MEDLINE

DOCUMENT NUMBER: 9395627 PubMed ID: 10466133

TITLE: Status of protozoan genome analysis: trypanosomatids.

AUTHOR: Blackwell J M; Melville S E

CORPORATE SOURCE: Cambridge Institute of Medical Research, Addenbrooke's
 Hospital.

SOURCE: PARASITOLOGY, (1999) 118 Suppl S11-4. Ref: 25
 Journal code: 0401121. ISSN: 0031-1820.

PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, TUTORIAL)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199909

ENTRY DATE: Entered STN: 19991012
 Last Updated on STN: 19991012
 Entered Medline: 19990930

L8 ANSWER 235 OF 355 MEDLINE

ACCESSION NUMBER: 1999246514 MEDLINE

DOCUMENT NUMBER: 99246514 PubMed ID: 10228186

TITLE: Identifying and mapping novel retinal-expressed ESTs from
 humans.

AUTHOR: Malone K; Sohocki M M; Sullivan L S; Daiger S P

CORPORATE SOURCE: Human Genetics Center, School of Public Health, The
 University of Texas Health Science Center, Houston, TX,
 USA.. kmalone@gsbs3.gs.uth.tmc.edu

CONTRACT NUMBER: EY07024 (NEI)
 EY07142 (NEI)

SOURCE: MOLECULAR VISION, (1999 May 4) 5 5.
 Journal code: 9605351. ISSN: 1090-0535.

PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-G42336; GENBANK-G42337; GENBANK-G42338;
 GENBANK-G42339; GENBANK-G42340; GENBANK-G42341;
 GENBANK-G42342; GENBANK-G42343; GENBANK-G42344;
 GENBANK-G42345; GENBANK-G42346; GENBANK-G42347;
 GENBANK-G42348; GENBANK-G42349; GENBANK-G42350;
 GENBANK-G42351; GENBANK-G42352; GENBANK-G42353;
 GENBANK-G42354; GENBANK-G42355; GENBANK-G42356;
 GENBANK-G42357; GENBANK-G42358; GENBANK-G42359;

GENBANK-G42360; GENBANK-G42361; GENBANK-G42362;
GENBANK-G42363; GENBANK-G42364; GENBANK-G42365
ENTRY MONTH: 199905
ENTRY DATE: Entered STN: 19990525
Last Updated on STN: 19990525
Entered Medline: 19990513

L8 ANSWER 236 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2000:102316 BIOSIS
DOCUMENT NUMBER: PREV200000102316
TITLE: Identifying and mapping novel retinal-expressed ESTs from humans.
AUTHOR(S): Malone, Kimberly; Sohocki, Melanie M.; Sullivan, Lori S.; Daiger, Stephen P. (1)
CORPORATE SOURCE: (1) Human Genetics Center, School of Public Health, Houston, TX, 77225-0334 USA
SOURCE: Molecular Vision, (May 4, 1999) Vol. 5, No. 5 CITED NOV. 18, 1999, pp. No Pagination.
ISSN: 1090-0535.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

L8 ANSWER 237 OF 355 CANCERLIT
ACCESSION NUMBER: 1999137667 CANCERLIT
DOCUMENT NUMBER: 99137667
TITLE: Cloning of the human kidney PAH transporter: narrow substrate specificity and regulation by protein kinase C.
AUTHOR: Lu R; Chan B S; Schuster V L
CORPORATE SOURCE: Departments of Medicine, Physiology and Biophysics, Albert Einstein College of Medicine, Bronx, New York 10461, USA.
CONTRACT NUMBER: DK-49688 (NIDDK)
SOURCE: AMERICAN JOURNAL OF PHYSIOLOGY, (1999). 276 (2 Pt. 2):F295-303.
Journal code: 3U8. ISSN: 0002-9513.
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
FILE SEGMENT: MEDL; L; Priority Journals
LANGUAGE: English
OTHER SOURCE: MEDLINE 99137667
ENTRY MONTH: 199905

L8 ANSWER 238 OF 355 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI
ACCESSION NUMBER: 1999-03571 BIOTECHDS
TITLE: DNA encoding protein with very long chain fatty-acid-elongase activity;
used for transgenic plant construction, with modified very long chain fatty acid composition, seed oil composition, epicuticular wax layer or conditional male sterility
AUTHOR: Kunst L; Millar A A
PATENT ASSIGNEE: Univ.British-Columbia
LOCATION: Vancouver, British Columbia, Canada.
PATENT INFO: WO 9846766 22 Oct 1998
APPLICATION INFO: WO 1998-CA343 14 Apr 1998
PRIORITY INFO: US 1998-958947 10 Apr 1998; US 1997-43831 14 Apr 1997
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 1999-080740 [07]

L8 ANSWER 239 OF 355 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI

ACCESSION NUMBER: 1998-06888 BIOTECHDS
 TITLE: Method for detecting a target PS112 polynucleotide;
 mRNA sequence for prostate cancer diagnosis, prevention,
 therapy or gene therapy
 AUTHOR: Cohen M; Friedman P N; Gordon J; Hodges S C; Klass M R;
 Kratochvil J D; Roberts-Rapp L; Russell J C; Stroupe S D
 PATENT ASSIGNEE: Abbott-Lab.
 LOCATION: Abbott Park, IL, USA.
 PATENT INFO: WO 9815657 16 Apr 1998
 APPLICATION INFO: WO 1997-US18290 8 Oct 1997
 PRIORITY INFO: US 1996-727688 8 Oct 1996
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 OTHER SOURCE: WPI: 1998-240838 [21]

L8 ANSWER 240 OF 355 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI
 ACCESSION NUMBER: 1999-01454 BIOTECHDS
 TITLE: Nucleic acid encoding delta-sarcoglycan polypeptide;
 recombinant protein production via vector expression in
 host cell for Duchenne muscular dystrophy therapy
 AUTHOR: Campbell K P; Jung D; Duclos F; Straub V; McPherson J
 PATENT ASSIGNEE: Univ.Washington-St.Louis; Univ.Iowa-Res.Found.
 LOCATION: St. Louis, MO, USA; Iowa City, IA, USA.
 PATENT INFO: US 5837537 17 Nov 1998
 APPLICATION INFO: US 1996-7197758 25 Sep 1996
 PRIORITY INFO: US 1996-719758 25 Sep 1996
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 OTHER SOURCE: WPI: 1999-023460 [02]

L8 ANSWER 241 OF 355 MEDLINE DUPLICATE 153
 ACCESSION NUMBER: 1999007314 MEDLINE
 DOCUMENT NUMBER: 99007314 PubMed ID: 9789088
 TITLE: Gene discovery in the wood-forming tissues of poplar:
 analysis of 5, 692 expressed sequence tags.
 AUTHOR: Sterky F; Regan S; Karlsson J; Hertzberg M; Rohde A;
 Holmberg A; Amini B; Bhalerao R; Larsson M; Villarroel R;
 Van Montagu M; Sandberg G; Olsson O; Teeri T T; Boerjan W;
 Gustafsson P; Uhlen M; Sundberg B; Lundeberg J
 CORPORATE SOURCE: Department of Biotechnology, Kungl Tekniska Hogskolan,
 Royal Institute of Technology, SE-10044 Stockholm,
 Sweden.
 SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE
 UNITED STATES OF AMERICA, (1998 Oct 27) 95 (22) 13330-5.
 Journal code: 7505876. ISSN: 0027-8424.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AI161440; GENBANK-AI161441; GENBANK-AI161442;
 GENBANK-AI161443; GENBANK-AI161444; GENBANK-AI161445;
 GENBANK-AI161446; GENBANK-AI161447; GENBANK-AI161448;
 GENBANK-AI161449; GENBANK-AI161450; GENBANK-AI161451;
 GENBANK-AI161452; GENBANK-AI161453; GENBANK-AI161454;
 GENBANK-AI161455; GENBANK-AI161456; GENBANK-AI161457;
 GENBANK-AI161458; GENBANK-AI161459; GENBANK-AI161460;
 GENBANK-AI161461; GENBANK-AI161462; GENBANK-AI161463;
 GENBANK-AI161464; GENBANK-AI161465; GENBANK-AI161466;
 GENBANK-AI161467; GENBANK-AI161468; GENBANK-AI161469; +
 ENTRY MONTH: 199811
 ENTRY DATE: Entered STN: 19990106

Last Updated on STN: 19990106
Entered Medline: 19981124

L8 ANSWER 242 OF 355 MEDLINE DUPLICATE 154
ACCESSION NUMBER: 1998356220 MEDLINE
DOCUMENT NUMBER: 98356220 PubMed ID: 9689143
TITLE: Analysis of xylem formation in pine by cDNA sequencing.
AUTHOR: Allona I; Quinn M; Shoop E; Swope K; St Cyr S; Carlis J;
Riedl J; Retzel E; Campbell M M; Sederoff R; Whetten R W
CORPORATE SOURCE: Forest Biotechnology Group, Department of Forestry, North
Carolina State University, Raleigh, NC 27695-8008, USA.
iallona@etsi.montes.upm.es.
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE
UNITED STATES OF AMERICA, (1998 Aug 4) 95 (16) 9693-8.
Journal code: 7505876. ISSN: 0027-8424.
(Investigators: Davies E, NC St U, Raleigh)
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
OTHER SOURCE: GENBANK-AA556146; GENBANK-AA556147; GENBANK-AA556148;
GENBANK-AA556149; GENBANK-AA556150; GENBANK-AA556151;
GENBANK-AA556152; GENBANK-AA556153; GENBANK-AA556154;
GENBANK-AA556155; GENBANK-AA556156; GENBANK-AA556157;
GENBANK-AA556158; GENBANK-AA556159; GENBANK-AA556160;
GENBANK-AA556161; GENBANK-AA556162; GENBANK-AA556163;
GENBANK-AA556164; GENBANK-AA556165; GENBANK-AA556166;
GENBANK-AA556167; GENBANK-AA556168; GENBANK-AA556169;
GENBANK-AA556170; GENBANK-AA556171; GENBANK-AA556172;
GENBANK-AA556173; GENBANK-AA556174; GENBANK-AA556175; +
ENTRY MONTH: 199809
ENTRY DATE: Entered STN: 19980917
Last Updated on STN: 20010517
Entered Medline: 19980908

L8 ANSWER 243 OF 355 MEDLINE DUPLICATE 155
ACCESSION NUMBER: 1999003155 MEDLINE
DOCUMENT NUMBER: 99003155 PubMed ID: 9784549
TITLE: Gene discovery through expressed sequence Tag sequencing
in
Trypanosoma cruzi.
AUTHOR: Verdun R E; Di Paolo N; Urmenyi T P; Rondinelli E; Frasch
A
C; Sanchez D O
CORPORATE SOURCE: Instituto de Investigaciones Biotecnologicas, Universidad
Nacional de General San Martin, Buenos Aires, Argentina.
SOURCE: INFECTION AND IMMUNITY, (1998 Nov) 66 (11) 5393-8.
Journal code: 0246127. ISSN: 0019-9567.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AA867894; GENBANK-AA867895; GENBANK-AA867896;
GENBANK-AA867897; GENBANK-AA867898; GENBANK-AA867899;
GENBANK-AA867900; GENBANK-AA867901; GENBANK-AA867902;
GENBANK-AA867903; GENBANK-AA867904; GENBANK-AA867905;
GENBANK-AA867906; GENBANK-AA867907; GENBANK-AA867908;
GENBANK-AA867909; GENBANK-AA867910; GENBANK-AA867911;
GENBANK-AA867912; GENBANK-AA867913; GENBANK-AA867914;
GENBANK-AA867915; GENBANK-AA867916; GENBANK-AA867917;
GENBANK-AA867918; GENBANK-AA867919; GENBANK-AA867920;

ENTRY MONTH: GENBANK-AA867921; GENBANK-AA867922; GENBANK-AA867923; +
199811
ENTRY DATE: Entered STN: 19990106
Last Updated on STN: 19990106
Entered Medline: 19981123

L8 ANSWER 244 OF 355 MEDLINE DUPLICATE 156
ACCESSION NUMBER: 1998352212 MEDLINE
DOCUMENT NUMBER: 98352212 PubMed ID: 9685493
TITLE: Hex1: a new human Rad2 nuclease family member with
homology
to yeast exonuclease 1.
AUTHOR: Wilson D M 3rd; Carney J P; Coleman M A; Adamson A W;
Christensen M; Lamerdin J E
CORPORATE SOURCE: Biology and Biotechnology Research Program, L-452,
Lawrence
Livermore National Laboratory, Livermore, CA 94551, USA..
wilson61@llnl.gov
CONTRACT NUMBER: CA09215-12 (NCI)
SOURCE: NUCLEIC ACIDS RESEARCH, (1998 Aug 15) 26 (16) 3762-8.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AC004783; GENBANK-AF042282
ENTRY MONTH: 199809
ENTRY DATE: Entered STN: 19981006
Last Updated on STN: 20000303
Entered Medline: 19980922

L8 ANSWER 245 OF 355 MEDLINE DUPLICATE 157
ACCESSION NUMBER: 1998264342 MEDLINE
DOCUMENT NUMBER: 98264342 PubMed ID: 9603203
TITLE: SCLIP: a novel SCG10-like protein of the stathmin family
expressed in the nervous system.
AUTHOR: Ozon S; Byk T; Sobel A
CORPORATE SOURCE: INSERM U440, Paris, France.
SOURCE: JOURNAL OF NEUROCHEMISTRY, (1998 Jun) 70 (6) 2386-96.
Journal code: 2985190R. ISSN: 0022-3042.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF026530; GENBANK-AF069708; GENBANK-AF069709;
GENBANK-AF069710
ENTRY MONTH: 199806
ENTRY DATE: Entered STN: 19980618
Last Updated on STN: 20000303
Entered Medline: 19980605

L8 ANSWER 246 OF 355 MEDLINE DUPLICATE 158
ACCESSION NUMBER: 1998158621 MEDLINE
DOCUMENT NUMBER: 98158621 PubMed ID: 9490669
TITLE: Molecular cloning of translocation t(1;14)(q21;q32)
defines
a novel gene (BCL9) at chromosome 1q21.
AUTHOR: Willis T G; Zalcborg I R; Coignet L J; Wlodarska I; Stul
M;
Jadayel D M; Bastard C; Treleaven J G; Catovsky D; Silva M
L; Dyer M J

CORPORATE SOURCE: Academic Department of Haematology and Cytogenetics,
Institute of Cancer Research, Haddow Laboratories, Sutton,
Surrey, UK.
SOURCE: BLOOD, (1998 Mar 15) 91 (6) 1873-81.
Journal code: 7603509. ISSN: 0006-4971.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 199804
ENTRY DATE: Entered STN: 19980416
Last Updated on STN: 19980416
Entered Medline: 19980409

L8 ANSWER 247 OF 355 MEDLINE DUPLICATE 159
ACCESSION NUMBER: 1998136197 MEDLINE
DOCUMENT NUMBER: 98136197 PubMed ID: 9469824
TITLE: Isolation and characterization of RAD51C, a new human
member of the RAD51 family of related genes.
AUTHOR: Dosanjh M K; Collins D W; Fan W; Lennon G G; Albala J S;
Shen Z; Schild D
CORPORATE SOURCE: Life Sciences Division, Lawrence Berkeley National
Laboratory, Berkeley, CA 94720, USA.
CONTRACT NUMBER: ES08353 (NIEHS)
GM30990 (NIGMS)
SOURCE: NUCLEIC ACIDS RESEARCH, (1998 Mar 1) 26 (5) 1179-84.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF029669; GENBANK-AF029670
ENTRY MONTH: 199804
ENTRY DATE: Entered STN: 19980410
Last Updated on STN: 19980410
Entered Medline: 19980402

L8 ANSWER 248 OF 355 MEDLINE DUPLICATE 160
ACCESSION NUMBER: 1998392085 MEDLINE
DOCUMENT NUMBER: 98392085 PubMed ID: 9724873
TITLE: Toxoplasma gondii: ESTs and gene discovery.
AUTHOR: Ajioka J W
CORPORATE SOURCE: Department of Pathology, University of Cambridge, U.K..
jwa@mole.bio.cam.ac.uk
SOURCE: INTERNATIONAL JOURNAL FOR PARASITOLOGY, (1998 Jul) 28 (7)
1025-31. Ref: 6
Journal code: 0314024. ISSN: 0020-7519.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199810
ENTRY DATE: Entered STN: 19990106
Last Updated on STN: 19990106
Entered Medline: 19981027

L8 ANSWER 249 OF 355 MEDLINE DUPLICATE 161
ACCESSION NUMBER: 1999011327 MEDLINE
DOCUMENT NUMBER: 99011327 PubMed ID: 9792926

TITLE: Serine protease inhibitors expressed in the process of budding of tunicates as revealed by EST analysis.
 AUTHOR: Kawamura K; Hayata D; Fujiwara S; Yubisui T
 CORPORATE SOURCE: Laboratory of Cellular and Molecular Biotechnology, Faculty of Science, Kochi University, Kochi, 780, Japan..
 SOURCE: JOURNAL OF BIOCHEMISTRY, (1998 Nov) 124 (5) 1004-12.
 PUB. COUNTRY: Japan
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199902
 ENTRY DATE: Entered STN: 19990223
 Last Updated on STN: 19990223
 Entered Medline: 19990211

L8 ANSWER 250 OF 355 MEDLINE DUPLICATE 162
 ACCESSION NUMBER: 1999003530 MEDLINE
 DOCUMENT NUMBER: 99003530 PubMed ID: 9784418
 TITLE: Molecular cloning and characterization of human PDE8B, a novel thyroid-specific isozyme of 3',5'-cyclic nucleotide phosphodiesterase.
 AUTHOR: Hayashi M; Matsushima K; Ohashi H; Tsunoda H; Murase S; Kwarada Y; Tanaka T
 CORPORATE SOURCE: Department of Molecular and Cellular Pharmacology, Department of Medical Informatics, First Department of Surgery, Mie University School of Medicine, 2-174 Edobashi,
 SOURCE: Tsu, Mie, 514, Japan.
 BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1998 Sep 29) 250 (3) 751-6.
 Journal code: 0372516. ISSN: 0006-291X.
 PUB. COUNTRY: United States
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF079529
 ENTRY MONTH: 199811
 ENTRY DATE: Entered STN: 19990106
 Last Updated on STN: 19990106
 Entered Medline: 19981123

L8 ANSWER 251 OF 355 MEDLINE DUPLICATE 163
 ACCESSION NUMBER: 1998187249 MEDLINE
 DOCUMENT NUMBER: 98187249 PubMed ID: 9526501
 TITLE: NAD(+)-dependent isocitrate dehydrogenase from Arabidopsis thaliana. Characterization of two closely related subunits.
 AUTHOR: Behal R H; Oliver D J
 CORPORATE SOURCE: Department of Botany, Iowa State University, Ames 50011-1020, USA.
 SOURCE: PLANT MOLECULAR BIOLOGY, (1998 Mar) 36 (5) 691-8.
 Journal code: 9106343. ISSN: 0167-4412.
 PUB. COUNTRY: Netherlands
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF015923; GENBANK-U81993; GENBANK-U81994; GENBANK-U82203

ENTRY MONTH: 199804
ENTRY DATE: Entered STN: 19980430
Last Updated on STN: 20000303
Entered Medline: 19980421

L8 ANSWER 252 OF 355 MEDLINE DUPLICATE 164
ACCESSION NUMBER: 1998162595 MEDLINE
DOCUMENT NUMBER: 98162595 PubMed ID: 9500987
TITLE: CYP86A1 from Arabidopsis thaliana encodes a cytochrome
P450-dependent fatty acid omega-hydroxylase.
AUTHOR: Benveniste I; Tijet N; Adas F; Philipps G; Salaun J P;
Durst F
CORPORATE SOURCE: Institut de Biologie Moleculaire des Plantes-CNRS,
Departement d'Enzymologie Cellulaire et Moleculaire,
Strasbourg, France..
irene.benveniste@bota-ulp.u-strasbg.fr
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1998
Feb 24) 243 (3) 688-93.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X90458
ENTRY MONTH: 199803
ENTRY DATE: Entered STN: 19980410
Last Updated on STN: 20020420
Entered Medline: 19980330

L8 ANSWER 253 OF 355 MEDLINE DUPLICATE 165
ACCESSION NUMBER: 1999155804 MEDLINE
DOCUMENT NUMBER: 99155804 PubMed ID: 10036779
TITLE: Use of a proteome strategy for tagging proteins present at
the plasma membrane.
AUTHOR: Santoni V; Rouquie D; Doumas P; Mansion M; Boutry M;
Degand
H; Dupree P; Packman L; Sherrier J; Prime T; Bauw G;
Posada
E; Rouze P; Dehais P; Sahnoun I; Barlier I; Rossignol M
CORPORATE SOURCE: Biochimie et Physiologie Moleculaire des Plantes,
INRA/ENSA-M/CNRS URA 2133, Montpellier, France.
SOURCE: PLANT JOURNAL, (1998 Dec) 16 (5) 633-41.
Journal code: 9207397. ISSN: 0960-7412.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990402
Last Updated on STN: 19990402
Entered Medline: 19990325

L8 ANSWER 254 OF 355 MEDLINE
ACCESSION NUMBER: 1999072164 MEDLINE
DOCUMENT NUMBER: 99072164 PubMed ID: 9856344
TITLE: Expressed sequence tags of fruits, peels, and carpels and
analysis of mRNA expression levels of the tagged cDNAs of
fruits from the Fuji apple.
AUTHOR: Sung S K; Jeong D H; Nam J; Kim S H; Kim S R; An G
CORPORATE SOURCE: Department of Life Science, Pohang University of Science
and Technology, Korea.

SOURCE: MOLECULES AND CELLS, (1998 Oct 31) 8 (5) 565-77.
Journal code: 9610936. ISSN: 1016-8478.

PUB. COUNTRY: KOREA
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AT000010; GENBANK-AT000029; GENBANK-AT000047;
GENBANK-AT000062; GENBANK-AT000091; GENBANK-AT000094;
GENBANK-AT000096; GENBANK-AT000097; GENBANK-AT000107;
GENBANK-AT000109; GENBANK-AT000124; GENBANK-AT000134;
GENBANK-AT000140; GENBANK-AT000157; GENBANK-AT000165;
GENBANK-AT000178; GENBANK-AT000216; GENBANK-AT000243;
GENBANK-AT000253; GENBANK-AT000294; GENBANK-AT000295;
GENBANK-AT000297; GENBANK-AT000307; GENBANK-AT000344;
GENBANK-AT000349; GENBANK-AT000382; GENBANK-AT000406;
GENBANK-AT000413; GENBANK-AT000417; GENBANK-AT000425; +

ENTRY MONTH: 199903

ENTRY DATE: Entered STN: 19990316
Last Updated on STN: 19990316
Entered Medline: 19990304

L8 ANSWER 255 OF 355 MEDLINE DUPLICATE 166

ACCESSION NUMBER: 1999097352 MEDLINE

DOCUMENT NUMBER: 99097352 PubMed ID: 9878255

TITLE: Molecular cloning of a gene on chromosome 19q12 coding for
a novel intracellular protein: analysis of expression in
human and mouse tissues and in human tumor cells,
particularly Reed-Sternberg cells in Hodgkin disease.

AUTHOR: Van Leuven F; Torrekens S; Moechars D; Hilliker C;
Buellens

CORPORATE SOURCE: M; Bollen M; Delabie J
Experimental Genetics Group, Center for Human Genetics,
Flemish Institute for Biotechnology, Department of
Biochemistry, K.U. Leuven, Campus Gasthuisberg, Louvain,
B-3000, Belgium.. FREDVL@MED.KULEUVEN.AC.BE

SOURCE: GENOMICS, (1998 Dec 15) 54 (3) 511-20.
Journal code: 8800135. ISSN: 0888-7543.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AF091095; GENBANK-AF091096

ENTRY MONTH: 199902

ENTRY DATE: Entered STN: 19990311
Last Updated on STN: 19990311
Entered Medline: 19990223

L8 ANSWER 256 OF 355 MEDLINE DUPLICATE 167

ACCESSION NUMBER: 1999097349 MEDLINE

DOCUMENT NUMBER: 99097349 PubMed ID: 9878252

TITLE: Evolutionarily conserved, "acatalytic" carbonic
anhydrase-related protein XI contains a sequence motif
present in the neuropeptide sauvagine: the human CA-RP XI
gene (CA11) is embedded between the secretor gene cluster
and the DBP gene at 19q13.3.

AUTHOR: Lovejoy D A; Hewett-Emmett D; Porter C A; Cepoi D;
Sheffield A; Vale W W; Tashian R E

CORPORATE SOURCE: The Clayton Foundation Laboratories for Peptide Biology,
The Salk Institute, 10010 North Torrey Pines Road, La
Jolla, California, 92037, USA.

CONTRACT NUMBER: DK-26741 (NIDDK)

SOURCE: GM 24681 (NIGMS)
GENOMICS, (1998 Dec 15) 54 (3) 484-93.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF050105; GENBANK-AF050106; GENBANK-Y07785
ENTRY MONTH: 199902
ENTRY DATE: Entered STN: 19990311
Last Updated on STN: 20000303
Entered Medline: 19990223

L8 ANSWER 257 OF 355 MEDLINE DUPLICATE 168
ACCESSION NUMBER: 1999013437 MEDLINE
DOCUMENT NUMBER: 99013437 PubMed ID: 9799093
TITLE: In silico-initiated cloning and molecular characterization
of a novel human member of the L1 gene family of neural
cell adhesion molecules.
AUTHOR: Wei M H; Karavanova I; Ivanov S V; Popescu N C; Keck C L;
Pack S; Eisen J A; Lerman M I
CORPORATE SOURCE: Intramural Research Support Program, SAIC Frederick,
National Cancer Institute-Frederick Cancer Research and
Development Center, MD 21702-1201, USA.
CONTRACT NUMBER: NO1-CO-56000 (NCI)
SOURCE: HUMAN GENETICS, (1998 Sep) 103 (3) 355-64.
Journal code: 7613873. ISSN: 0340-6717.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199811
ENTRY DATE: Entered STN: 19990106
Last Updated on STN: 19990106
Entered Medline: 19981119

L8 ANSWER 258 OF 355 MEDLINE DUPLICATE 169
ACCESSION NUMBER: 1998149982 MEDLINE
DOCUMENT NUMBER: 98149982 PubMed ID: 9480748
TITLE: FACL4, a new gene encoding long-chain acyl-CoA synthetase
4, is deleted in a family with Alport syndrome,
elliptocytosis, and mental retardation.
AUTHOR: Piccini M; Vitelli F; Bruttini M; Pober B R; Jonsson J J;
Villanova M; Zollo M; Borsani G; Ballabio A; Renieri A
CORPORATE SOURCE: Genetica Medica, Policlinico le Scotte, 53100 Siena,
Italy.
SOURCE: GENOMICS, (1998 Feb 1) 47 (3) 350-8.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-Y12777; GENBANK-Y13058
ENTRY MONTH: 199804
ENTRY DATE: Entered STN: 19980416
Last Updated on STN: 19980416
Entered Medline: 19980408

L8 ANSWER 259 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1998:404999 BIOSIS
DOCUMENT NUMBER: PREV199800404999

TITLE: Partial sequence analysis of Hibiscus syriacus cDNA clones.
 AUTHOR(S): Um, Bo Young; Pak, Chun Ho (1); Ok, Seung Han; Chung, Young
 CORPORATE SOURCE: Soo; Shin, Jeong Sheop
 (1) Dep. Horticultural Sci., Korea Univ., Seoul 136-701 South Korea
 SOURCE: Journal of the Korean Society for Horticultural Science, (June, 1998) Vol. 39, No. 3, pp. 350-354.
 ISSN: 0253-6498.
 DOCUMENT TYPE: Article
 LANGUAGE: English
 SUMMARY LANGUAGE: English; Korean

L8 ANSWER 260 OF 355 MEDLINE DUPLICATE 170
 ACCESSION NUMBER: 1998268130 MEDLINE
 DOCUMENT NUMBER: 98268130 PubMed ID: 9604771
 TITLE: Sequence analysis of libraries from individual human blastocysts.
 AUTHOR: Morozov G; Verlinsky O; Rechitsky S; Kukharensko V; Goltsman
 Y
 CORPORATE SOURCE: Reproductive Genetics Institute, Chicago, Illinois 60657, USA.
 SOURCE: JOURNAL OF ASSISTED REPRODUCTION AND GENETICS, (1998 May) 15 (5) 338-43.
 Journal code: 9206495. ISSN: 1058-0468.
 PUB. COUNTRY: United States
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199808
 ENTRY DATE: Entered STN: 19980828
 Last Updated on STN: 19980828
 Entered Medline: 19980818

L8 ANSWER 261 OF 355 MEDLINE DUPLICATE 171
 ACCESSION NUMBER: 1998342085 MEDLINE
 DOCUMENT NUMBER: 98342085 PubMed ID: 9675132
 TITLE: JH8, a gene highly homologous to the mouse jerky gene, maps
 to the region for childhood absence epilepsy on 8q24.
 COMMENT: Erratum in: Biochem Biophys Res Commun 1998 Sep 18;250(2):536
 AUTHOR: Morita R; Miyazaki E; Fong C Y; Chen X N; Korenberg J R; Delgado-Escueta A V; Yamakawa K
 CORPORATE SOURCE: Brain Science Institute, The Institute of Physical and Chemical Research (RIKEN), 2-1 Hirosawa, Wako-shi, Saitama,
 351-0198, Japan.
 CONTRACT NUMBER: 5P01-NS21908 (NINDS)
 P01 HD17449 (NICHD)
 SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1998 Jul 20) 248 (2) 307-14.
 Journal code: 0372516. ISSN: 0006-291X.
 PUB. COUNTRY: United States
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF072467; GENBANK-AF072468; GENBANK-AF072469

ENTRY MONTH: 199808
ENTRY DATE: Entered STN: 19980903
Last Updated on STN: 20000303
Entered Medline: 19980827

L8 ANSWER 262 OF 355 MEDLINE DUPLICATE 172
ACCESSION NUMBER: 1998248992 MEDLINE
DOCUMENT NUMBER: 98248992 PubMed ID: 9587421
TITLE: Identification of a novel human glutathione S-transferase
using bioinformatics.
AUTHOR: Liu S; Stoesz S P; Pickett C B
CORPORATE SOURCE: Schering-Plough Research Institute, Kenilworth, New Jersey
07033, USA.
SOURCE: ARCHIVES OF BIOCHEMISTRY AND BIOPHYSICS, (1998 Apr 15) 352
(2) 306-13.
Journal code: 0372430. ISSN: 0003-9861.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF025887
ENTRY MONTH: 199806
ENTRY DATE: Entered STN: 19980611
Last Updated on STN: 19980611
Entered Medline: 19980603

L8 ANSWER 263 OF 355 MEDLINE DUPLICATE 173
ACCESSION NUMBER: 1998207242 MEDLINE
DOCUMENT NUMBER: 98207242 PubMed ID: 9545632
TITLE: Structure and methylation-based silencing of a gene
(DBCCR1) within a candidate bladder cancer tumor
suppressor
region at 9q32-q33.
AUTHOR: Habuchi T; Luscombe M; Elder P A; Knowles M A
CORPORATE SOURCE: Molecular Genetics Laboratory, Marie Curie Research
Institute, Oxted, Surrey, United Kingdom.
SOURCE: GENOMICS, (1998 Mar 15) 48 (3) 277-88.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF027734
ENTRY MONTH: 199806
ENTRY DATE: Entered STN: 19980618
Last Updated on STN: 20000303
Entered Medline: 19980608

L8 ANSWER 264 OF 355 MEDLINE DUPLICATE 174
ACCESSION NUMBER: 1998317539 MEDLINE
DOCUMENT NUMBER: 98317539 PubMed ID: 9653652
TITLE: A putative human zinc-finger gene (ZFPL1) on 11q13, highly
conserved in the mouse and expressed in exocrine pancreas.
The European Consortium on MEN 1.
AUTHOR: Hoppener J W; De Wit M J; Simarro-Doorten A Y; Roijers J
F;
van Herrewaarden H M; Lips C J; Parente F; Quincey D;
Gaudray P; Khodaei S; Weber G; Teh B; Farnebo F; Larsson
C;
Zhang C X; Calender A; Pannett A A; Forbes S A; Bassett J
H; Thakker R V; Lemmens I; Van de Ven W J; Kas K

CORPORATE SOURCE: Department of Internal Medicine, Utrecht University
Hospital, The Netherlands.. j.w.m.hoeppener@lab.azu.nl
SOURCE: GENOMICS, (1998 Jun 1) 50 (2) 251-9.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199810
ENTRY DATE: Entered STN: 19981008
Last Updated on STN: 19981008
Entered Medline: 19981001

L8 ANSWER 265 OF 355 MEDLINE
ACCESSION NUMBER: 2000194935 MEDLINE
DOCUMENT NUMBER: 20194935 PubMed ID: 10732797
TITLE: Isolation and characterization of trinucleotide repeat
containing partial transcripts in human spinal cord.
AUTHOR: Kaushik N; Malaspina A; Schalling M; Baas F; de Bellerocche
J
CORPORATE SOURCE: Department of Neuromuscular Diseases, Imperial College
School of Medicine at Charing Cross Hospital, London, UK.
SOURCE: NEUROGENETICS, (1998 Aug) 1 (4) 239-47.
Journal code: 9709714. ISSN: 1364-6745.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200004
ENTRY DATE: Entered STN: 20000421
Last Updated on STN: 20000421
Entered Medline: 20000413

L8 ANSWER 266 OF 355 MEDLINE DUPLICATE 175
ACCESSION NUMBER: 1998390186 MEDLINE
DOCUMENT NUMBER: 98390186 PubMed ID: 9722946
TITLE: Cloning of the human interferon-related developmental
regulator (IFRD1) gene coding for the PC4 protein, a
member
of a novel family of developmentally regulated genes.
AUTHOR: Buanne P; Incerti B; Guardavaccaro D; Avvantaggiato V;
Simeone A; Tirone F
CORPORATE SOURCE: Istituto di Neurobiologia CNR, Rome, Italy.
SOURCE: GENOMICS, (1998 Jul 15) 51 (2) 233-42.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-J04511; GENBANK-Y10313
ENTRY MONTH: 199811
ENTRY DATE: Entered STN: 19990106
Last Updated on STN: 20000303
Entered Medline: 19981105

L8 ANSWER 267 OF 355 MEDLINE DUPLICATE 176
ACCESSION NUMBER: 1998433873 MEDLINE
DOCUMENT NUMBER: 98433873 PubMed ID: 9762909
TITLE: cDNA cloning of Brassica napus malonyl-CoA:ACP
transacylase
(MCAT) (fab D) and complementation of an E. coli MCAT

mutant.
 AUTHOR: Simon J W; Slabas A R
 CORPORATE SOURCE: Department of Biological Sciences, University of Durham,
 Science Laboratories, UK.. j.w.simon@durham.ac.uk
 SOURCE: FEBS LETTERS, (1998 Sep 18) 435 (2-3) 204-6.
 Journal code: 0155157. ISSN: 0014-5793.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AJ007046
 ENTRY MONTH: 199810
 ENTRY DATE: Entered STN: 19981029
 Last Updated on STN: 19981029
 Entered Medline: 19981022

L8 ANSWER 268 OF 355 MEDLINE DUPLICATE 177
 ACCESSION NUMBER: 1999000838 MEDLINE
 DOCUMENT NUMBER: 99000838 PubMed ID: 9782084
 TITLE: Cloning and localization of a human diphthamide
 biosynthesis-like protein-2 gene, DPH2L2.
 AUTHOR: Schultz D C; Balasara B R; Testa J R; Godwin A K
 CORPORATE SOURCE: Department of Medical Oncology, Fox Chase Cancer Center,
 Philadelphia, Pennsylvania, 19111, USA.
 CONTRACT NUMBER: CA-06927 (NCI)
 R01CA70329 (NCI)
 SOURCE: GENOMICS, (1998 Sep 1) 52 (2) 186-91.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF053003
 ENTRY MONTH: 199812
 ENTRY DATE: Entered STN: 19990115
 Last Updated on STN: 19990115
 Entered Medline: 19981207

L8 ANSWER 269 OF 355 MEDLINE DUPLICATE 178
 ACCESSION NUMBER: 1998146269 MEDLINE
 DOCUMENT NUMBER: 98146269 PubMed ID: 9473664
 TITLE: Expression analysis and chromosomal mapping of a novel
 human gene, APRIL, encoding an acidic protein rich in
 leucines.
 AUTHOR: Mencinger M; Panagopoulos I; Contreras J A; Mitelman F;
 Aman P
 CORPORATE SOURCE: Department of Clinical Genetics, University Hospital,
 Lund,
 Sweden.. marina.mencinger@klingen.lu.se
 SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (1998 Jan 21) 1395 (2)
 176-80.
 Journal code: 0217513. ISSN: 0006-3002.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-Y07569; GENBANK-Y07570; GENBANK-Y07969
 ENTRY MONTH: 199803
 ENTRY DATE: Entered STN: 19980326
 Last Updated on STN: 20020420
 Entered Medline: 19980319

L8 ANSWER 270 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1998:318589 BIOSIS

DOCUMENT NUMBER: PREV199800318589

TITLE: Expressed sequence tags (ESTs) of *Biomphalaria glabrata*,
an

intermediate snail host of *Schistosoma mansoni*: Use in the
identification of RFLP markers.

AUTHOR(S): Knight, Matty (1); Miller, Andre N. (1); Geoghagen, Neil
S.

M.; Lewis, Fred A. (1); Kerlavage, Anthony R.

CORPORATE SOURCE: (1) Biomed. Res. Inst., Rockville, MD 20852 USA

SOURCE: Malacologia, (1998) Vol. 39, No. 1-2, pp. 175-182.

ISSN: 0076-2997.

DOCUMENT TYPE: Article

LANGUAGE: English

L8 ANSWER 271 OF 355 MEDLINE

DUPLICATE 179

ACCESSION NUMBER: 1998201609 MEDLINE

DOCUMENT NUMBER: 98201609 PubMed ID: 9524256

TITLE: A novel 52 kDa protein induces apoptosis and concurrently
activates c-Jun N-terminal kinase 1 (JNK1) in mouse
C3H10T1/2 fibroblasts.

AUTHOR: Sun L; Liu Y; Fremont M; Schwarz S; Siegmann M; Matthies
R;

Jost J P

CORPORATE SOURCE: Friedrich Miescher Institute, Basel, Switzerland.

SOURCE: GENE, (1998 Feb 27) 208 (2) 157-66.

Journal code: 7706761. ISSN: 0378-1119.

PUB. COUNTRY: Netherlands

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AF029071

ENTRY MONTH: 199805

ENTRY DATE: Entered STN: 19980514

Last Updated on STN: 20000303

Entered Medline: 19980504

L8 ANSWER 272 OF 355 MEDLINE

DUPLICATE 180

ACCESSION NUMBER: 1998121324 MEDLINE

DOCUMENT NUMBER: 98121324 PubMed ID: 9461426

TITLE: Molecular cloning and characterization of a highly
conserved human 67-kDa laminin receptor pseudogene mapping
to Xq21.3.

AUTHOR: Richardson M P; Braybrook C; Tham M; Moore G E; Stanier P

CORPORATE SOURCE: Molecular Biology Laboratory, Institute of Obstetrics and
Gynaecology, Queen Charlotte's and Chelsea Hospital,
London, UK.

SOURCE: GENE, (1998 Jan 5) 206 (1) 145-50.

Journal code: 7706761. ISSN: 0378-1119.

PUB. COUNTRY: Netherlands

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199802

ENTRY DATE: Entered STN: 19980306

Last Updated on STN: 19980306

Entered Medline: 19980226

L8 ANSWER 273 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1998:404898 BIOSIS
 DOCUMENT NUMBER: PREV199800404898
 TITLE: Analysis of 176 expressed sequence tags generated from
 cDNA clones of hot pepper by single-pass sequencing.
 AUTHOR(S): Hong, Sung-Tae; Chung, Jae-Eun; An, Gynheung; Kim,
 Seong-Ryong (1)
 CORPORATE SOURCE: (1) Dep. Life Sci., Sogang Univ., Seoul 121-742 South
 Korea
 SOURCE: Journal of Plant Biology, (June, 1998) Vol. 41, No. 2, pp.
 116-124.
 DOCUMENT TYPE: Article
 LANGUAGE: English

L8 ANSWER 274 OF 355 MEDLINE DUPLICATE 181
 ACCESSION NUMBER: 1998234549 MEDLINE
 DOCUMENT NUMBER: 98234549 PubMed ID: 9570954
 TITLE: Identification, characterization, and genetic mapping of
 Rad51d, a new mouse and human RAD51/RecA-related gene.
 AUTHOR: Pittman D L; Weinberg L R; Schimenti J C
 CORPORATE SOURCE: Jackson Laboratory, Bar Harbor, Maine 04609, USA.
 CONTRACT NUMBER: CA34196 (NCI)
 GM45415 (NIGMS)
 HD07065 (NICHD)
 +
 SOURCE: GENOMICS, (1998 Apr 1) 49 (1) 103-11.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF034955; GENBANK-AF034956
 ENTRY MONTH: 199806
 ENTRY DATE: Entered STN: 19980708
 Last Updated on STN: 19980708
 Entered Medline: 19980625

L8 ANSWER 275 OF 355 MEDLINE DUPLICATE 182
 ACCESSION NUMBER: 1998364425 MEDLINE
 DOCUMENT NUMBER: 98364425 PubMed ID: 9699269
 TITLE: Characterization of FSH-regulated genes isolated by mRNA
 differential display from pig ovarian granulosa cells.
 AUTHOR: Clouscard-Martinato C; Mulsant P; Robic A; Bonnet A;
 Gasser
 F; Hatey F
 CORPORATE SOURCE: Laboratoire de Genetique Cellulaire, INRA, Castanet
 Tolosan, France.
 SOURCE: ANIMAL GENETICS, (1998 Apr) 29 (2) 98-106.
 Journal code: 8605704. ISSN: 0268-9146.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199809
 ENTRY DATE: Entered STN: 19981006
 Last Updated on STN: 19981006
 Entered Medline: 19980924

L8 ANSWER 276 OF 355 MEDLINE DUPLICATE 183
 ACCESSION NUMBER: 1999070056 MEDLINE
 DOCUMENT NUMBER: 99070056 PubMed ID: 9852954

TITLE: Generation of expressed sequence tags as physical landmarks
in the genome of Trypanosoma brucei.
AUTHOR: Djikeng A; Agufa C; Donelson J E; Majiwa P A
CORPORATE SOURCE: International Livestock Research Institute (ILRI), Nairobi, Kenya.
SOURCE: GENE, (1998 Oct 9) 221 (1) 93-106.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199812
ENTRY DATE: Entered STN: 19990115
Last Updated on STN: 19990115
Entered Medline: 19981231

L8 ANSWER 277 OF 355 MEDLINE
ACCESSION NUMBER: 1999449047 MEDLINE
DOCUMENT NUMBER: 99449047 PubMed ID: 10520737
TITLE: Sequencing of 42kb of the APO E-C2 gene cluster reveals a new gene: PEREC1.
AUTHOR: Freitas E M; Zhang W J; Lalonde J P; Tay G K; Gaudieri S; Ashworth L K; Van Bockxmeer F M; Dawkins R L
CORPORATE SOURCE: Centre for Molecular Immunology and Instrumentation, University of Western Australia, Nedlands.
SOURCE: DNA SEQUENCE, (1998) 9 (2) 89-100.
Journal code: 9107800. ISSN: 1042-5179.
PUB. COUNTRY: Switzerland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB012576
ENTRY MONTH: 199912
ENTRY DATE: Entered STN: 20000113
Last Updated on STN: 20000113
Entered Medline: 19991209

L8 ANSWER 278 OF 355 MEDLINE DUPLICATE 184
ACCESSION NUMBER: 1998324444 MEDLINE
DOCUMENT NUMBER: 98324444 PubMed ID: 9662067
TITLE: Digital cloning: identification of human cDNAs homologous to novel kinases through expressed sequence tag database searching.
AUTHOR: Chen H C; Kung H J; Robinson D
CORPORATE SOURCE: Molecular and Genomic Medicine Division, National Health Research Institutes, Taipei, Taiwan, ROC.
CONTRACT NUMBER: CA 57179 (NCI)
CA39207 (NCI)
DK52659 (NIDDK)
SOURCE: JOURNAL OF BIOMEDICAL SCIENCE, (1998) 5 (2) 86-92.
Journal code: 9421567. ISSN: 1021-7770.
PUB. COUNTRY: Switzerland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199809
ENTRY DATE: Entered STN: 19980925
Last Updated on STN: 19980925
Entered Medline: 19980916

L8 ANSWER 279 OF 355 MEDLINE DUPLICATE 185
 ACCESSION NUMBER: 1998163747 MEDLINE
 DOCUMENT NUMBER: 98163747 PubMed ID: 9503017
 TITLE: The hyaluronidase gene HYAL1 maps to chromosome 3p21.2-p21.3 in human and 9F1-F2 in mouse, a conserved candidate tumor suppressor locus.
 AUTHOR: Csoka T B; Frost G I; Heng H H; Scherer S W; Mohapatra G; Stern R
 CORPORATE SOURCE: Department of Gerontology, University Medical School of Debrecen, Hungary.
 CONTRACT NUMBER: GM46765 (NIGMS)
 SOURCE: GENOMICS, (1998 Feb 15) 48 (1) 63-70.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF011567; GENBANK-U96078
 ENTRY MONTH: 199804
 ENTRY DATE: Entered STN: 19980507
 Last Updated on STN: 20000303
 Entered Medline: 19980424

L8 ANSWER 280 OF 355 MEDLINE DUPLICATE 186
 ACCESSION NUMBER: 1998400255 MEDLINE
 DOCUMENT NUMBER: 98400255 PubMed ID: 9731529
 TITLE: Mass spectrometry and EST-database searching allows characterization of the multi-protein spliceosome complex.
 COMMENT: Comment in: Nat Genet. 1998 Sep;20(1):5-6
 AUTHOR: Neubauer G; King A; Rappsilber J; Calvio C; Watson M; Ajuh P; Sleeman J; Lamond A; Mann M
 CORPORATE SOURCE: Protein & Peptide Group, European Molecular Biology Laboratory, Heidelberg, Germany.
 SOURCE: NATURE GENETICS, (1998 Sep) 20 (1) 46-50.
 Journal code: 9216904. ISSN: 1061-4036.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF081788; GENBANK-AF083383; GENBANK-AF083384; GENBANK-AF083385
 ENTRY MONTH: 199810
 ENTRY DATE: Entered STN: 19981029
 Last Updated on STN: 20000303
 Entered Medline: 19981022

L8 ANSWER 281 OF 355 MEDLINE DUPLICATE 187
 ACCESSION NUMBER: 1998234542 MEDLINE
 DOCUMENT NUMBER: 98234542 PubMed ID: 9570947
 TITLE: Divergently transcribed overlapping genes expressed in liver and kidney and located in the 11p15.5 imprinted domain.
 AUTHOR: Cooper P R; Smilinich N J; Day C D; Nowak N J; Reid L H; Pearsall R S; Reece M; Prawitt D; Landers J; Housman D E; Winterpacht A; Zabel B U; Pelletier J; Weissman B E; Shows T B; Higgins M J
 CORPORATE SOURCE: Department of Human Genetics, Roswell Park Cancer Institute, Buffalo, New York 14263, USA.
 CONTRACT NUMBER: CA63176 (NCI)

SOURCE: CA63333 (NCI)
 HG00333 (NHGRI)
 GENOMICS, (1998 Apr 1) 49 (1) 38-51.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AC001228; GENBANK-AF087428
 ENTRY MONTH: 199806
 ENTRY DATE: Entered STN: 19980708
 Last Updated on STN: 20000512
 Entered Medline: 19980625

L8 ANSWER 282 OF 355 MEDLINE DUPLICATE 188
 ACCESSION NUMBER: 1999077824 MEDLINE
 DOCUMENT NUMBER: 99077824 PubMed ID: 9858671
 TITLE: Fluorescent differential display analysis of gene
 expression in apoptotic neuroblastoma cells.
 AUTHOR: Choi D K; Ito T; Mitsui Y; Sakaki Y
 CORPORATE SOURCE: Human Genome Center, Institute of Medical Science,
 University of Tokyo, 4-6-1 Shirokanedai, Minato-ku, Tokyo
 108, Japan.
 SOURCE: GENE, (1998 Nov 26) 223 (1-2) 21-31.
 Journal code: 7706761. ISSN: 0378-1119.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-U63289
 ENTRY MONTH: 199903
 ENTRY DATE: Entered STN: 19990316
 Last Updated on STN: 19990316
 Entered Medline: 19990303

L8 ANSWER 283 OF 355 MEDLINE DUPLICATE 189
 ACCESSION NUMBER: 1998234205 MEDLINE
 DOCUMENT NUMBER: 98234205 PubMed ID: 9574906
 TITLE: Differentially expressed genes in the Trypanosoma brucei
 life cycle identified by RNA fingerprinting.
 AUTHOR: Mathieu-Daude F; Welsh J; Davis C; McClelland M
 CORPORATE SOURCE: Sidney Kimmel Cancer Center, San Diego, CA 92121, USA.
 CONTRACT NUMBER: AI 34829 (NIAID)
 CA 68822 (NCI)
 NS 33377 (NINDS)
 +
 SOURCE: MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (1998 Apr 1) 92
 (1)
 15-28.
 Journal code: 8006324. ISSN: 0166-6851.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF009703; GENBANK-AF009704; GENBANK-AF009705;
 GENBANK-AF009706; GENBANK-AF009707; GENBANK-AF009708;
 GENBANK-AF009709; GENBANK-AF009710; GENBANK-AF009711;
 GENBANK-AF009712; GENBANK-AF009713; GENBANK-AF009714;
 GENBANK-AF009715; GENBANK-AF009716; GENBANK-AF009717;
 GENBANK-AF009718; GENBANK-AF009719; GENBANK-AF009720;
 GENBANK-AF009721; GENBANK-AF009722; GENBANK-AF009723;

GENBANK-AF009724; GENBANK-AF009725; GENBANK-AF009726;
GENBANK-AF009727; GENBANK-AF009728; GENBANK-AF009729;
GENBANK-AF009730; GENBANK-U49237; GENBANK-U53929

ENTRY MONTH: 199806
ENTRY DATE: Entered STN: 19980708
Last Updated on STN: 20000303
Entered Medline: 19980622

L8 ANSWER 284 OF 355 MEDLINE DUPLICATE 190
ACCESSION NUMBER: 1998126432 MEDLINE
DOCUMENT NUMBER: 98126432 PubMed ID: 9465292
TITLE: An expressed-sequence-tag database of the human prostate:
sequence analysis of 1168 cDNA clones.
AUTHOR: Nelson P S; Ng W L; Schummer M; True L D; Liu A Y;
Bumgarner R E; Ferguson C; Dimak A; Hood L
CORPORATE SOURCE: Department of Molecular Biotechnology, University of
Washington, Seattle 98195, USA.. psnels@u.washington.edu
SOURCE: GENOMICS, (1998 Jan 1) 47 (1) 12-25.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AA447269; GENBANK-AA447270; GENBANK-AA447271;
GENBANK-AA447272; GENBANK-AA447273; GENBANK-AA447274;
GENBANK-AA447275; GENBANK-AA447276; GENBANK-AA447277;
GENBANK-AA447278; GENBANK-AA447279; GENBANK-AA447280;
GENBANK-AA447281; GENBANK-AA447282; GENBANK-AA447283;
GENBANK-AA447284; GENBANK-AA447285; GENBANK-AA447286;
GENBANK-AA447287; GENBANK-AA447288; GENBANK-AA447289;
GENBANK-AA447290; GENBANK-AA447291; GENBANK-AA447292;
GENBANK-AA447293; GENBANK-AA447294; GENBANK-AA447295;
GENBANK-AA447296; GENBANK-AA447297; GENBANK-AA447298; +
ENTRY MONTH: 199804
ENTRY DATE: Entered STN: 19980430
Last Updated on STN: 19980430
Entered Medline: 19980420

L8 ANSWER 285 OF 355 MEDLINE DUPLICATE 191
ACCESSION NUMBER: 1998324209 MEDLINE
DOCUMENT NUMBER: 98324209 PubMed ID: 9520496
TITLE: The Merck Gene Index browser: an extensible data
integration system for gene finding, gene characterization
and EST data mining.
AUTHOR: Eckman B A; Aaronson J S; Borkowski J A; Bailey W J;
Elliston K O; Williamson A R; Blevins R A
CORPORATE SOURCE: Department of Bioinformatics, Merck Research Laboratories,
West Point, PA, USA.. barbara_eckman@sbphrd.com
SOURCE: BIOINFORMATICS, (1998) 14 (1) 2-13.
Journal code: 9808944. ISSN: 1367-4803.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199809
ENTRY DATE: Entered STN: 19980917
Last Updated on STN: 19980917
Entered Medline: 19980908

L8 ANSWER 286 OF 355 MEDLINE
ACCESSION NUMBER: 97264341 MEDLINE

DOCUMENT NUMBER: 97264341 PubMed ID: 9110174
 TITLE: Large-scale concatenation cDNA sequencing.
 AUTHOR: Yu W; Andersson B; Worley K C; Muzny D M; Ding Y; Liu W;
 Ricafrente J Y; Wentland M A; Lennon G; Gibbs R A
 CONTRACT NUMBER: 1F32 HG00169-01 (NHGRI)
 P30 HG00210-05 (NHGRI)
 R01 HG00823 (NHGRI)
 SOURCE: GENOME RESEARCH, (1997 Apr) 7 (4) 353-8.
 Journal code: 9518021. ISSN: 1088-9051.
 PUB. COUNTRY: United States
 Letter
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF007128; GENBANK-AF007129; GENBANK-AF007130;
 GENBANK-AF007131; GENBANK-AF007132; GENBANK-AF007133;
 GENBANK-AF007134; GENBANK-AF007135; GENBANK-AF007136;
 GENBANK-AF007137; GENBANK-AF007138; GENBANK-AF007139;
 GENBANK-AF007140; GENBANK-AF007141; GENBANK-AF007142;
 GENBANK-AF007143; GENBANK-AF007144; GENBANK-AF007145;
 GENBANK-AF007146; GENBANK-AF007147; GENBANK-AF007148;
 GENBANK-AF007149; GENBANK-AF007150; GENBANK-AF007151;
 GENBANK-AF007152; GENBANK-AF007153; GENBANK-AF007154
 ENTRY MONTH: 199706
 ENTRY DATE: Entered STN: 19970630
 Last Updated on STN: 20000303
 Entered Medline: 19970617

L8 ANSWER 287 OF 355 MEDLINE DUPLICATE 192
 ACCESSION NUMBER: 1998038808 MEDLINE
 DOCUMENT NUMBER: 98038808 PubMed ID: 9372971
 TITLE: Molecular cloning and characterization of human JNKK2, a
 novel Jun NH2-terminal kinase-specific kinase.
 AUTHOR: Wu Z; Wu J; Jacinto E; Karin M
 CORPORATE SOURCE: Department of Pharmacology, University of California, San
 Diego, La Jolla 92093-0636, USA.
 CONTRACT NUMBER: ES04151 (NIEHS)
 SOURCE: MOLECULAR AND CELLULAR BIOLOGY, (1997 Dec) 17 (12)
 7407-16.
 Journal code: 8109087. ISSN: 0270-7306.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF014401
 ENTRY MONTH: 199712
 ENTRY DATE: Entered STN: 19980109
 Last Updated on STN: 20000606
 Entered Medline: 19971216

L8 ANSWER 288 OF 355 MEDLINE DUPLICATE 193
 ACCESSION NUMBER: 97422886 MEDLINE
 DOCUMENT NUMBER: 97422886 PubMed ID: 9276951
 TITLE: Construction of a Lotus japonicus late nodulin expressed
 sequence tag library and identification of novel
 nodule-specific genes.
 AUTHOR: Szczyglowski K; Hamburger D; Kapranov P; de Bruijn F J
 CORPORATE SOURCE: Department of Energy Plant Research Laboratory, Michigan
 State University, East Lansing 48824, USA..
 szczyglw@pilot.msu.edu
 SOURCE: PLANT PHYSIOLOGY, (1997 Aug) 114 (4) 1335-46.
 Journal code: 0401224. ISSN: 0032-0889.

PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF000382; GENBANK-AF000383; GENBANK-AF000384;
 GENBANK-AF000385; GENBANK-AF000386; GENBANK-AF000387;
 GENBANK-AF000388; GENBANK-AF000389; GENBANK-AF000390;
 GENBANK-AF000391; GENBANK-AF000392; GENBANK-AF000393;
 GENBANK-AF000394; GENBANK-AF000395; GENBANK-AF000396;
 GENBANK-AF000397; GENBANK-AF000398; GENBANK-AF000399;
 GENBANK-AF000400; GENBANK-AF000401; GENBANK-AF000402;
 GENBANK-AF000403; GENBANK-AF000404; GENBANK-AF000405;
 GENBANK-AF000406; GENBANK-AF000407; GENBANK-AF000408
 ENTRY MONTH: 199709
 ENTRY DATE: Entered STN: 19971008
 Last Updated on STN: 20000303
 Entered Medline: 19970925

L8 ANSWER 289 OF 355 MEDLINE DUPLICATE 194
 ACCESSION NUMBER: 97376836 MEDLINE
 DOCUMENT NUMBER: 97376836 PubMed ID: 9233607
 TITLE: A novel human CC chemokine PARC that is most homologous to
 macrophage-inflammatory protein-1 alpha/LD78 alpha and
 chemotactic for T lymphocytes, but not for monocytes.
 AUTHOR: Hieshima K; Imai T; Baba M; Shoudai K; Ishizuka K;
 Nakagawa
 CORPORATE SOURCE: T; Tsuruta J; Takeya M; Sakaki Y; Takatsuki K; Miura R;
 Opdenakker G; Van Damme J; Yoshie O; Nomiyama H
 Department of Biochemistry, Kumamoto University Medical
 School, Japan.
 SOURCE: JOURNAL OF IMMUNOLOGY, (1997 Aug 1) 159 (3) 1140-9.
 Journal code: 2985117R. ISSN: 0022-1767.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
 OTHER SOURCE: GENBANK-AB000221
 ENTRY MONTH: 199708
 ENTRY DATE: Entered STN: 19970825
 Last Updated on STN: 19970825
 Entered Medline: 19970814

L8 ANSWER 290 OF 355 MEDLINE DUPLICATE 195
 ACCESSION NUMBER: 97336304 MEDLINE
 DOCUMENT NUMBER: 97336304 PubMed ID: 9193080
 TITLE: Identification of members of gene families in Arabidopsis
 thaliana by contig construction from partial cDNA
 sequences: 106 genes encoding 50 cytoplasmic ribosomal
 proteins.
 AUTHOR: Cooke R; Raynal M; Laudie M; Delseny M
 CORPORATE SOURCE: Laboratoire de Physiologie et Biologie Moleculaires
 Vegetales, UMR5545 du CNRS, Universite de Perpignan,
 France.
 SOURCE: PLANT JOURNAL, (1997 May) 11 (5) 1127-40.
 Journal code: 9207397. ISSN: 0960-7412.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-A34571; GENBANK-A36571; GENBANK-B24028;
 GENBANK-C36571; GENBANK-D38010; GENBANK-L27461;

GENBANK-L31645; GENBANK-M62396; GENBANK-S11393;
 GENBANK-S19164; GENBANK-S22789; GENBANK-S32578;
 GENBANK-S39486; GENBANK-S42260; GENBANK-S51347;
 GENBANK-U10046; GENBANK-U30454; GENBANK-U30495;
 GENBANK-X77456; GENBANK-X91958; GENBANK-X91959;
 SWISSPROT-P17094; SWISSPROT-P23358; SWISSPROT-P29766;
 SWISSPROT-P35685; SWISSPROT-P38666; SWISSPROT-P41099;
 SWISSPROT-P41127; SWISSPROT-P46286; SWISSPROT-Q07760; +
 199708
 ENTRY MONTH: Entered STN: 19970813
 ENTRY DATE: Last Updated on STN: 19990129
 Entered Medline: 19970805

L8 ANSWER 291 OF 355 LIFESCI COPYRIGHT 2002 CSA
 ACCESSION NUMBER: 1998:11835 LIFESCI
 TITLE: Long human-mouse sequence alignments reveal novel
 regulatory elements: A reason to sequence the mouse genome
 AUTHOR: Hardison, R.C.; Oeltjen, J.; Miller, W.*
 CORPORATE SOURCE: Cent. for Gene Regulation, Pennsylvania State Univ.,
 University Park, PA 16802, USA
 SOURCE: GENOME RES., (19971000) vol. 7, no. 10, pp. 959-966.
 ISSN: 1088-9051.
 DOCUMENT TYPE: Journal
 FILE SEGMENT: G
 LANGUAGE: English

L8 ANSWER 292 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 1998:6246 BIOSIS
 DOCUMENT NUMBER: PREV199800006246
 TITLE: Expressed sequence tags of citrus fruit during rapid cell
 development phase.
 AUTHOR(S): Hisada, Sunao; Akihama, Tomoya; Endo, Tomoko; Moriguchi,
 Takaya (1); Omura, Mitsuo
 CORPORATE SOURCE: (1) Dep. Citriculture, Natl. Inst. Fruit Tree Sci.,
 Okitsu,
 Shimizu, Shizuoka 424-02 Japan
 SOURCE: Journal of the American Society for Horticultural Science,
 (Nov., 1997) Vol. 122, No. 6, pp. 808-812.
 ISSN: 0003-1062.
 DOCUMENT TYPE: Article
 LANGUAGE: English

L8 ANSWER 293 OF 355 MEDLINE DUPLICATE 196
 ACCESSION NUMBER: 97312490 MEDLINE
 DOCUMENT NUMBER: 97312490 PubMed ID: 9168931
 TITLE: Molecular cloning and expression analysis of rat Rgs12 and
 Rgs14.
 AUTHOR: Snow B E; Antonio L; Suggs S; Gutstein H B; Siderovski D P
 CORPORATE SOURCE: Quantitative Biology Laboratory, Amgen Institute, Toronto,
 Ontario, Canada.
 SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1997
 Apr 28) 233 (3) 770-7.
 Journal code: 0372516. ISSN: 0006-291X.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-U92279; GENBANK-U92280
 ENTRY MONTH: 199706
 ENTRY DATE: Entered STN: 19970716
 Last Updated on STN: 20000303

Entered Medline: 19970630

L8 ANSWER 294 OF 355 MEDLINE DUPLICATE 197
ACCESSION NUMBER: 97238476 MEDLINE
DOCUMENT NUMBER: 97238476 PubMed ID: 9132061
TITLE: Sequence and RT-PCR expression analysis of two peroxidases
from Arabidopsis thaliana belonging to a novel
evolutionary
branch of plant peroxidases.
AUTHOR: Kjaersgard I V; Jespersen H M; Rasmussen S K; Welinder K G
CORPORATE SOURCE: Department of Protein Chemistry, University of Copenhagen,
Denmark.
SOURCE: PLANT MOLECULAR BIOLOGY, (1997 Mar) 33 (4) 699-708.
Journal code: 9106343. ISSN: 0167-4412.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X98189; GENBANK-X98190; GENBANK-X98313;
GENBANK-X98317
ENTRY MONTH: 199704
ENTRY DATE: Entered STN: 19970507
Last Updated on STN: 19980206
Entered Medline: 19970428

L8 ANSWER 295 OF 355 MEDLINE DUPLICATE 198
ACCESSION NUMBER: 97396144 MEDLINE
DOCUMENT NUMBER: 97396144 PubMed ID: 9245698
TITLE: Analysis of expressed sequence tags (ESTs) of the
parasitic
protozoa Entamoeba histolytica.
AUTHOR: Tanaka T; Tanaka M; Mitsui Y
CORPORATE SOURCE: Division of Host Defense Mechanism, Tokai University
School
of Medicine, Isehara, Kanagawa, Japan..
ttanaka@is.icc.u-tokai.ac.jp
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1997
Jul 30) 236 (3) 611-5.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB002699; GENBANK-AB002700; GENBANK-AB002701;
GENBANK-AB002702; GENBANK-AB002703; GENBANK-AB002704;
GENBANK-AB002705; GENBANK-AB002706; GENBANK-AB002707;
GENBANK-AB002708; GENBANK-AB002709; GENBANK-AB002710;
GENBANK-AB002711; GENBANK-AB002712; GENBANK-AB002713;
GENBANK-AB002714; GENBANK-AB002715; GENBANK-AB002716;
GENBANK-AB002717; GENBANK-AB002718; GENBANK-AB002719;
GENBANK-AB002720; GENBANK-AB002721; GENBANK-AB002722;
GENBANK-AB002723; GENBANK-AB002724; GENBANK-AB002725
ENTRY MONTH: 199709
ENTRY DATE: Entered STN: 19970926
Last Updated on STN: 20000303
Entered Medline: 19970915

L8 ANSWER 296 OF 355 MEDLINE DUPLICATE 199
ACCESSION NUMBER: 97275308 MEDLINE
DOCUMENT NUMBER: 97275308 PubMed ID: 9129202
TITLE: The chemokine information source: identification and

WorldWideWeb characterization of novel chemokines using the
 and expressed sequence tag databases.
 AUTHOR: Wells T N; Peitsch M C
 CORPORATE SOURCE: Geneva Biomedical Research Institute, Switzerland.
 SOURCE: JOURNAL OF LEUKOCYTE BIOLOGY, (1997 May) 61 (5) 545-50.
 Ref: 16
 Journal code: 8405628. ISSN: 0741-5400.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 General Review; (REVIEW)
 (REVIEW, TUTORIAL)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals; AIDS
 OTHER SOURCE: GENBANK-U67775; PDB-1HUM; PDB-1IL8
 ENTRY MONTH: 199705
 ENTRY DATE: Entered STN: 19970602
 Last Updated on STN: 19970602
 Entered Medline: 19970521

L8 ANSWER 297 OF 355 MEDLINE DUPLICATE 200
 ACCESSION NUMBER: 97295295 MEDLINE
 DOCUMENT NUMBER: 97295295 PubMed ID: 9150937
 TITLE: A comparison of selected mRNA and protein abundances in
 human liver.
 AUTHOR: Anderson L; Seilhamer J
 CORPORATE SOURCE: Large Scale Biology Corporation, Rockville, MD 20850-3338,
 USA.. leigh@lsbc.com
 SOURCE: ELECTROPHORESIS, (1997 Mar-Apr) 18 (3-4) 533-7.
 Journal code: 8204476. ISSN: 0173-0835.
 PUB. COUNTRY: GERMANY: Germany, Federal Republic of
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199707
 ENTRY DATE: Entered STN: 19970812
 Last Updated on STN: 19970812
 Entered Medline: 19970728

L8 ANSWER 298 OF 355 MEDLINE DUPLICATE 201
 ACCESSION NUMBER: 1998035876 MEDLINE
 DOCUMENT NUMBER: 98035876 PubMed ID: 9367677
 TITLE: Identification and characterization of BRDT: A
 testis-specific gene related to the bromodomain genes
 RING3
 and Drosophila fsh.
 AUTHOR: Jones M H; Numata M; Shimane M
 CORPORATE SOURCE: Chugai Research Institute for Molecular Medicine, 153-2
 Nagai, Niihari, Ibaraki, 300-41, Japan.
 SOURCE: GENOMICS, (1997 Nov 1) 45 (3) 529-34.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF019085
 ENTRY MONTH: 199801
 ENTRY DATE: Entered STN: 19980129
 Last Updated on STN: 20020420
 Entered Medline: 19980113

L8 ANSWER 299 OF 355 LIFESCI COPYRIGHT 2002 CSA
 ACCESSION NUMBER: 1999:17786 LIFESCI
 TITLE: Identification and mapping of a novel human gene, HRMT1L1, homologous to the rat protein arginine N-methyltransferase 1 (PRMT1) gene
 AUTHOR: Katsanis, N.; Yaspo, M.-L.; Fisher, E.M.C.*
 CORPORATE SOURCE: Neurogenetics Unit, Imperial Coll. Sch. Med. at St. Mary's,
 Norfolk Place, London W2 1PG, UK
 SOURCE: MAMM. GENOME, (19970700) vol. 8, no. 7, pp. 526-529.
 ISSN: 0938-8990.
 DOCUMENT TYPE: Journal
 FILE SEGMENT: G
 LANGUAGE: English

L8 ANSWER 300 OF 355 MEDLINE DUPLICATE 202
 ACCESSION NUMBER: 1998004295 MEDLINE
 DOCUMENT NUMBER: 98004295 PubMed ID: 9346309
 TITLE: Characterisation of macrophage inflammatory protein-5/human
 CC cytokine-2, a member of the macrophage-inflammatory-protein family of chemokines.
 AUTHOR: Coulin F; Power C A; Alouani S; Peitsch M C; Schroeder J M;
 Moshizuki M; Clark-Lewis I; Wells T N
 CORPORATE SOURCE: Geneva Biomedical Research Institute, Switzerland.
 SOURCE: EUROPEAN JOURNAL OF BIOCHEMISTRY, (1997 Sep 1) 248 (2) 507-15.
 Journal code: 0107600. ISSN: 0014-2956.
 PUB. COUNTRY: GERMANY: Germany, Federal Republic of
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-Z70293; SWISSPROT-Q16663
 ENTRY MONTH: 199711
 ENTRY DATE: Entered STN: 19971224
 Last Updated on STN: 19971224
 Entered Medline: 19971121

L8 ANSWER 301 OF 355 MEDLINE DUPLICATE 203
 ACCESSION NUMBER: 1998110589 MEDLINE
 DOCUMENT NUMBER: 98110589 PubMed ID: 9441757
 TITLE: Subregional localization of 21 chromosome 7-specific expressed sequence tags (ESTs) by FISH using newly identified YACs and Pls.
 AUTHOR: Morton S M; Veile R A; Helms C; Lee M; Kuo W L; Gray J; Donis-Keller H
 CORPORATE SOURCE: Department of Surgery, Washington University School of Medicine, St. Louis, Missouri 63110, USA.
 CONTRACT NUMBER: P41 HG01066 (NHGRI)
 RO1 HG00469 (NHGRI)
 SOURCE: GENOMICS, (1997 Dec 15) 46 (3) 491-4.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199803
 ENTRY DATE: Entered STN: 19980319
 Last Updated on STN: 19990129
 Entered Medline: 19980309

L8 ANSWER 302 OF 355 MEDLINE DUPLICATE 204
 ACCESSION NUMBER: 1998110580 MEDLINE
 DOCUMENT NUMBER: 98110580 PubMed ID: 9441748
 TITLE: Analysis of a human gene homologous to rat ventral prostate.1 protein.
 AUTHOR: Peacock R E; Keen T J; Inglehearn C F
 CORPORATE SOURCE: Molecular Medicine Unit, St James University Hospital, Leeds, United Kingdom.
 SOURCE: GENOMICS, (1997 Dec 15) 46 (3) 443-9.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF007189
 ENTRY MONTH: 199803
 ENTRY DATE: Entered STN: 19980319
 Last Updated on STN: 19980319
 Entered Medline: 19980309

L8 ANSWER 303 OF 355 MEDLINE DUPLICATE 205
 ACCESSION NUMBER: 97224466 MEDLINE
 DOCUMENT NUMBER: 97224466 PubMed ID: 9119374
 TITLE: Two novel human members of an emerging mammalian gene family related to mono-ADP-ribosylating bacterial toxins.
 COMMENT: Erratum in: Genomics 1999 Jan 1;55(1):130
 AUTHOR: Koch-Nolte F; Haag F; Braren R; Kuhl M; Hoovers J; Balasubramanian S; Bazan F; Thiele H G
 CORPORATE SOURCE: Department of Immunology, University Hospital, Hamburg, Federal Republic of Germany.. nolte@uke.uni-hamburg.de
 SOURCE: GENOMICS, (1997 Feb 1) 39 (3) 370-6.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-X95826; GENBANK-X95827
 ENTRY MONTH: 199704
 ENTRY DATE: Entered STN: 19970506
 Last Updated on STN: 20020420
 Entered Medline: 19970424

L8 ANSWER 304 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC. DUPLICATE 206
 ACCESSION NUMBER: 1997:226552 BIOSIS
 DOCUMENT NUMBER: PREV199799518268
 TITLE: Large-scale concatenation cDNA sequencing.
 AUTHOR(S): Yu, Wei; Andersson, Bjorn; Worley, Kim C.; Muzny, Donna M.;
 Ding, Yan; Liu, Wen; Ricafrente, Jennifer Y.; Wentland, Meredith A.; Lennon, Greg; Gibbs, Richard A. (1)
 CORPORATE SOURCE: (1) Dep. Molecular Human Genetics, Baylor College Med., Houston, TX 77030 USA
 SOURCE: Genome Research, (1997) Vol. 7, No. 4, pp. 353-358.
 ISSN: 1088-9051.
 DOCUMENT TYPE: Article
 LANGUAGE: English

L8 ANSWER 305 OF 355 MEDLINE DUPLICATE 207
 ACCESSION NUMBER: 97435549 MEDLINE

DOCUMENT NUMBER: 97435549 PubMed ID: 9290248
 TITLE: Expressed sequences from conidial, mycelial, and sexual stages of *Neurospora crassa*.
 AUTHOR: Nelson M A; Kang S; Braun E L; Crawford M E; Dolan P L; Leonard P M; Mitchell J; Armijo A M; Bean L; Blueyes E; Cushing T; Errett A; Fleharty M; Gorman M; Judson K; Miller
 R; Ortega J; Pavlova I; Perea J; Todisco S; Trujillo R; Valentine J; Wells A; Werner-Washburne M; Natvig D O; +
 CORPORATE SOURCE: Department of Biology, University of New Mexico, Albuquerque 87131, USA.
 CONTRACT NUMBER: GM47374 (NIGMS)
 GM52576 (NIGMS)
 SOURCE: FUNGAL GENETICS AND BIOLOGY, (1997 Jun) 21 (3) 348-63.
 Journal code: 9607601. ISSN: 1087-1845.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AA574464; GENBANK-AA574465; GENBANK-AA601776;
 GENBANK-AA601777; GENBANK-AA738494; GENBANK-AA738495;
 GENBANK-AA738496; GENBANK-AA738497; GENBANK-AA738498;
 GENBANK-AA738499; GENBANK-AA738500; GENBANK-AA738501;
 GENBANK-AA774383; GENBANK-AA774384; GENBANK-AA774385;
 GENBANK-AA774386; GENBANK-AA774387; GENBANK-AA897792;
 GENBANK-AA897793; GENBANK-AA897794; GENBANK-AA897795;
 GENBANK-AA897796; GENBANK-AA897797; GENBANK-AA897798;
 GENBANK-AA897799; GENBANK-AA897800; GENBANK-AA897801
 ENTRY MONTH: 199710
 ENTRY DATE: Entered STN: 19971024
 Last Updated on STN: 20000303
 Entered Medline: 19971014

L8 ANSWER 306 OF 355 MEDLINE DUPLICATE 208
 ACCESSION NUMBER: 1998008921 MEDLINE
 DOCUMENT NUMBER: 98008921 PubMed ID: 9344656
 TITLE: Identification of two novel human putative serine/threonine kinases, VRK1 and VRK2, with structural similarity to vaccinia virus B1R kinase.
 AUTHOR: Nezu J; Oku A; Jones M H; Shimane M
 CORPORATE SOURCE: Gene Search Program, Chugai Research Institute for Molecular Medicine, 153-2 Nagai, Niihari, Ibaraki, 300-41, Japan.. nezuj@tk.chugai-pharm.co.jp
 SOURCE: GENOMICS, (1997 Oct 15) 45 (2) 327-31.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AB000449; GENBANK-AB000450
 ENTRY MONTH: 199802
 ENTRY DATE: Entered STN: 19980224
 Last Updated on STN: 19990129
 Entered Medline: 19980212

L8 ANSWER 307 OF 355 MEDLINE DUPLICATE 209
 ACCESSION NUMBER: 97424381 MEDLINE
 DOCUMENT NUMBER: 97424381 PubMed ID: 9280303
 TITLE: Characterization of three cDNA species encoding plastid RNA

polymerase sigma factors in *Arabidopsis thaliana*: evidence for the sigma factor heterogeneity in higher plant plastids.

AUTHOR: Tanaka K; Tozawa Y; Mochizuki N; Shinozaki K; Nagatani A; Wakasa K; Takahashi H
CORPORATE SOURCE: Institute of Molecular and Cellular Biosciences, University of Tokyo, Japan.
SOURCE: FEBS LETTERS, (1997 Aug 18) 413 (2) 309-13. Journal code: 0155157. ISSN: 0014-5793.
PUB. COUNTRY: Netherlands
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB004293; GENBANK-D89993; GENBANK-D89994
ENTRY MONTH: 199709
ENTRY DATE: Entered STN: 19971008
Last Updated on STN: 20000303
Entered Medline: 19970923

L8 ANSWER 308 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1998:6152 BIOSIS
DOCUMENT NUMBER: PREV199800006152
TITLE: Expressed sequence tags (ESTs) from the marine red alga *Gracilaria gracilis*.
AUTHOR(S): Lluisma, Arturo O.; Ragan, Mark A. (1)
CORPORATE SOURCE: (1) Inst. Marine Biosciences, Natl. Res. Council Canada, 1411 Oxford St., Halifax, NS B3H 3Z1 Canada
SOURCE: Journal of Applied Phycology, (June, 1997) Vol. 9, No. 3, pp. 287-293.
ISSN: 0921-8971.
DOCUMENT TYPE: Article
LANGUAGE: English

L8 ANSWER 309 OF 355 MEDLINE DUPLICATE 210

ACCESSION NUMBER: 97311420 MEDLINE
DOCUMENT NUMBER: 97311420 PubMed ID: 9168137
TITLE: Myelin and lymphocyte protein (MAL/MVP17/VIP17) and plasmolipin are members of an extended gene family.
AUTHOR: Magyar J P; Ebensperger C; Schaeren-Wiemers N; Suter U
CORPORATE SOURCE: Department of Biology, Institute of Cell Biology, Swiss Federal Institute of Technology, Zurich.
SOURCE: GENE, (1997 Apr 21) 189 (2) 269-75.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-Y07626; GENBANK-Y07627; GENBANK-Y07628; GENBANK-Y07629; GENBANK-Y07630
ENTRY MONTH: 199706
ENTRY DATE: Entered STN: 19970630
Last Updated on STN: 19970630
Entered Medline: 19970616

L8 ANSWER 310 OF 355 MEDLINE DUPLICATE 211

ACCESSION NUMBER: 97289529 MEDLINE
DOCUMENT NUMBER: 97289529 PubMed ID: 9144434
TITLE: cDNA cloning and tissue-specific expression of a novel basic helix-loop-helix/PAS protein (BMAL1) and identification of alternatively spliced variants with

alternative translation initiation site usage.
 AUTHOR: Ikeda M; Nomura M
 CORPORATE SOURCE: Department of Physiology, Saitama Medical School,
 Moroyama,
 Japan.. mikeda@saitama-med.ac.jp
 SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1997
 Apr 7) 233 (1) 258-64.
 Journal code: 0372516. ISSN: 0006-291X.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AB000812; GENBANK-AB000813; GENBANK-AB000814;
 GENBANK-AB000815; GENBANK-AB000816; GENBANK-D89722
 ENTRY MONTH: 199706
 ENTRY DATE: Entered STN: 19970612
 Last Updated on STN: 20000303
 Entered Medline: 19970605

L8 ANSWER 311 OF 355 MEDLINE DUPLICATE 212
 ACCESSION NUMBER: 1998094278 MEDLINE
 DOCUMENT NUMBER: 98094278 PubMed ID: 9434189
 TITLE: MSG1 and its related protein MRG1 share a transcription
 activating domain.
 AUTHOR: Shioda T; Fenner M H; Isselbacher K J
 CORPORATE SOURCE: Laboratory of Tumor Biology, MGH Cancer Center,
 Massachusetts General Hospital-East, Charlestown 02129,
 USA.. shioda@helix.mgh.harvard.edu
 SOURCE: GENE, (1997 Dec 19) 204 (1-2) 235-41.
 Journal code: 7706761. ISSN: 0378-1119.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-U86445
 ENTRY MONTH: 199802
 ENTRY DATE: Entered STN: 19980224
 Last Updated on STN: 19990129
 Entered Medline: 19980212

L8 ANSWER 312 OF 355 MEDLINE DUPLICATE 213
 ACCESSION NUMBER: 97446139 MEDLINE
 DOCUMENT NUMBER: 97446139 PubMed ID: 9299237
 TITLE: Gene structure and subcellular localization of FMR2, a
 member of a new family of putative transcription
 activators.
 AUTHOR: Gecz J; Bielby S; Sutherland G R; Mulley J C
 CORPORATE SOURCE: Department of Cytogenetics and Molecular Genetics, Women's
 and Children's Hospital, Adelaide, SA 5006, Australia..
 jgecz@mad.adelaide.edu.au
 SOURCE: GENOMICS, (1997 Sep 1) 44 (2) 201-13.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF012603; GENBANK-AF012604; GENBANK-AF012605;
 GENBANK-AF012606; GENBANK-AF012607; GENBANK-AF012608;
 GENBANK-AF012609; GENBANK-AF012610; GENBANK-AF012611;
 GENBANK-AF012612; GENBANK-AF012613; GENBANK-AF012614;
 GENBANK-AF012615; GENBANK-AF012616; GENBANK-AF012617;

GENBANK-AF012618; GENBANK-AF012619; GENBANK-AF012620;
GENBANK-AF012621; GENBANK-AF012622; GENBANK-AF012623;
GENBANK-AF012624; GENBANK-AF012625; GENBANK-AF012626;
GENBANK-U48436

ENTRY MONTH: 199712
ENTRY DATE: Entered STN: 19980109
Last Updated on STN: 20000303
Entered Medline: 19971208

L8 ANSWER 313 OF 355 MEDLINE DUPLICATE 214
ACCESSION NUMBER: 97473513 MEDLINE
DOCUMENT NUMBER: 97473513 PubMed ID: 9332367
TITLE: Cloning of a human multispanning membrane protein cDNA:
evidence for a new protein family.
AUTHOR: Chluba-de Tapia J; de Tapia M; Jaggin V; Eberle A N
CORPORATE SOURCE: Department of Research (ZLF), University Hospital, Basel,
Switzerland.. chluba@aspirine.u-strasbg.fr
SOURCE: GENE, (1997 Sep 15) 197 (1-2) 195-204.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-R19112; GENBANK-U94831
ENTRY MONTH: 199711
ENTRY DATE: Entered STN: 19971224
Last Updated on STN: 19971224
Entered Medline: 19971119

L8 ANSWER 314 OF 355 MEDLINE DUPLICATE 215
ACCESSION NUMBER: 97366618 MEDLINE
DOCUMENT NUMBER: 97366618 PubMed ID: 9223448
TITLE: cDNA cloning of a novel amphiphysin isoform and
variants.
tissue-specific expression of its multiple splice
AUTHOR: Tsutsui K; Maeda Y; Tsutsui K; Seki S; Tokunaga A
CORPORATE SOURCE: Department of Molecular Biology, Institute of Cellular and
Molecular Biology, Okayama University Medical School,
Shikata-cho, Japan.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1997
Jul 9) 236 (1) 178-83.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF001383; GENBANK-U07616; GENBANK-U60884;
GENBANK-U68485
ENTRY MONTH: 199708
ENTRY DATE: Entered STN: 19970813
Last Updated on STN: 19970813
Entered Medline: 19970807

L8 ANSWER 315 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1998:126837 BIOSIS
DOCUMENT NUMBER: PREV199800126837
TITLE: ATMRK1, an Arabidopsis protein kinase related to mammal
mixed-lineage kinases and Raf protein kinases.
AUTHOR(S): Ichimura, Kazuya; Mizoguchi, Tsuyoshi; Shinozaki, Kazuo
(1)
CORPORATE SOURCE: (1) Lab. Plant Mol. Biol., Tsukuba Life Sci. Cent., Inst.

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Physical Chemical Res., 3-1-1 Koyadai, Tsukuba, Ibaraki

Japan

SOURCE: Plant Science (Shannon), (Dec., 1997) Vol. 130, No. 2, pp. 171-179.

ISSN: 0168-9452.

DOCUMENT TYPE: Article

LANGUAGE: English

L8 ANSWER 316 OF 355 LIFESCI COPYRIGHT 2002 CSA

ACCESSION NUMBER: 97:62895 LIFESCI

TITLE: Cell biology and the genome projects - A concerted strategy

for characterizing multiprotein complexes by using mass spectrometry

AUTHOR: Lamond, A.I.; Mann, M.

CORPORATE SOURCE: Dep. Biochem., Univ. Dundee, Dundee, UK DD1 4HN

SOURCE: TRENDS CELL BIOL., (1997) vol. 7, no. 4, pp. 139-142. ISSN: 0962-8924.

DOCUMENT TYPE: Journal

TREATMENT CODE: General Review

FILE SEGMENT: W3; G

LANGUAGE: English

SUMMARY LANGUAGE: English

L8 ANSWER 317 OF 355 MEDLINE DUPLICATE 216

ACCESSION NUMBER: 97420696 MEDLINE

DOCUMENT NUMBER: 97420696 PubMed ID: 9276681

TITLE: A survey of genes expressed in mouse embryonal carcinoma F9

cells: characterization of expressed sequence tags

matching

no known genes.

AUTHOR: Nomura M; Nishiguchi S; Motaleb M A; Takiyara Y; Takagi T; Yasunaga T; Shimada K

CORPORATE SOURCE: Department of Medical Genetics, Research Institute for Microbial Diseases, Osaka University.

SOURCE: JOURNAL OF BIOCHEMISTRY, (1997 Jul) 122 (1) 129-47. Journal code: 0376600. ISSN: 0021-924X.

PUB. COUNTRY: Japan

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-D21355; GENBANK-D21356; GENBANK-U21357; GENBANK-U21358; GENBANK-U21359; GENBANK-U21360; GENBANK-U21361; GENBANK-U21362; GENBANK-U21363; GENBANK-U21364; GENBANK-U21365; GENBANK-U21366; GENBANK-U21367; GENBANK-U21368; GENBANK-U21369; GENBANK-U21370; GENBANK-U21371; GENBANK-U21372; GENBANK-U21373; GENBANK-U21374; GENBANK-U21375; GENBANK-U21376; GENBANK-U21377; GENBANK-U21378; GENBANK-U21379; GENBANK-U21380; GENBANK-U21381; GENBANK-U21382

ENTRY MONTH: 199710

ENTRY DATE: Entered STN: 19971021

Last Updated on STN: 19971021

Entered Medline: 19971006

L8 ANSWER 318 OF 355 MEDLINE DUPLICATE 217

ACCESSION NUMBER: 97306278 MEDLINE

DOCUMENT NUMBER: 97306278 PubMed ID: 9162095

TITLE: Cloning of a new human gene with short consensus repeats using the EST database.
 AUTHOR: Nangaku M; Shankland S J; Kurokawa K; Bomsztyk K; Johnson R
 J; Couser W G
 CORPORATE SOURCE: Division of Nephrology, Box 356 521, University of Washington, Seattle, WA, USA.
 CONTRACT NUMBER: DK02142 (NIDDK)
 DK34198 (NIDDK)
 DK43422 (NIDDK)
 +
 SOURCE: IMMUNOGENETICS, (1997) 46 (2) 99-103.
 Journal code: 0420404. ISSN: 0093-7711.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199707
 ENTRY DATE: Entered STN: 19970805
 Last Updated on STN: 19970805
 Entered Medline: 19970723

L8 ANSWER 319 OF 355 MEDLINE DUPLICATE 218
 ACCESSION NUMBER: 97186437 MEDLINE
 DOCUMENT NUMBER: 97186437 PubMed ID: 9034012
 TITLE: Novel transcribed sequences neighbouring a translocation breakpoint associated with schizophrenia.
 AUTHOR: Devon R S; Evans K L; Maule J C; Christie S; Anderson S; Brown J; Shibasaki Y; Porteous D J; Brookes A J
 CORPORATE SOURCE: MRC Human Genetics Unit, Western General Hospital, Edinburgh, United Kingdom.
 SOURCE: AMERICAN JOURNAL OF MEDICAL GENETICS, (1997 Feb 21) 74 (1) 82-90.
 Journal code: 7708900. ISSN: 0148-7299.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-UNKNOWN; SWISSPROT-UNKNOWN
 ENTRY MONTH: 199704
 ENTRY DATE: Entered STN: 19970507
 Last Updated on STN: 19970507
 Entered Medline: 19970430

L8 ANSWER 320 OF 355 LIFESCI COPYRIGHT 2002 CSA
 ACCESSION NUMBER: 97:62796 LIFESCI
 TITLE: DRES search engine: Of flies, men and ESTs
 AUTHOR: Guffanti, A.; Banfi, S.; Simon, G.; Ballabio, A.; Borsani, G.
 CORPORATE SOURCE: Telethon Inst. Genet. and Med. (Tigem), San Raffaele Biomedical Science Park, Via Olgettina 58, 20132 Milano, Italy
 SOURCE: TRENDS GENET., (1997) vol. 13, no. 2, pp. 79-80.
 ISSN: 0168-9525.
 DOCUMENT TYPE: Journal
 TREATMENT CODE: General Review
 FILE SEGMENT: G; Z
 LANGUAGE: English
 SUMMARY LANGUAGE: English

L8 ANSWER 321 OF 355 MEDLINE DUPLICATE 219

ACCESSION NUMBER: 97480716 MEDLINE
 DOCUMENT NUMBER: 97480716 PubMed ID: 9339361
 TITLE: Cosmid contig and transcriptional map of three regions of human chromosome 21q22: identification of 37 novel transcripts by direct selection.
 AUTHOR: Guimera J; Pucharcos C; Domenech A; Casas C; Solans A; Gallardo T; Ashley J; Lovett M; Estivill X; Pritchard M
 CORPORATE SOURCE: Molecular Genetics Department, Cancer Research Institute, Hospital Duran i Reynals, Barcelona, Spain.
 SOURCE: GENOMICS, (1997 Oct 1) 45 (1) 59-67.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-U81187; GENBANK-U81188; GENBANK-U81189;
 GENBANK-U81190; GENBANK-U81191; GENBANK-U81192;
 GENBANK-U81193; GENBANK-U81194; GENBANK-U81195;
 GENBANK-U81196; GENBANK-U81197; GENBANK-U81198;
 GENBANK-U81199; GENBANK-U81200; GENBANK-U81201;
 GENBANK-U81202; GENBANK-U81203; GENBANK-U81204;
 GENBANK-U81205; GENBANK-U81206; GENBANK-U81207;
 GENBANK-U81208; GENBANK-U81209; GENBANK-U81210;
 GENBANK-U81211; GENBANK-U81212; GENBANK-U81213;
 GENBANK-U81214; GENBANK-U81215; GENBANK-U81216; +
 ENTRY MONTH: 199711
 ENTRY DATE: Entered STN: 19971224
 Last Updated on STN: 19971224
 Entered Medline: 19971120

L8 ANSWER 322 OF 355 MEDLINE DUPLICATE 220
 ACCESSION NUMBER: 97320163 MEDLINE
 DOCUMENT NUMBER: 97320163 PubMed ID: 9177047
 TITLE: Evaluation of 515 expressed sequence tags obtained from guard cells of Brassica campestris.
 AUTHOR: Kwak J M; Kim S A; Hong S W; Nam H G
 CORPORATE SOURCE: Department of Life Science and School of Environmental Engineering, Pohang University of Science and Technology, Republic of Korea.
 SOURCE: PLANTA, (1997) 202 (1) 9-17.
 Journal code: 1250576. ISSN: 0032-0935.
 PUB. COUNTRY: GERMANY: Germany, Federal Republic of
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Biotechnology
 OTHER SOURCE: GENBANK-AT000431; GENBANK-AT000432; GENBANK-AT000433;
 GENBANK-AT000434; GENBANK-AT000435; GENBANK-AT000436;
 GENBANK-AT000437; GENBANK-AT000438; GENBANK-AT000439;
 GENBANK-AT000440; GENBANK-AT000441; GENBANK-AT000442;
 GENBANK-AT000443; GENBANK-AT000444; GENBANK-AT000445;
 GENBANK-AT000446; GENBANK-AT000447; GENBANK-AT000448;
 GENBANK-AT000449; GENBANK-AT000450; GENBANK-AT000451;
 GENBANK-AT000452; GENBANK-AT000453; GENBANK-AT000454;
 GENBANK-AT000455; GENBANK-AT000456; GENBANK-AT000457
 ENTRY MONTH: 199708
 ENTRY DATE: Entered STN: 19970908
 Last Updated on STN: 20000303
 Entered Medline: 19970826

L8 ANSWER 323 OF 355 MEDLINE DUPLICATE 221
 ACCESSION NUMBER: 97432815 MEDLINE

DOCUMENT NUMBER: 97432815 PubMed ID: 9286695
 TITLE: Genomic organization of two novel genes on human Xq28: compact head to head arrangement of IDH gamma and TRAP delta is conserved in rat and mouse.
 AUTHOR: Brenner V; Nyakatura G; Rosenthal A; Platzer M
 CORPORATE SOURCE: Institut fur Molekulare Biotechnologie, Jena, Germany.
 SOURCE: GENOMICS, (1997 Aug 15) 44 (1) 8-14.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-U52111; GENBANK-U52112; GENBANK-U63009;
 GENBANK-U68564; GENBANK-U69268; GENBANK-U69269;
 GENBANK-U73205; GENBANK-Z68907; GENBANK-Z69043
 ENTRY MONTH: 199711
 ENTRY DATE: Entered STN: 19971224
 Last Updated on STN: 19990129
 Entered Medline: 19971118

L8 ANSWER 324 OF 355 MEDLINE DUPLICATE 222
 ACCESSION NUMBER: 97364947 MEDLINE
 DOCUMENT NUMBER: 97364947 PubMed ID: 9221896
 TITLE: Identification of preferentially expressed cochlear genes by systematic sequencing of a rat cochlea cDNA library.
 AUTHOR: Soto-Prior A; Lavigne-Rebillard M; Lenoir M; Ripoll C; Rebillard G; Vago P; Pujol R; Hamel C P
 CORPORATE SOURCE: INSERM U254 and Universites de Montpellier 1 et 2, CHU Hopital Saint Charles, France.
 SOURCE: BRAIN RESEARCH. MOLECULAR BRAIN RESEARCH, (1997 Jul) 47 (1-2) 1-10.
 Journal code: 8908640. ISSN: 0169-328X.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AA108262; GENBANK-AA108263; GENBANK-AA108264;
 GENBANK-AA108265; GENBANK-AA108266; GENBANK-AA108267;
 GENBANK-AA108268; GENBANK-AA108269; GENBANK-AA108270;
 GENBANK-AA108271; GENBANK-AA108272; GENBANK-AA108273;
 GENBANK-AA108274; GENBANK-AA108275; GENBANK-AA108276;
 GENBANK-AA108277; GENBANK-AA108278; GENBANK-AA108279;
 GENBANK-AA108280; GENBANK-AA108281; GENBANK-AA108282;
 GENBANK-AA108283; GENBANK-AA108284; GENBANK-AA108285;
 GENBANK-AA108286; GENBANK-AA108287; GENBANK-AA108288
 ENTRY MONTH: 199709
 ENTRY DATE: Entered STN: 19970926
 Last Updated on STN: 20000303
 Entered Medline: 19970917

L8 ANSWER 325 OF 355 CANCERLIT
 ACCESSION NUMBER: 97610391 CANCERLIT
 DOCUMENT NUMBER: 97610391
 TITLE: Mass spectrometry identification of cancer cell-line proteins resolved by two-dimensional (2D) electrophoresis (Meeting abstract).
 AUTHOR: Li G; Waltham M; Treston A; Mulshine J; Anderson N L; Kohn K W; Weinstein J N
 CORPORATE SOURCE: NCI, Bethesda, MD 20892.
 SOURCE: Proc Annu Meet Am Assoc Cancer Res, (1996). Vol. 37, pp. A3661.

DOCUMENT TYPE: ISSN: 0197-016X.
(MEETING ABSTRACTS)
FILE SEGMENT: ICDB
LANGUAGE: English
ENTRY MONTH: 199705

L8 ANSWER 326 OF 355 CANCERLIT
ACCESSION NUMBER: 96649792 CANCERLIT
DOCUMENT NUMBER: 96649792
TITLE: Alterations in human HT29 colon cell gene expression following glutathione S-transferase inhibitor treatment (Meeting abstract).
AUTHOR: Ciaccio P J; Barone L R; Tew K D
CORPORATE SOURCE: Dept. of Pharmacology and Medical Oncology, Fox Chase Cancer Center, Philadelphia, PA 19111.
SOURCE: Proc Annu Meet Am Assoc Cancer Res, (1996). Vol. 37, pp. A2090.

ISSN: 0197-016X.
DOCUMENT TYPE: (MEETING ABSTRACTS)
FILE SEGMENT: ICDB
LANGUAGE: English
ENTRY MONTH: 199608

L8 ANSWER 327 OF 355 MEDLINE DUPLICATE 223
ACCESSION NUMBER: 97137266 MEDLINE
DOCUMENT NUMBER: 97137266 PubMed ID: 8982603
TITLE: cDNA expression and human two-dimensional gel protein databases: towards integrating DNA and protein information.
AUTHOR: Leffers H; Dejgaard K; Honore B; Madsen P; Nielsen M S; Celis J E
CORPORATE SOURCE: Institute of Medical Biochemistry, Aarhus University, Denmark.. lef@biobase.dk
SOURCE: ELECTROPHORESIS, (1996 Nov) 17 (11) 1713-9.
PUB. COUNTRY: JOURNAL code: 8204476. ISSN: 0173-0835.
GERMANY: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199705
ENTRY DATE: Entered STN: 19970609
Last Updated on STN: 19970609
Entered Medline: 19970529

L8 ANSWER 328 OF 355 MEDLINE DUPLICATE 224
ACCESSION NUMBER: 97092854 MEDLINE
DOCUMENT NUMBER: 97092854 PubMed ID: 8938416
TITLE: The construction of Arabidopsis expressed sequence tag assemblies. A new resource to facilitate gene identification.
AUTHOR: Rounsley S D; Glodek A; Sutton G; Adams M D; Somerville C R; Venter J C; Kerlavage A R
CORPORATE SOURCE: Institute for Genomic Research, Rockville, Maryland 20850, USA.. rounsley@tigr.org
SOURCE: PLANT PHYSIOLOGY, (1996 Nov) 112 (3) 1177-83.
Journal code: 0401224. ISSN: 0032-0889.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-H77094; GENBANK-L00638; GENBANK-L00640;

GENBANK-R65559; GENBANK-R90720; GENBANK-T04012;
GENBANK-T45221; GENBANK-T45942; GENBANK-T76127;
GENBANK-T76497; GENBANK-Z26215; GENBANK-Z26506;
GENBANK-Z34662; PIR-S29435; PIR-S31971; PIR-S32674;
PIR-S36468; PIR-S36769; PIR-S39483; SWISSPROT-P28263;
SWISSPROT-P33296; SWISSPROT-P35128

ENTRY MONTH: 199702
ENTRY DATE: Entered STN: 19970219
Last Updated on STN: 19970219
Entered Medline: 19970204

L8 ANSWER 329 OF 355 MEDLINE DUPLICATE 225
ACCESSION NUMBER: 96174661 MEDLINE
DOCUMENT NUMBER: 96174661 PubMed ID: 8600462
TITLE: Molecular cloning and functional analysis of a human cDNA
encoding an Escherichia coli AlkB homolog, a protein
involved in DNA alkylation damage repair.
AUTHOR: Wei Y F; Carter K C; Wang R P; Shell B K
CORPORATE SOURCE: Department of Molecular Biology, Human Genome Sciences
Inc., Rockville, MD 20850-3338, USA.
SOURCE: NUCLEIC ACIDS RESEARCH, (1996 Mar 1) 24 (5) 931-37.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X91992
ENTRY MONTH: 199605
ENTRY DATE: Entered STN: 19960513
Last Updated on STN: 19980206
Entered Medline: 19960501

L8 ANSWER 330 OF 355 MEDLINE DUPLICATE 226
ACCESSION NUMBER: 96359152 MEDLINE
DOCUMENT NUMBER: 96359152 PubMed ID: 8703118
TITLE: A survey of the goat genome transcribed in the lactating
mammary gland.
AUTHOR: Le Provost F; Lepingle A; Martin P
CORPORATE SOURCE: Laboratoire de Genetique Biochimique et de Cytogenetique,
Institut National de la Recherche Agronomique, 78352
Jouy-en-Josas Cedex, France.
SOURCE: MAMMALIAN GENOME, (1996 Sep) 7 (9) 657-66.
Journal code: 9100916. ISSN: 0938-8990.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X73542; GENBANK-X73543; GENBANK-X73544;
GENBANK-X73545; GENBANK-X73546; GENBANK-X73547;
GENBANK-X73548; GENBANK-X73704; GENBANK-X73705;
GENBANK-X73706; GENBANK-X73707; GENBANK-X73708;
GENBANK-X73709; GENBANK-X73710; GENBANK-X73711;
GENBANK-X73712; GENBANK-X73713; GENBANK-X73714;
GENBANK-X73715; GENBANK-X73716; GENBANK-X73717;
GENBANK-X73718; GENBANK-X73719; GENBANK-X73720;
GENBANK-X73721; GENBANK-X73722; GENBANK-X73723;
GENBANK-X73724; GENBANK-X73725; GENBANK-X73726; +
ENTRY MONTH: 199610
ENTRY DATE: Entered STN: 19961025
Last Updated on STN: 19980206
Entered Medline: 19961017

L8 ANSWER 331 OF 355 MEDLINE DUPLICATE 227
 ACCESSION NUMBER: 96327632 MEDLINE
 DOCUMENT NUMBER: 96327632 PubMed ID: 8678978
 TITLE: Genetic mapping and embryonic expression of a novel,
 maternally transcribed gene Mem3.
 AUTHOR: Hwang S; Benjamin L E; Oh B; Rothstein J L; Ackerman S L;
 Beddington R S; Solter D; Knowles B B
 CORPORATE SOURCE: Jackson Laboratory, 600 Main Street, Bar Harbor, Maine
 04609, USA.
 CONTRACT NUMBER: P30 CA34196 (NCI)
 RO1 CA37225 (NCI)
 SOURCE: MAMMALIAN GENOME, (1996 Aug) 7 (8) 586-90.
 Journal code: 9100916. ISSN: 0938-8990.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-U47024
 ENTRY MONTH: 199610
 ENTRY DATE: Entered STN: 19961025
 Last Updated on STN: 19961025
 Entered Medline: 19961017

L8 ANSWER 332 OF 355 MEDLINE DUPLICATE 228
 ACCESSION NUMBER: 96255495 MEDLINE
 DOCUMENT NUMBER: 96255495 PubMed ID: 8787028
 TITLE: Expressed sequence tags of Chinese cabbage flower bud
 cDNA.
 AUTHOR: Lim C O; Kim H Y; Kim M G; Lee S I; Chung W S; Park S H;
 Hwang I; Cho M J
 CORPORATE SOURCE: Department of Biochemistry, Gyeongsang National
 University,
 Chinju, Korea.
 SOURCE: PLANT PHYSIOLOGY, (1996 Jun) 111 (2) 577-88.
 Journal code: 0401224. ISSN: 0032-0889.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-L33494; GENBANK-L33495; GENBANK-L33496;
 GENBANK-L33497; GENBANK-L33498; GENBANK-L33499;
 GENBANK-L33500; GENBANK-L33501; GENBANK-L33502;
 GENBANK-L33503; GENBANK-L33504; GENBANK-L33505;
 GENBANK-L33506; GENBANK-L33507; GENBANK-L33508;
 GENBANK-L33510; GENBANK-L33511; GENBANK-L33512;
 GENBANK-L33513; GENBANK-L33514; GENBANK-L33515;
 GENBANK-L33516; GENBANK-L33517; GENBANK-L33518;
 GENBANK-L33519; GENBANK-L33520; GENBANK-L33521;
 GENBANK-L33522; GENBANK-L33523; GENBANK-L33524
 ENTRY MONTH: 199609
 ENTRY DATE: Entered STN: 19961008
 Last Updated on STN: 19980206
 Entered Medline: 19960920

L8 ANSWER 333 OF 355 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI
 ACCESSION NUMBER: 1997-02401 BIOTECHDS
 TITLE: A shortcut to interesting human genes: peptide sequence
 tags,
 expressed-sequence tags and computers;
 human gene cloning method

AUTHOR: Mann M
CORPORATE SOURCE: EMBL
LOCATION: Group Leader Proteins & Peptides, EMBL, Heidelberg, Germany.
SOURCE: Trends Biochem.Sci.; (1996) 21, 12, 494-95
CODEN: TBSCDB
ISSN: 0376-5067
DOCUMENT TYPE: Journal
LANGUAGE: English

L8 ANSWER 334 OF 355 MEDLINE DUPLICATE 229
ACCESSION NUMBER: 96254978 MEDLINE
DOCUMENT NUMBER: 96254978 PubMed ID: 8845841
TITLE: Cloning and characterization of the human homologue of a dystrophin related phosphoprotein found at the Torpedo electric organ post-synaptic membrane.
AUTHOR: Sadoulet-Puccio H M; Khurana T S; Cohen J B; Kunkel L M
CORPORATE SOURCE: Department of Genetics, Harvard Medical School, Boston, MA 02115, USA.
CONTRACT NUMBER: 5 R01 NS 23740-10 (NINDS)
NS29343 (NINDS)
SOURCE: HUMAN MOLECULAR GENETICS, (1996 Apr) 5 (4) 489-96.
Journal code: 9208958. ISSN: 0964-6906.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U26742; GENBANK-U26743; GENBANK-U26744;
GENBANK-U46744; GENBANK-U46745; GENBANK-U46746
ENTRY MONTH: 199610
ENTRY DATE: Entered STN: 19961106
Last Updated on STN: 19980206
Entered Medline: 19961024

L8 ANSWER 335 OF 355 MEDLINE DUPLICATE 230
ACCESSION NUMBER: 97064805 MEDLINE
DOCUMENT NUMBER: 97064805 PubMed ID: 8908355
TITLE: Cloning of a cDNA encoding a developmentally regulated 22 kDa polypeptide from tobacco leaf plasma membrane.
AUTHOR: Gantet P; Masson F; Domergue O; Marquis-Mention M; Bauw G; Inze D; Rossignol M; de la Serve B T
CORPORATE SOURCE: INRA/ENSA-M/CNRS URA 573, Laboratoire de Biochimie et Physiologie Vegetales, Montpellier, France.
SOURCE: BIOCHEMISTRY AND MOLECULAR BIOLOGY INTERNATIONAL, (1996 Oct) 40 (3) 469-77.
Journal code: 9306673. ISSN: 1039-9712.
PUB. COUNTRY: Australia
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X95957
ENTRY MONTH: 199703
ENTRY DATE: Entered STN: 19970313
Last Updated on STN: 19990129
Entered Medline: 19970304

L8 ANSWER 336 OF 355 MEDLINE DUPLICATE 231
ACCESSION NUMBER: 97128831 MEDLINE
DOCUMENT NUMBER: 97128831 PubMed ID: 8973371
TITLE: Sequences of two expressed sequence tags (EST) from rice encoding different cap-binding proteins.
AUTHOR: Aliyeva E; Metz A M; Browning K S

CORPORATE SOURCE: Department of Chemistry and Biochemistry, University of Texas at Austin 78712, USA.
 SOURCE: GENE, (1996 Nov 21) 180 (1-2) 221-3.
 Journal code: 7706761. ISSN: 0378-1119.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-U34597; GENBANK-U34598
 ENTRY MONTH: 199701
 ENTRY DATE: Entered STN: 19970219
 Last Updated on STN: 19980206
 Entered Medline: 19970122

L8 ANSWER 337 OF 355 MEDLINE DUPLICATE 232
 ACCESSION NUMBER: 96398134 MEDLINE
 DOCUMENT NUMBER: 96398134 PubMed ID: 8804996
 TITLE: Molecular cloning of two novel transmembrane ligands for Eph-related kinases (LERKS) that are related to LERK-2.
 AUTHOR: Nicola N A; Viney E; Hilton D J; Roberts B; Willson T
 CORPORATE SOURCE: Walter and Eliza Hall Institute of Medical Research, Royal Melbourne Hospital, Victoria, Australia.
 CONTRACT NUMBER: CA22556 (NCI)
 SOURCE: GROWTH FACTORS, (1996) 13 (1-2) 141-9.
 Journal code: 9000468. ISSN: 0897-7194.
 PUB. COUNTRY: Switzerland
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199612
 ENTRY DATE: Entered STN: 19970128
 Last Updated on STN: 19970128
 Entered Medline: 19961203

L8 ANSWER 338 OF 355 MEDLINE
 ACCESSION NUMBER: 97191470 MEDLINE
 DOCUMENT NUMBER: 97191470 PubMed ID: 9039428
 TITLE: Sequencing and mapping the Arabidopsis genome: a weed model
 for real crops.
 AUTHOR: Delseny M; Raynal M; Laudie M; Varoquaux F; Comella P; Wu H
 J; Cooke R; Grellet F
 CORPORATE SOURCE: Physiologie et Biologie Moleculaire des Plantes, CNRS Unite
 565, University of Perpignan, France.
 SOURCE: SYMPOSIA OF THE SOCIETY FOR EXPERIMENTAL BIOLOGY, (1996) 50,
 5-9.
 Journal code: 0404517. ISSN: 0081-1386.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199703
 ENTRY DATE: Entered STN: 19970327
 Last Updated on STN: 19970327
 Entered Medline: 19970320

L8 ANSWER 339 OF 355 MEDLINE DUPLICATE 233
 ACCESSION NUMBER: 96090247 MEDLINE

DOCUMENT NUMBER: 96090247 PubMed ID: 7581366
TITLE: Model for a transcript map of human chromosome 21:
isolation of new coding sequences from exon and enriched
cDNA libraries.
AUTHOR: Yaspo M L; Gellen L; Mott R; Korn B; Nizetic D; Poustka A
M; Lehrach H
CORPORATE SOURCE: Imperial Cancer Research Fund, Genome Analysis Laboratory,
London, UK.
SOURCE: HUMAN MOLECULAR GENETICS, (1995 Aug) 4 (8) 1291-304.
Journal code: 9208958. ISSN: 0964-6906.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199512
ENTRY DATE: Entered STN: 19960124
Last Updated on STN: 19960124
Entered Medline: 19951215

L8 ANSWER 340 OF 355 MEDLINE DUPLICATE 234
ACCESSION NUMBER: 96191284 MEDLINE
DOCUMENT NUMBER: 96191284 PubMed ID: 8616217
TITLE: The macrophage-specific membrane protein Nramp controlling
natural resistance to infections in mice has homologues
expressed in the root system of plants.
AUTHOR: Belouchi A; Cellier M; Kwan T; Saini H S; Leroux G; Gros P
CORPORATE SOURCE: Department of Biochemistry, McGill University, Montreal,
Quebec, Canada.
SOURCE: PLANT MOLECULAR BIOLOGY, (1995 Dec) 29 (6) 1181-96.
Journal code: 9106343. ISSN: 0167-4412.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-S81897
ENTRY MONTH: 199606
ENTRY DATE: Entered STN: 19960620
Last Updated on STN: 19960620
Entered Medline: 19960613

L8 ANSWER 341 OF 355 MEDLINE DUPLICATE 235
ACCESSION NUMBER: 95228954 MEDLINE
DOCUMENT NUMBER: 95228954 PubMed ID: 7713329
TITLE: Alterations in gene expression associated with changes in
the state of endothelial differentiation.
AUTHOR: Shima D T; Saunders K B; Gougos A; D'Amore P A
CORPORATE SOURCE: Laboratory for Surgical Research, Children's Hospital,
Boston, MA 02115.
CONTRACT NUMBER: CA45548 (NCI)
EY05318 (NEI)
SOURCE: DIFFERENTIATION, (1995 Feb) 58 (3) 217-26.
Journal code: 0401650. ISSN: 0301-4681.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-S77716; GENBANK-S77721; GENBANK-S77727;
GENBANK-S77728; GENBANK-S77729; GENBANK-S77733
ENTRY MONTH: 199505
ENTRY DATE: Entered STN: 19950524
Last Updated on STN: 19950524

Entered Medline: 19950517

L8 ANSWER 342 OF 355 MEDLINE DUPLICATE 236
ACCESSION NUMBER: 96043858 MEDLINE
DOCUMENT NUMBER: 96043858 PubMed ID: 8531660
TITLE: Sequencing and identification of expressed Schistosoma
mansoni genes by random selection of cDNA clones from a
directional library.
AUTHOR: Franco G R; Simpson A J; Pena S D
CORPORATE SOURCE: Departamento de Bioquimica e Imunologia, Instituto de
Ciencias Biologicas-UFGM, Belo Horizonte, Brasil.
SOURCE: MEMORIAS DO INSTITUTO OSWALDO CRUZ, (1995 Mar-Apr) 90 (2)
215-6.
Journal code: 7502619. ISSN: 0074-0276.
PUB. COUNTRY: Brazil
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199602
ENTRY DATE: Entered STN: 19960220
Last Updated on STN: 19960220
Entered Medline: 19960201

L8 ANSWER 343 OF 355 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI
ACCESSION NUMBER: 1996-13413 BIOTECHDS
TITLE: Construction and characterization of Brugia malayi adult
male, microfilaria and L3 cDNA libraries;
Brugia malayi adult male microfilaria, adult male and L3
infective larva cDNA library construction and
characterization (conference abstract)
AUTHOR: Saunders L J; Lu W; Ling N; Williams S A
CORPORATE SOURCE: Univ.Massachusetts; Smith-Coll.Massachusetts
LOCATION: Molecular and Cellular Biology, University of Massachusetts,
Amherst, MA, USA.
SOURCE: Am.J.Trop.Med.Hyg.; (1995) 53, 2, Suppl., 173
CODEN: AJTHAB
ISSN: 0002-9637
American Society of Tropical Medicine and Hygiene, 44th
Annual Meeting, San Antonio, Texas, USA, on 17-21 November,
1995.
DOCUMENT TYPE: Journal
LANGUAGE: English

L8 ANSWER 344 OF 355 MEDLINE DUPLICATE 237
ACCESSION NUMBER: 95137379 MEDLINE
DOCUMENT NUMBER: 95137379 PubMed ID: 7835692
TITLE: Identification of new Schistosoma mansoni genes by the EST
strategy using a directional cDNA library.
AUTHOR: Franco G R; Adams M D; Soares M B; Simpson A J; Venter J
C;
Pena S D
CORPORATE SOURCE: Departamento de Bioquimica, Universidade Federal de Minas
Gerais, Belo Horizonte, Brazil.
SOURCE: GENE, (1995 Jan 23) 152 (2) 141-7.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199503
ENTRY DATE: Entered STN: 19950314

Last Updated on STN: 19950314
Entered Medline: 19950301

L8 ANSWER 345 OF 355 MEDLINE DUPLICATE 238
ACCESSION NUMBER: 96123380 MEDLINE
DOCUMENT NUMBER: 96123380 PubMed ID: 8577350
TITLE: cDNA expressed sequence tags of Trypanosoma brucei
rhodesiense provide new insights into the biology of the
parasite.
AUTHOR: el-Sayed N M; Alarcon C M; Beck J C; Sheffield V C;
Donelson J E
CORPORATE SOURCE: Department of Biochemistry, University of Iowa, Iowa City
52242, USA.
SOURCE: MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (1995 Jul) 73
(1-2)
75-90.
Journal code: 8006324. ISSN: 0166-6851.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U24677; GENBANK-U24678; GENBANK-U26666;
PIR-A02647;
PIR-A23060; PIR-A23082; PIR-A35273; PIR-A38145;
PIR-B38145;
PIR-C48328; PIR-S00939; PIR-S05199; PIR-S07328;
PIR-S11393;
PIR-S11557; PIR-S11623; PIR-S15658; PIR-S17351;
PIR-S17521;
PIR-S18806; PIR-S20418; PIR-S27823; PIR-S30653;
PIR-S30823;
PIR-S31359; PIR-S36423; PIR-S37271; PIR-S37576;
PIR-SA33823; PIR-SA48583; +
ENTRY MONTH: 199603
ENTRY DATE: Entered STN: 19960321
Last Updated on STN: 20000303
Entered Medline: 19960308

L8 ANSWER 346 OF 355 MEDLINE DUPLICATE 239
ACCESSION NUMBER: 96026280 MEDLINE
DOCUMENT NUMBER: 96026280 PubMed ID: 7566098
TITLE: Initial assessment of human gene diversity and expression
patterns based upon 83 million nucleotides of cDNA
sequence.
AUTHOR: Adams M D; Kerlavage A R; Fleischmann R D; Fuldner R A;
Bult C J; Lee N H; Kirkness E F; Weinstock K G; Gocayne J
D; White O; +
CORPORATE SOURCE: Institute for Genomic Research, Rockville, Maryland 20850,
USA.
SOURCE: NATURE, (1995 Sep 28) 377 (6547 Suppl) 3-174.
Journal code: 0410462. ISSN: 0028-0836.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-L49534; GENBANK-L49535; GENBANK-L49536;
GENBANK-L49537; GENBANK-L49538; GENBANK-L49539;
GENBANK-L49540; GENBANK-L49541; GENBANK-L49542;
GENBANK-L49543; GENBANK-L49544; GENBANK-L49545;
GENBANK-L49546; GENBANK-L49547; GENBANK-L49548;
GENBANK-L49549; GENBANK-L49550; GENBANK-L49551;

GENBANK-L49552; GENBANK-L49553; GENBANK-L49554;
GENBANK-L49555; GENBANK-L49556; GENBANK-L49557;
GENBANK-L49558; GENBANK-L49559; GENBANK-L49560;
GENBANK-L49561; GENBANK-L49562; GENBANK-L49563

ENTRY MONTH:

199511

ENTRY DATE:

Entered STN: 19951227

Last Updated on STN: 19951227

Entered Medline: 19951108

L8 ANSWER 347 OF 355 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI
ACCESSION NUMBER: 1996-01289 BIOTECHDS

TITLE: Cross referencing yeast genetics and mammalian genomes;
XREFdb database for Saccharomyces cerevisiae and mouse
and

human genome mapping data correlation (conference
abstract)

AUTHOR: Bassett D; Boguski M; Goebel M; Hieter P; Kim R; Reeves R;
Spencer F; Tugendreich S

CORPORATE SOURCE: Univ.Johns-Hopkins; Univ.Indiana;
Nat.Cent.Biotechnol.Inform.Bethesda;
Nat.Inst.Health-Bethesda

LOCATION: Johns Hopkins Medical School, Baltimore, MD 21205, USA.
Email: xref_info@biochem1.iupui.edu

SOURCE: Yeast; (1995) 11, Spec.Iss., S631

CODEN: YESTE3

ISSN: 0749-503X

17th International Conference on Yeast Genetics and

Molecular

Biology, Lisbon, Portugal, 10-16 June, 1995.

DOCUMENT TYPE: Journal

LANGUAGE: English

L8 ANSWER 348 OF 355 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI
ACCESSION NUMBER: 1995-14478 BIOTECHDS

TITLE: The determination of differential gene expression patterns
in

prostate carcinoma utilizing a high through-put cDNA
sequencing approach;

high throughput cDNA sequencing and expressed sequence

tag

cDNA library screening (conference abstract)

AUTHOR: Nelson P S; Huang G M; Ng W L; Yu J; Farkas J; Peterson E;
Liang H A; Chen L; Hood L

CORPORATE SOURCE: Univ.Washington-Seattle

LOCATION: Department of Molecular Biotechnology, University of
Washington, Seattle, WA 98195, USA.

SOURCE: FASEB J.; (1995) 9, 4, A834

CODEN: FAJOEC

ISSN: 0892-6638

Experimental Biology 95, Atlanta, Georgia, 9-13 April, 1995.

DOCUMENT TYPE: Journal

LANGUAGE: English

L8 ANSWER 349 OF 355 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI
ACCESSION NUMBER: 1995-01676 BIOTECHDS

TITLE: Genes galore: a summary of methods for accessing results
from

large-scale partial sequencing of anonymous Arabidopsis cDNA
clones;

Arabidopsis thaliana expressed sequence tag coding
capacity analysis

AUTHOR: Newman T; de Bruijn F J; Green P; Keegstra K; Kende H;
McIntosh L; Ohlrogge J; Raikhel N; Somerville S; Thomasow M;
Retzel E; *Somerville C
CORPORATE SOURCE: Univ.Michigan-State; Univ.Minnesota; Carnegie-Inst.
LOCATION: Carnegie Institution of Washington, Department of Plant
Biology, 290 Panama Street, Stanford, CA 94305-4101, USA.
SOURCE: Plant Physiol.; (1994) 106, 4, 1241-55
CODEN: PLPHAY
ISSN: 0032-0889
DOCUMENT TYPE: Journal
LANGUAGE: English

L8 ANSWER 350 OF 355 MEDLINE DUPLICATE 240
ACCESSION NUMBER: 94324994 MEDLINE
DOCUMENT NUMBER: 94324994 PubMed ID: 8048971
TITLE: Cataloging of the genes expressed in human keratinocytes:
analysis of 607 randomly isolated cDNA sequences.
AUTHOR: Konishi K; Morishima Y; Ueda E; Kibe Y; Nonomura K;
Yamanishi K; Yasuno H
CORPORATE SOURCE: Department of Dermatology, Kyoto Prefectural University of
Medicine, Japan.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1994
Jul 29) 202 (2) 976-83.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-D29018; GENBANK-D29019; GENBANK-D29020;
GENBANK-D29021; GENBANK-D29022; GENBANK-D29023;
GENBANK-D29024; GENBANK-D29025; GENBANK-D29026;
GENBANK-D29027; GENBANK-D29028; GENBANK-D29029;
GENBANK-D29030; GENBANK-D29031; GENBANK-D29032;
GENBANK-D29033; GENBANK-D29034; GENBANK-D29035;
GENBANK-D29036; GENBANK-D29037; GENBANK-D29038;
GENBANK-D29039; GENBANK-D29040; GENBANK-D29041;
GENBANK-D29042; GENBANK-D29043; GENBANK-D29044;
GENBANK-D29045; GENBANK-D29046; GENBANK-D29047
ENTRY MONTH: 199409
ENTRY DATE: Entered STN: 19940909
Last Updated on STN: 19960129
Entered Medline: 19940901

L8 ANSWER 351 OF 355 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
DUPLICATE 241
ACCESSION NUMBER: 1994:400086 BIOSIS
DOCUMENT NUMBER: PREV199497413086
TITLE: Cloning and characterization of pig muscle cDNAs by an
expressed sequence tag approach.
AUTHOR(S): Tuggle, C. K.; Schmitz, C. B.
CORPORATE SOURCE: Dep. Anim. Sci., Iowa State Univ., Ames, IA 50011 USA
SOURCE: Animal Biotechnology, (1994) Vol. 5, No. 1, pp. 1-13.
ISSN: 1049-5398.
DOCUMENT TYPE: Article
LANGUAGE: English

L8 ANSWER 352 OF 355 MEDLINE DUPLICATE 242
ACCESSION NUMBER: 94004965 MEDLINE
DOCUMENT NUMBER: 94004965 PubMed ID: 8401585
TITLE: Rapid cDNA sequencing (expressed sequence tags) from a
directionally cloned human infant brain cDNA library.

AUTHOR: Adams M D; Soares M B; Kerlavage A R; Fields C; Venter J C
 CORPORATE SOURCE: Receptor Biochemistry and Molecular Biology Section,
 NINDS/NIH, Bethesda, Maryland 20892.
 SOURCE: NATURE GENETICS, (1993 Aug) 4 (4) 373-80.
 Journal code: 9216904. ISSN: 1061-4036.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-T07956; GENBANK-T07957; GENBANK-T07958;
 GENBANK-T07959; GENBANK-T07960; GENBANK-T07961;
 GENBANK-T07962; GENBANK-T07963; GENBANK-T07964;
 GENBANK-T07965; GENBANK-T07966; GENBANK-T07967;
 GENBANK-T07968; GENBANK-T07969; GENBANK-T07970;
 GENBANK-T07971; GENBANK-T07972; GENBANK-T07973;
 GENBANK-T07974; GENBANK-T07975; GENBANK-T07976;
 GENBANK-T07977; GENBANK-T07978; GENBANK-T07979;
 GENBANK-T07980; GENBANK-T07981; GENBANK-T07982;
 GENBANK-T07983; GENBANK-T07984; GENBANK-T07985; +
 ENTRY MONTH: 199311
 ENTRY DATE: Entered STN: 19940117
 Last Updated on STN: 19950307
 Entered Medline: 19931105

L8 ANSWER 353 OF 355 MEDLINE DUPLICATE 243
 ACCESSION NUMBER: 93364420 MEDLINE
 DOCUMENT NUMBER: 93364420 PubMed ID: 8358434
 TITLE: 3,400 new expressed sequence tags identify diversity of
 transcripts in human brain.
 COMMENT: Comment in: Nat Genet. 1994 Dec;8(4):321-2
 AUTHOR: Adams M D; Kerlavage A R; Fields C; Venter J C
 CORPORATE SOURCE: Receptor Biochemistry and Molecular Biology Section,
 National Institute of Neurological Disorders and Stroke,
 National Institutes of Health, Bethesda, Maryland 20892.
 SOURCE: NATURE GENETICS, (1993 Jul) 4 (3) 256-67.
 Journal code: 9216904. ISSN: 1061-4036.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-T04839; GENBANK-T04840; GENBANK-T04841;
 GENBANK-T04842; GENBANK-T04843; GENBANK-T04844;
 GENBANK-T04845; GENBANK-T04846; GENBANK-T04847;
 GENBANK-T04848; GENBANK-T04849; GENBANK-T04850;
 GENBANK-T04851; GENBANK-T04852; GENBANK-T04853;
 GENBANK-T04854; GENBANK-T04855; GENBANK-T04856;
 GENBANK-T04857; GENBANK-T04858; GENBANK-T04859;
 GENBANK-T04860; GENBANK-T04861; GENBANK-T04862;
 GENBANK-T04863; GENBANK-T04864; GENBANK-T04865;
 GENBANK-T04866; GENBANK-T04867; GENBANK-T04868; +
 ENTRY MONTH: 199309
 ENTRY DATE: Entered STN: 19931015
 Last Updated on STN: 19970203
 Entered Medline: 19930924

L8 ANSWER 354 OF 355 MEDLINE DUPLICATE 244
 ACCESSION NUMBER: 93271973 MEDLINE
 DOCUMENT NUMBER: 93271973 PubMed ID: 8499912
 TITLE: Cloning of the X-linked glycerol kinase deficiency gene
 and
 its identification by sequence comparison to the Bacillus

COMMENT: subtilis homologue.
 Comment in: Hum Mol Genet. 1993 Feb;2(2):95-6
 AUTHOR: Sargent C A; Affara N A; Bentley E; Pelmear A; Bailey D M;
 Davey P; Dow D; Leversha M; Aplin H; Besley G T; +
 CORPORATE SOURCE: Cambridge University, Department of Pathology, UK.
 SOURCE: HUMAN MOLECULAR GENETICS, (1993 Feb) 2 (2) 97-106.
 Journal code: 9208958. ISSN: 0964-6906.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-X68285
 ENTRY MONTH: 199307
 ENTRY DATE: Entered STN: 19930716
 Last Updated on STN: 19930716
 Entered Medline: 19930701

L8 ANSWER 355 OF 355 MEDLINE DUPLICATE 245
 ACCESSION NUMBER: 93250983 MEDLINE
 DOCUMENT NUMBER: 93250983 PubMed ID: 1302005
 TITLE: Caenorhabditis elegans expressed sequence tags identify
 gene families and potential disease gene homologues.
 AUTHOR: McCombie W R; Adams M D; Kelley J M; FitzGerald M G;
 Utterback T R; Khan M; Dubnick M; Kerlavage A R; Venter J
 C; Fields C
 CORPORATE SOURCE: Receptor Biochemistry and Molecular Biology Section,
 National Institute of Neurological Disorders and Stroke,
 NIH, Bethesda, Maryland 20892.
 SOURCE: NATURE GENETICS, (1992 May) 1 (2) 124-31.
 Journal code: 9216904. ISSN: 1061-4036.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199306
 ENTRY DATE: Entered STN: 19930618
 Last Updated on STN: 19970203
 Entered Medline: 19930610

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	ENTRY	SESSION
FULL ESTIMATED COST	208.79	209.00

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PASSWORD:
 * * * * * RECONNECTED TO STN INTERNATIONAL * * * * *
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 AT 19:57:25 ON 08 JUL 2002
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FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
19:04:09
ON 08 JUL 2002

L1 13496 S EST
L2 34 S L1(S) (NO#(W) CORRELAT?)
L3 21 DUP REM L2 (13 DUPLICATES REMOVED)
L4 3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5 1972 S L4(S) (PROTEIN OR PEPTIDE)
L6 1748 S L5(S) (EXPRESS?)
L7 775 S L6(S) DATABASE#
L8 355 DUP REM L7 (420 DUPLICATES REMOVED)

=> s l8(s) (prostate or bladder or lung or kidney or bone or skin or breast or
uterus or cervi? or testis or testes or ovar?)

3 FILES SEARCHED...

L9 96 L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN OR
BREAST OR UTERUS OR CERVI? OR TESTIS OR TESTES OR OVAR?)

=> s l8(s) genbank

L10 47 L8(S) GENBANK

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L10 ANSWER 1 OF 47 MEDLINE
ACCESSION NUMBER: 2002328673 IN-PROCESS
DOCUMENT NUMBER: 22056133 PubMed ID: 12060780
TITLE: Identification of gene expression profile of dorsal root
neuropathic ganglion in the rat peripheral axotomy model of
pain.
AUTHOR: Xiao Hua-Sheng; Huang Qiu-Hua; Zhang Fang-Xiong; Bao Lan;
Lu Ying-Jin; Guo Chao; Yang Liang; Huang Wein-Jing; Fu
Gang; Xu Shu-Hua; Cheng Xi-Ping; Yan Qing; Zhu Zhi-Dong;
Zhang Xin; Chen Zhu; Han Ze-Guang; Zhang Xu
CORPORATE SOURCE: Laboratory of Sensory System, Institute of Neuroscience,
Shanghai Institutes for Biological Sciences, Chinese
Academy of Sciences, 320 Yue Yang Road, Shanghai 200031,
China.
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE
UNITED STATES OF AMERICA, (2002 Jun 11) 99 (12) 8360-5.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
OTHER SOURCE: GENBANK-BG662484; GENBANK-BG662485; GENBANK-BG662486;
GENBANK-BG662487; GENBANK-BG662488; GENBANK-BG662489;

[illegible]

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GENBANK-BG663405; GENBANK-BG663406; GENBANK-BG663407;
 GENBANK-BG663408; GENBANK-BG663409; GENBANK-BG663410;
 GENBANK-BG663411; GENBANK-BG663412; GENBANK-BG663413;
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 GENBANK-BG663456; GENBANK-BG663457; GENBANK-BG663458;
 GENBANK-BG663459; GENBANK-BG663460; GENBANK-BG663461;
 GENBANK-BG663462; GENBANK-BG663463; GENBANK-BG663464;
 GENBANK-BG663465; GENBANK-BG663466; GENBANK-BG663467;
 GENBANK-BG663468; GENBANK-BG663469; GENBANK-BG663470;
 GENBANK-BG663471; GENBANK-BG663472; GENBANK-BG663473;
 GENBANK-BG663474; GENBANK-BG663475; GENBANK-BG663476;
 GENBANK-BG663477; GENBANK-BG663478; GENBANK-BG663479;
 GENBANK-BG663480; GENBANK-BG663481; GENBANK-BG663482;
 GENBANK-BG663483

ENTRY DATE:

Entered STN: 20020620

Last Updated on STN: 20020620

AB Phenotypic modification of dorsal root ganglion (DRG) neurons represents an important mechanism underlying neuropathic pain. However, the nerve injury-induced molecular changes are not fully identified. To determine the molecular alterations in a broader way, we have carried out **cdNA** array on the genes mainly made from the **cdNA** libraries of lumbar DRGs of normal rats and of rats 14 days after peripheral axotomy. Of the 7,523 examined genes and **expressed** sequence tags (**ESTs**), the **expression** of 122 genes and 51 **expressed** sequence tags is strongly changed. These genes encompass a large number of members of distinct families, including neuropeptides, receptors, ion channels, signal transduction molecules, synaptic vesicle **proteins**, and others. Of particular interest is the up-regulation of gamma-aminobutyric acid(A) receptor alpha5 subunit, peripheral benzodiazepine receptor, nicotinic acetylcholine receptor alpha7 subunit, P2Y1 purinoceptor, Na(+) channel beta2 subunit, and

L-type

Ca(2+) channel alpha2delta-1 subunit. Our findings therefore reveal dynamic and complex changes in molecular diversity among DRG neurons after

axotomy. Sequences reported in this paper have been deposited in the **GenBank database** (accession numbers BG 662484-BG 673712)

L10 ANSWER 2 OF 47

MEDLINE

ACCESSION NUMBER: 2002302237 MEDLINE

DOCUMENT NUMBER: 22039529 PubMed ID: 12043562

TITLE: Molecular cloning, characterization, chromosomal assignment, genomic organization and verification of SFRS12(SRrp508), a novel member of human SR protein superfamily and a human homolog of rat SRrp86.

AUTHOR: Zhang De-Li; Sun Xiao-Jing; Ling Lun-Jiang; Chen

Run-Sheng;

Ma Da-Long

CORPORATE SOURCE: Peking University Center for Human Disease Genomics, China
National Center for Human Genome Research, Beijing 100083,
China.. delizhang@bjmu.edu

SOURCE: I CHUAN HSUEH PAO. ACTA GENETICA SINICA, (2002 May) 29 (5)
377-83.
Journal code: 7900784. ISSN: 0379-4172.

PUB. COUNTRY: China
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: Chinese

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AF459094

ENTRY MONTH: 200207

ENTRY DATE: Entered STN: 20020605
Last Updated on STN: 20020704
Entered Medline: 20020703

AB We have identified and characterized a novel human serine-arginine-rich (SR) splicing regulatory **protein** 508 (SRrp508) gene that is related to other members of the growing SR superfamily, but only homologous to rat (*Rattus norvegicus*) serine-arginine-rich splicing regulatory **protein** 86 (SRrp86) gene. The full-length **cDNA** of 3811 bp for human SRrp508 was cloned through a blast search of public **databases** following the identification of a **cDNA** contig of 658 bp obtained by **EST** assembly with full robotization in supercomputer in large-scale. Structurally, human SRrp508 encodes a polypeptide of 508 amino acids, which contains a single amino-terminal RNA recognition motif (RRM) and two carboxy-terminal domains rich in serine-arginine dipeptides that are highly conserved among other members of the SR superfamily. The conserved SR and RRM domains emphasize the biological importance of this gene. The SRrp508 gene, which contains 12 exons ranging from 0.096 to 2.093 kb and 11 introns ranging from 0.14 to 5.153 kb, is mapped to the human cytogenetic region 5q11.2-q12.1 using the bioinformatic analysis, and it does not link to any other genes. Furthermore, we have experimentally cloned and sequenced a **cDNA** fragment of 1680 bp containing the full-length ORF of 1527 bp in this novel human gene by RT-PCR from the single-stranded human pancreas **cDNA** library (Clontech), which is fully identical with that of the in silico cloning determined by the nucleotide sequencing. Thus, we in silico cloned his gene with **GenBank** accession number of AF459094 identified solely by bioinformatic analysis of the nucleotide and **protein**. This novel gene has promoters, TATA-box, several stop codons in the upstream of ORF, and PolyA signal in the downstream of ORF. Based on the above results, it can be concluded that we have obtained a complete novel human gene. The gene sequence exhibits good overall homology to that of rat SRrp86 gene, with 84% and 86% identity over the full-length nucleotide and **protein**, respectively, and with 96% and 86% identity over the serine-rich domain (RS) or arginine-rich domain (RA), respectively. The full-length sequence exhibits little overall homology to any other known **protein** at either the nucleotide or the amino acid level. The other two most closely related **proteins**, with 34% and 35% identity over the full-length **protein**, respectively, or with 51% and 54% identity over the full-length nucleotide of ORF, respectively, are drosophila serine-arginine-rich **protein** 54 (SRp54) and human arginine-rich nuclear **protein** 54 (p54). When comparisons are restricted to the RS or RA domains, the percent identity increased for both SRp54 and p54 are 44% and 54% or 38% and 43%, respectively. These results well demonstrate that only the novel human **protein** of 508 amino acids cloned is the human homolog of rat

SRrp86, thus correcting the standpoint made by Barnard and Patton (Barnard

DC, Patton JG. Identification and Characterization of a Novel Serine-Arginine-Rich Splicing Regulatory **Protein**. Molecular and Cellular Biology, 2000, 20(9): 3049-3057) that human arginine-rich nuclear

protein 54 (p54) is the human homolog of the rat SRrp86, and suggesting that human SRrp508 is a new member of this growing superfamily of SR **proteins**. SRrp508 has an extensive **expression** profile, and may be a transcriptional factor. On the basis of its sequence

and functional properties, we have named this **protein** SRrp508 for SR-related splicing regulatory **protein** of 508 amino acids. In summary, by combining bioinformatic analysis with experimental verification, we have successfully cloned the human **cDNA** homolog of rat SRrp86, which is verified by a series of theoretical and experimental evidence. The HGNC has just given SRrp508 gene entry the nomenclature information containing APPROVED SYMBOL: SFRS12; NAME: splicing factor, arginine/serine-rich 12; and ALIAS: DKFZp564B176, SRrp86.

We have cloned this gene for near one year with no person landing the **GenBank** for registering the same gene. Our newly-established technique line will be helpful in discovering much more novel human genes.

L10 ANSWER 3 OF 47 MEDLINE

ACCESSION NUMBER: 2002258011 IN-PROCESS

DOCUMENT NUMBER: 21993152 PubMed ID: 11997173

TITLE: Reexamining the polyadenylation signal: were we wrong about

AAUAAA?.

AUTHOR: MacDonald Clinton C; Redondo Jose Luis

CORPORATE SOURCE: Department of Cell Biology & Biochemistry and Southwest Cancer Center at University Medical Center, Texas Tech University Health Sciences Center, 3601 4th Street, 79430, Lubbock, TX, USA.

SOURCE: MOLECULAR AND CELLULAR ENDOCRINOLOGY, (2002 Apr 25) 190 (1-2) 1-8.

Journal code: 7500844. ISSN: 0303-7207.

PUB. COUNTRY: Ireland

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals

ENTRY DATE: Entered STN: 20020509

Last Updated on STN: 20020509

AB Polyadenylation is the process by which most eukaryotic **mRNAs** form their 3' ends. It was long held that polyadenylation required the sequence AAUAAA and that 90% of **mRNAs** had AAUAAA within 30 nucleotides of the site of poly(A) addition. More recent studies, aided by

computer analysis of sequences made available in **GenBank** and **expressed** sequence tag (**EST**) **databases**, have suggested that the actual incidence of AAUAAA is much lower, perhaps as low as 50-60%. Reproductive biologists have long recognized that a large number of **mRNAs** in male germ cells of mammals lack AAUAAA but are otherwise normally polyadenylated. Recent research in our laboratory has uncovered a new form of an essential polyadenylation **protein**, tauCstF-64, that is most highly **expressed** in male germ cells, and to a smaller extent in the brain, and which we propose plays a significant role in AAUAAA-independent **mRNA** polyadenylation in germ cells.

L10 ANSWER 4 OF 47 MEDLINE
 ACCESSION NUMBER: 2002090551 IN-PROCESS
 DOCUMENT NUMBER: 21676815 PubMed ID: 11818518
 TITLE: A set of 1542 mouse blastocyst and pre-blastocyst genes with well-matched human homologues.
 AUTHOR: Stanton J L; Green D P L
 CORPORATE SOURCE: Department of Anatomy and Structural Biology, University of Otago Medical School, P.O. Box 913, Dunedin, New Zealand.
 SOURCE: MOLECULAR HUMAN REPRODUCTION, (2002 Feb) 8 (2) 149-66.
 Journal code: 9513710. ISSN: 1360-9947.
 PUB. COUNTRY: England: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
 ENTRY DATE: Entered STN: 20020131
 Last Updated on STN: 20020131

AB **GenBank** contains 57 151 **Expressed** Sequence Tags (**EST**) derived from 11 preimplantation embryo mouse **cDNA** libraries ranging from the 2-cell embryo to the blastocyst. **EST** were matched to UniGene clusters to identify a composite set of 11 291 UniGenes. These 11 291 UniGenes were screened using HomoloGene to identify a subset of 3467 mouse UniGenes with matches in at least two other species, one of which was human. Of the 3467 matches, 1542 are for named human **proteins**. Four of the 11 preimplantation embryo libraries were for blastocysts and contain 22 307 **EST**. These blastocyst **EST** generate 5762 UniGenes, of which 2246 have matches in at least two other species. Of the 2246 matches, 1170 are for named human **proteins**. Comparison of the **expression** profile of the blastocyst set with a similarly derived set from the mouse oocyte identified a number of transcripts that are significantly up-regulated during preimplantation development. The set of named blastocyst and pre-blastocyst genes complements the similar set published recently for the mouse oocyte. They provide a **database** for identifying signalling pathways that may play a role in determining cell fate in preimplantation embryo development.

L10 ANSWER 5 OF 47 MEDLINE
 ACCESSION NUMBER: 2002054749 MEDLINE
 DOCUMENT NUMBER: 21639644 PubMed ID: 11780420
 TITLE: Molecular cloning and characterization of NAG-7: a novel gene downregulated in human nasopharyngeal carcinoma.
 AUTHOR: Xie Y; Bin L; Yang J; Li Z; Yu Y; Zhang X; Cao L; Li G
 CORPORATE SOURCE: Laboratory of Cellular/Molecular Genetics, Cancer Research Institute, Hunan Medical University, Changsha 410078, China.
 SOURCE: CHINESE MEDICAL JOURNAL, (2001 May) 114 (5) 530-4.
 Journal code: 7513795. ISSN: 0366-6999.
 PUB. COUNTRY: China
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200202
 ENTRY DATE: Entered STN: 20020125
 Last Updated on STN: 20020222
 Entered Medline: 20020221

AB OBJECTIVE: To identify novel tumor suppressor genes at chromosome 3p24-26 in human nasopharyngeal carcinoma (NPC). METHODS: Twenty epithelial-derived **expressed** sequence tags (**EST**) were

selected from chromosome 3p24-26. RT-PCR and Northern blot were used to detect the **expression** of the **ESTs** in NPC cell line, HNE-1, and primary cultures of normal nasopharyngeal epithelial cells.

One

EST, which was substantially downregulated in the HNE-1 cell line, was detected in 19 NPC biopsy samples. **cDNA** library screening was used to get its full sequence and the sequence of this novel gene was analyzed. **RESULTS**: A novel gene located at chromosome 3p25.3 was obtained and named NAG-7. It was downregulated in 26.3% (5/19) of NPC biopsy samples. Its 1677 bp full length **cDNA** had a potential open reading frame predicting a 94 amino acid **protein** with a molecular weight of 11,023.87 Dalton. Analysis of the NAG-7 gene showed that it was a transmembrane **protein** containing a **protein** kinase C phosphorylation site and a myristyl site. It has no significant homology to any reported genes in the **database** of **GenBank**. **CONCLUSION**: NAG-7 is a novel gene downregulated in NPC, suggesting that it may be involved in the development of NPC.

L10 ANSWER 6 OF 47 MEDLINE
ACCESSION NUMBER: 2002013892 MEDLINE
DOCUMENT NUMBER: 21310278 PubMed ID: 11417722
TITLE: The analysis of expressed genes in the kidney of Japanese flounder, *Paralichthys olivaceus*, injected with the immunostimulant peptidoglycan.
AUTHOR: Kono T; Sakai M
CORPORATE SOURCE: United Graduate School of Agricultural Sciences, Kagoshima University, Japan.
SOURCE: FISH & SHELLFISH IMMUNOLOGY, (2001 May) 11 (4) 357-66.
Journal code: 9505220. ISSN: 1050-4648.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20020121
Last Updated on STN: 20020121
Entered Medline: 20011204

AB Immunostimulants are widely used in aquaculture, but there are few reports

on the genes that are **expressed** by their stimulation. Therefore, in this study, **expressed** genes in the kidney of Japanese flounder *Paralichthys olivaceus* injected with the immunostimulant peptidoglycan were analysed. The results of single-pass sequencing of **ESTs** from 198 clones (AU090255-AU090451, AU090935) from kidney **cDNA** are presented. Sequences of the **cDNA** clones were compared with sequences in the **GenBank database**. One hundred and six clones (53.5%) appeared to be completely unknown and are likely to represent newly described genes, whereas 92 clones (46.5%) were identified based on matches to sequences in the **database**. The results contain the genes such as alpha globin (AU090287), several ribosomal **proteins** (AU090-263, 274, 299, 351, 365, 375, 377, 382, 434, 445), heat shock **protein** 90 (AU090374) and cytochrome oxidase subunit (AU090385). Immune related **cDNAs** identified from the kidney were immunoglobulin heavy (AU090291) and light chain (AU090352), beta2-microglobulin (AU090280), macrophage inflammatory **protein** 1-alpha precursor (AU090535), thymosin beta-10 (AU090391), lysozyme (AU090322) and MHC class IIalpha (AU090435). It is possible that **expression** of macrophage inflammatory **protein** 1-alpha results in macrophage activation as a consequence of peptidoglycan treatment.

L10 ANSWER 7 OF 47 MEDLINE
 ACCESSION NUMBER: 2001692422 MEDLINE
 DOCUMENT NUMBER: 21602807 PubMed ID: 11738710
 TITLE: Profiling the malaria genome: a gene survey of three species of malaria parasite with comparison to other apicomplexan species.
 AUTHOR: Carlton J M; Muller R; Yowell C A; Fluegge M R; Sturrock K A; Pritt J R; Vargas-Serrato E; Galinski M R; Barnwell J W;
 CORPORATE SOURCE: Mulder N; Kanapin A; Cawley S E; Hide W A; Dame J B
 Computational Biology Branch, National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, MD 20892, USA.. carlton@tigr.org
 CONTRACT NUMBER: N01-A1-65315
 SOURCE: MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (2001 Dec) 118 (2) 201-10.
 Journal code: 8006324. ISSN: 0166-6851.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AZ521913; GENBANK-AZ521914; GENBANK-AZ521915;
 GENBANK-AZ521916; GENBANK-AZ521917; GENBANK-AZ521918;
 GENBANK-AZ521919; GENBANK-AZ521920; GENBANK-AZ521921;
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 GENBANK-AZ521943; GENBANK-AZ521944; GENBANK-AZ521945;
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 GENBANK-AZ521976; GENBANK-AZ521977; GENBANK-AZ521978;
 GENBANK-AZ521979; GENBANK-AZ521980; GENBANK-AZ521981;
 GENBANK-AZ521982; GENBANK-AZ521983; GENBANK-AZ521984;
 GENBANK-AZ521985; GENBANK-AZ521986; GENBANK-AZ521987;
 GENBANK-AZ521988; GENBANK-AZ521989; GENBANK-AZ521990;
 GENBANK-AZ521991; GENBANK-AZ521992; GENBANK-AZ521993;
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 GENBANK-AZ522003; GENBANK-AZ522004; GENBANK-AZ522005;
 GENBANK-AZ522006; GENBANK-AZ522007; GENBANK-AZ522008;
 GENBANK-AZ522009; GENBANK-AZ522010; GENBANK-AZ522011;
 GENBANK-AZ522012; GENBANK-AZ522013; GENBANK-AZ522014;
 GENBANK-AZ522015; GENBANK-AZ522016; GENBANK-AZ522017;
 GENBANK-AZ522018; GENBANK-AZ522019; GENBANK-AZ522020;
 GENBANK-AZ522021; GENBANK-AZ522022; GENBANK-AZ522023;
 GENBANK-AZ522024; GENBANK-AZ522025; GENBANK-AZ522026;
 GENBANK-AZ522027; GENBANK-AZ522028; GENBANK-AZ522029;

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[illegible]

[illegible]

[illegible]

GENBANK-AZ522762; GENBANK-AZ522763; GENBANK-AZ522764;
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 GENBANK-AZ522858; GENBANK-AZ522859; GENBANK-AZ522860;
 GENBANK-AZ522861; GENBANK-AZ522862; GENBANK-AZ522863;
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 GENBANK-AZ522867; GENBANK-AZ522868; GENBANK-AZ522869;
 GENBANK-AZ522870; GENBANK-AZ522871; GENBANK-AZ522872;
 GENBANK-AZ522873; GENBANK-AZ522874; GENBANK-AZ522875;
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 GENBANK-AZ522888; GENBANK-AZ522889; GENBANK-AZ522890;
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 GENBANK-AZ522894; GENBANK-AZ522895; GENBANK-AZ522896;
 GENBANK-AZ522897; GENBANK-AZ522898; GENBANK-AZ522899;
 GENBANK-AZ522900; GENBANK-AZ522901; GENBANK-AZ522902;
 GENBANK-AZ522903; GENBANK-AZ522904; GENBANK-AZ522905;
 GENBANK-AZ522906; GENBANK-AZ522907; GENBANK-AZ522908;
 GENBANK-AZ522909; GENBANK-AZ522910; GENBANK-AZ522911;
 GENBANK-AZ522912

ENTRY MONTH:

200202

ENTRY DATE:

Entered STN: 20011213

Last Updated on STN: 20020228

Entered Medline: 20020227

AB We have undertaken the first comparative pilot gene discovery analysis of
 approximately 25,000 random genomic and **expressed** sequence tags
 (**ESTs**) from three species of Plasmodium, the infectious agent
 that causes malaria. A total of 5482 genome survey sequences (GSSs) and
 5582 **ESTs** were generated from mung bean nuclease (MBN) and
 cDNA libraries, respectively, of the ANKA line of the rodent

malaria parasite *Plasmodium berghei*, and 10,874 GSSs generated from MBN libraries of the Salvador I and Belem lines of *Plasmodium vivax*, the most geographically wide-spread human malaria pathogen. These tags, together with 2438 *Plasmodium falciparum* sequences present in **GenBank**, were used to perform first-pass assembly and transcript reconstruction, and non-redundant consensus sequence datasets created. The datasets were compared against public **protein databases** and more than 1000 putative new *Plasmodium* **proteins** identified based on sequence similarity. Homologs of previously characterized *Plasmodium* genes

were also identified, increasing the number of *P. vivax* and *P. berghei* sequences in public **databases** at least 10-fold. Comparative studies with other species of Apicomplexa identified interesting homologs of possible therapeutic or diagnostic value. A gene prediction program, Phat, was used to predict probable open reading frames for **proteins** in all three datasets. Predicted and non-redundant BLAST-matched **proteins** were submitted to InterPro, an integrated **database** of **protein** domains, signatures and families, for functional classification. Thus a partial predicted proteome was created for each species. This first comparative analysis of *Plasmodium* **protein** coding sequences represents a valuable resource for further studies on the biology of this important pathogen.

L10 ANSWER 8 OF 47 MEDLINE
 ACCESSION NUMBER: 2001691666 MEDLINE
 DOCUMENT NUMBER: 21601106 PubMed ID: 11738820
 TITLE: Application of differential display RT-PCR to identify porcine liver ESTs.
 AUTHOR: Ponsuksili S; Wimmers K; Schellander K
 CORPORATE SOURCE: Institute of Animal Breeding Science, University of Bonn, Endenicher Allee 15, 53115 Bonn, Germany.. spon@itz.uni-bonn.de
 SOURCE: GENE, (2001 Dec 12) 280 (1-2) 75-85. Journal code: 7706761. ISSN: 0378-1119.
 PUB. COUNTRY: Netherlands
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200202
 ENTRY DATE: Entered STN: 20011213
 Last Updated on STN: 20020301
 Entered Medline: 20020228

AB Differential display banding patterns of liver and nine other tissues were

produced in order to isolate porcine **expressed** sequence tags (**ESTs**), representing genes active in liver while avoiding redundant analysis of housekeeping genes. We cloned and sequenced those **cDNA** fragments that were unique to the liver banding pattern or that appeared in liver and a maximum of four other tissues. We analyzed 240 sequences that represent 200 distinct **ESTs**/genes and that make up the first list of liver **ESTs** in the pig. Ninety-one clones correspond to known genes and 109 clones showed no significant match with any gene or DNA sequence in **GenBank** and EMBL **databases**. Fifty-eight clones represent 18 distinct genes, the most abundant representing the albumin gene (13/240). The majority of genes that were represented by more than one clone code for **proteins** released by the liver into the plasma. We demonstrated the suitability of the differential display reverse transcription polymerase chain reaction approach for the detection of porcine liver **ESTs**. It is shown that this approach is appropriate to reduce redundant analysis of clones containing the same sequence.

L10 ANSWER 9 OF 47 MEDLINE

ACCESSION NUMBER: 2001528245 MEDLINE

DOCUMENT NUMBER: 21458557 PubMed ID: 11574155

TITLE: Discovery and mapping of ten novel G protein-coupled receptor genes.

AUTHOR: Lee D K; Nguyen T; Lynch K R; Cheng R; Vanti W B; Arkhitko O; Lewis T; Evans J F; George S R; O'Dowd B F

CORPORATE SOURCE: Department of Pharmacology, University of Toronto, Toronto,

Ontario, M5S 1A8, Canada.

SOURCE: GENE, (2001 Sep 5) 275 (1) 83-91.

Journal code: 7706761. ISSN: 0378-1119.

PUB. COUNTRY: Netherlands

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AF411107; GENBANK-AF411108; GENBANK-AF411109; GENBANK-AF411110; GENBANK-AF411111; GENBANK-AF411112; GENBANK-AF411113; GENBANK-AF411114; GENBANK-AF411115; GENBANK-AF411116; GENBANK-AF411117

ENTRY MONTH: 200112

ENTRY DATE: Entered STN: 20011001

Last Updated on STN: 20020122

Entered Medline: 20011213

AB We report the identification, cloning and tissue distributions of ten novel human genes encoding G **protein**-coupled receptors (GPCRs) GPR78, GPR80, GPR81, GPR82, GPR93, GPR94, GPR95, GPR101, GPR102, GPR103 and a pseudogene, psi GPR79. Each novel orphan GPCR (oGPCR) gene was discovered using customized searches of the **GenBank** high-throughput genomic sequences **database** with previously known GPCR-encoding sequences. The **expressed** genes can now be used in assays to determine endogenous and pharmacological ligands. GPR78 shared highest identity with the oGPCR gene GPR26 (56% identity in the transmembrane (TM) regions). psi GPR79 shared highest sequence identity with the P2Y(2) gene and contained a frame-shift truncating the encoded receptor in TM5, demonstrating a pseudogene. GPR80 shared highest identity with the P2Y(1) gene (45% in the TM regions), while GPR81, GPR82 and GPR93 shared TM identities with the oGPCR genes HM74 (70%), GPR17 (30%) and P2Y(5) (40%), respectively. Two other novel GPCR genes, GPR94 and GPR95, encoded a subfamily with the genes encoding the UDP-glucose and P2Y(12) receptors (sharing >50% identities in the TM regions). GPR101 demonstrated only distant identities with other GPCR genes and GPR102 shared identities with GPR57, GPR58 and PNR (35-42% in the TM regions). GPR103 shared identities with the neuropeptide FF 2, neuropeptide Y2 and galanin GalR1 receptors (34-38% in the TM regions). Northern analyses revealed GPR78 **mRNA expression** in the pituitary and placenta and GPR81 **expression** in the pituitary. A search of the **GenBank** **databases** with the GPR82 sequence retrieved an identical sequence in an **expressed** sequence tag (**EST**) partially encoding GPR82 from human colonic tissue. The GPR93 sequence retrieved an identical, human **EST** sequence from human primary tonsil B-cells and an **EST** partially encoding mouse GPR93 from small intestinal tissue. GPR94 was **expressed** in the frontal cortex, caudate putamen and thalamus of brain while GPR95 was **expressed** in the human prostate and rat stomach and fetal tissues. GPR101 revealed **mRNA** transcripts in caudate putamen and hypothalamus. GPR103

mRNA signals were detected in the cortex, pituitary, thalamus, hypothalamus, basal forebrain, midbrain and pons.

L10 ANSWER 10 OF 47 MEDLINE
ACCESSION NUMBER: 2001325836 MEDLINE
DOCUMENT NUMBER: 21226134 PubMed ID: 11327696
TITLE: Cloning, mapping, genomic organization, and expression of mouse M-LP, a new member of the peroxisomal membrane protein Mpv17 domain family.
AUTHOR: Iida R; Yasuda T; Tsubota E; Matsuki T; Kishi K
CORPORATE SOURCE: Department of Forensic Medicine, Fukui Medical University, Matsuoka-cho, Fukui, 910-1193, Japan..
ireiko@fmsrsa.fukui-med.ac.jp
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2001 May 4) 283 (2) 292-6.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AI482564
ENTRY MONTH: 200106
ENTRY DATE: Entered STN: 20010611
Last Updated on STN: 20010611
Entered Medline: 20010607
AB We have identified a mouse full-length cDNA and gene encoding a novel **protein** (M-LP), based on an **expressed** sequence tag (**EST**) sequence (**GenBank** Accession No. AI482564) obtained by differential display screening of age-dependently **expressed** genes in mouse kidney. The ML-P gene is composed of three exons, ranges over 5 kb on mouse chromosome 16B1-B2 and is **expressed** as two transcripts (1455 and 3058 bp), both of which include the same open-reading frame encoding 194 amino acids. M-LP is **expressed** mainly in kidney and spleen and shows age-dependent **expression**. M-LP has sequence homologies and membrane topologies very similar to the Mpv17 **protein**, a peroxisomal **protein** involved in the development of early-onset glomerulosclerosis. Search of the **protein** domain family **database** (ProDom) revealed that M-LP is a new member of the Mpv17 domain family (PD008400).

L10 ANSWER 11 OF 47 MEDLINE
ACCESSION NUMBER: 2001314104 MEDLINE
DOCUMENT NUMBER: 21280915 PubMed ID: 11386757
TITLE: Central nervous system, uterus, heart, and leukocyte expression of the LOXL3 gene, encoding a novel lysyl oxidase-like protein.
AUTHOR: Jourdan-Le Saux C; Tomsche A; Ujfalusi A; Jia L; Csiszar K
CORPORATE SOURCE: Pacific Biomedical Research Center, University of Hawaii, 1993 East-West Road, Honolulu, Hawaii, 96822.
CONTRACT NUMBER: CA76580 (NCI)
RR03061 (NCRR)
SOURCE: GENOMICS, (2001 Jun 1) 74 (2) 211-8.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AA852888; GENBANK-AF311313; GENBANK-AI752772;
GENBANK-R55706
ENTRY MONTH: 200110

ENTRY DATE: Entered STN: 20011008
Last Updated on STN: 20011008
Entered Medline: 20011004

AB A BLASTN search using the mouse lor-2 **cDNA** identified three overlapping **ESTs** (AI752772, AA852888, and R55706) in the **GenBank database**. These **expressed** sequence tags were assembled into a contig of 3121 nucleotides with an open reading frame of 2262 bp. The encoded putative polypeptide of 754 amino acids presented all structural characteristics of the lysyl oxidase (LOX) enzyme family, a copper-binding site with four histidyl residues, the lysyl and tyrosyl residues known to be involved in LOX enzyme in the formation of the quinone cofactor and surrounding sequences, and the cytokine receptor-like domain. In addition, four scavenger receptor cysteine-rich (SRCR) domains were found in the N-terminal region of the **protein**. The gene encoding this new **cDNA**, which we have referred to as human lysyl oxidase-like 3 (humanLOXL3), has been mapped to chromosome 2p13.3, overlapping at its 3' end the HtrA2 serine protease gene. The structure of the humanLOXL3 gene was deduced from the BAC clone bac91a19 sequence and contained 14 exons. The **expression** pattern of this new member of the LOX gene family appears to be different from that of the LOX and LOX-like genes, as the central nervous system, neurons, and also leukocytes **expressed** humanLOXL3. A BLASTN search of the human **EST database** indicated the presence of **ESTs**, corresponding to alternative splice variants of LOXL3, that lacked exon 5 and exon 8. The putative resulting **protein** retained the region encoding the structural and functional elements of the amine oxidase but the second and fourth SRCR domains were truncated and the potential BMP-1 cleavage site was not present. The presence of domains unrelated to the traditional amine oxidase activity is a strong indication that humanLOXL3 might fulfill other functions in addition to intrinsic enzyme activity. Copyright 2001 Academic Press.

L10 ANSWER 12 OF 47 MEDLINE
ACCESSION NUMBER: 2001312137 MEDLINE
DOCUMENT NUMBER: 21278998 PubMed ID: 11385108
TITLE: A set of 840 mouse oocyte genes with well-matched human homologues.
AUTHOR: Stanton J L; Green D P
CORPORATE SOURCE: Department of Anatomy and Structural Biology, University of Otago, Medical School, P.O.Box 913, Dunedin, New Zealand.
SOURCE: MOLECULAR HUMAN REPRODUCTION, (2001 Jun) 7 (6) 521-43.
JOURNAL code: 9513710. ISSN: 1360-9947.
PUB. COUNTRY: England: United Kingdom
JOURNAL; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010903
Last Updated on STN: 20010903
Entered Medline: 20010830
AB **GenBank** contains 14 477 **expressed** sequence tags (**EST**) derived from mouse oocyte **cDNA** libraries: 3499 of these are from two unfertilized oocyte libraries and 10 978 are from two fertilized oocyte libraries. Gene **expression** profiles were obtained for these libraries by matching library **EST** to UniGene clusters. The 14 477 **EST** identified 4226 UNIGENES: These were screened using HomoloGene to identify 1386 homologous UniGene clusters in

two other species with one of the matches being human. Within these human matches, 840 encoded named **proteins**, 223 encoded hypothetical **proteins**, and 323 encoded clustered **EST**. The set of named genes provides the first step in establishing a **database** of genes **expressed** in mouse oocytes and, by extension, human oocytes.

L10 ANSWER 13 OF 47 MEDLINE
ACCESSION NUMBER: 2001209051 MEDLINE
DOCUMENT NUMBER: 21193750 PubMed ID: 11300479
TITLE: Genetic approach to insight into the immunobiology of human dendritic cells and identification of CD84-H1, a novel CD84 homologue.
AUTHOR: Zhang W; Wan T; Li N; Yuan Z; He L; Zhu X; Yu M; Cao X
CORPORATE SOURCE: Department of Immunology, Second Military Medical University, Shanghai, People's Republic of China.
SOURCE: CLINICAL CANCER RESEARCH, (2001 Mar) 7 (3 Suppl) 822s-829s.
PUB. COUNTRY: Journal code: 9502500. ISSN: 1078-0432. United States
LANGUAGE: Journal; Article; (JOURNAL ARTICLE) English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010827
Last Updated on STN: 20010827
Entered Medline: 20010823

AB To better understand the immunobiology of dendritic cells (DCs), we took the **expressed** sequence tag (**EST**) approach to describe their transcript profile and discovered novel genes. **ESTs** (n = 25,668) were generated from monocyte-derived DCs, and 15,863 **ESTs** (61.8%) represented unique genes in **GenBank**. Integration of **ESTs** allowed for the generation of a profile of 4,367 known genes and identification of > 100 novel genes. HLA-DR invariant chain p33, cathepsin D, HLA-DR alpha chain, beta2-microglobulin, HLA-DP beta chain, CD11a, and mannose receptor were in the top 30 transcripts, and 451 known genes were potentially associated with the immunobiology of DCs. This transcript profile was consistent with the unique antigen-presenting capacity of DCs and provided invaluable information to better understand the immunobiology of DCs. On the basis of the **EST database**, a full-length novel gene was identified that exhibited close homology with CD84; it was designated CD84-H1. The full-length **cDNA** of CD84-H1 contained an open reading frame of 870 bp encoding a type I transmembrane **protein** of 289 amino acids. Consistent with the structural feature of the CD2 family, the predicted 270-amino acid mature **protein** of CD84-H1 contained two extracellular immunoglobulin-like domains that shared homology with CD2 family members, e.g., CD84, Ly-9, CD48, and signaling lymphocyte activation molecule. Its intracellular domain was short and contained no putative signaling structure. Northern blot analysis revealed that CD84-H1 **expression** was predominantly restricted in hematopoietic tissues. Reverse transcription-PCR analysis showed that it was widely **expressed** in the immune cells, including monocytes, DCs, B cells, and T cells.

These

data indicate that CD84-H1 may be relevant to immune responses.

L10 ANSWER 14 OF 47 MEDLINE
ACCESSION NUMBER: 2001182568 MEDLINE
DOCUMENT NUMBER: 21100433 PubMed ID: 11167026

TITLE: Transcriptome analysis of channel catfish (*Ictalurus punctatus*): genes and expression profile from the brain.
 AUTHOR: Ju Z; Karsi A; Kocabas A; Patterson A; Li P; Cao D; Dunham R; Liu Z
 CORPORATE SOURCE: The Fish Molecular Genetics and Biotechnology Laboratory, 203 Swingle Hall, Department of Fisheries and Allied Aquacultures and Program of Cell and Molecular Biosciences, Auburn University, AL, Auburn 36849, USA.
 SOURCE: GENE, (2000 Dec 31) 261 (2) 373-82.
 Journal code: 7706761. ISSN: 0378-1119.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200103
 ENTRY DATE: Entered STN: 20010404
 Last Updated on STN: 20010404
 Entered Medline: 20010329

AB **Expressed** sequence tag (**EST**) analysis was conducted using a complementary DNA (**cDNA**) library made from the brain **mRNA** of channel catfish (*Ictalurus punctatus*). As part of our transcriptome analysis in catfish to develop molecular reagents for comparative functional genomics, here we report analysis of 1201 brain **cDNA** clones. Of the 1201 clones, 595 clones (49.5%) were identified as known genes by BLAST searches and 606 clones (50.5%) as unknown genes. The 595 clones of known gene products represent transcripts of 251 genes. These known genes were categorized into 15 groups according to their biological functions. The largest group of known genes was the genes involved in translational machinery (21.4%) followed by mitochondrial genes (6.2%), structural genes (3.1%), genes homologous to sequences of unknown functions (2.3%), enzymes (2.7%), hormone and regulatory **proteins** (2.5%), genes involved in immune systems (2.1%), genes involved in sorting, transport, and metal metabolism (1.8%), transcriptional factors and DNA repair **proteins** (1.6%), proto-oncogenes (1.2%), lipid binding **proteins** (1.2%), stress-induced genes (0.7%), genes homologous to human genes involved in mental diseases (0.6%), and development or differentiation-related genes (0.3%). The number of genes represented by the 606 clones of unknown genes is not known at present, but the high percentage of clones showing no homology to any known genes in the **GenBank databases** may indicate that a great number of novel genes exist in teleost brain.

L10 ANSWER 15 OF 47 MEDLINE
 ACCESSION NUMBER: 2001155138 MEDLINE
 DOCUMENT NUMBER: 21092618 PubMed ID: 11162530
 TITLE: Molecular cloning of a novel human gene on chromosome 4p11 by immunoscreening of an ovarian carcinoma cDNA library.
 AUTHOR: Luo L Y; Soosaipillai A; Diamandis E P
 CORPORATE SOURCE: Department of Pathology and Laboratory Medicine, Mount Sinai Hospital, Toronto, Ontario, M5G 1X5, Canada.
 SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2001 Jan 12) 280 (1) 401-6.
 Journal code: 0372516. ISSN: 0006-291X.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals

ENTRY MONTH: 200103
ENTRY DATE: Entered STN: 20010404
Last Updated on STN: 20010404
Entered Medline: 20010322

AB In our efforts to identify immunoreactive antigens in ovarian cancer, we used the method of immunoscreening of an ovarian carcinoma **cDNA expression** library with ascites fluid from ovarian cancer patients. Among many positive clones, one was found to contain partial sequence of a novel gene. By searching **expressed** sequence tags (**ESTs**) and human genome project **databases** as well as by screening other **cDNA** libraries and by RT-PCR strategies, we were able to obtain the full-length **cDNA** sequence (1.4 kb) and establish the genomic organization of this new gene. We also identified two alternatively spliced forms, encoding for slightly different **proteins**. The longer form (1.4 kb) is predicted to encode for a 27.6 kDa **protein** of 245 amino acids. The shorter form (1.3 kb) encodes for a truncated **protein** of 20.7 kDa and 208 amino acids. These **proteins** are not significantly homologous to any known **protein** in the **GenBank database**. This gene is composed of nine exons and eight introns. By fluorescence in situ hybridization (FISH), it was mapped to chromosome 4p11. This gene is highly **expressed** in many tissues, including testis, brain, placenta, ovary, prostate, and mammary gland. The high level **expression** of the shorter form is restricted to the central nervous system, including brain, cerebellum, and spinal cord, suggesting that this form may have a unique function in the central nervous system. Copyright 2001 Academic Press.

L10 ANSWER 16 OF 47 MEDLINE
ACCESSION NUMBER: 2001123002 MEDLINE
DOCUMENT NUMBER: 21023480 PubMed ID: 11147971
TITLE: Mammalian HSP40/DNAJ homologs: cloning of novel cDNAs and
a
proposal for their classification and nomenclature.
AUTHOR: Ohtsuka K; Hata M
CORPORATE SOURCE: Laboratory of Experimental Radiology, Aichi Cancer Center
Research Institute, Nagoya, Japan.. kohtsuka@aichi-
cc.pref.aichi.jp
SOURCE: CELL STRESS AND CHAPERONES, (2000 Apr) 5 (2) 98-112.
Journal code: 9610925. ISSN: 1355-8145.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200102
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010222

AB We have cloned 10 novel full-length **cDNAs** of mouse and human HSP40/DNAJ homologs using **expressed** sequence tag (**EST**) clones found in the DDBJ/**GenBank**/EMBL DNA **database**. In this report, we tentatively designated them mHsp40, mDj3, mDj4, mDj5, mDj6, mDj7, mDj8, hDj9, mDj10, and mDj11. Based on the identity of the deduced amino acid sequences, mHsp40, mDj3, and mDj11 are orthologs of human Hsp40, rat Rdj2, and human Tpr2, respectively. We determined that mDj4 is identical with the recently isolated mouse Mrj (mammalian relative of DnaJ). PSORT analysis (a program that predicts the subcellular localization site of a given **protein** from its amino acid sequences) revealed that hDj9 has an N-terminal signal **peptide**; hence, its localization might be extracellular, suggesting that there may

be a partner Hsp70 **protein** that acts together with the hDj9 outside of the cell. The same analysis indicated that mDj7 and mDj10 may have transmembrane domains. In order to simplify the complicated and confusing nomenclature of recently identified mammalian HSP40/DNAJ homologs, we propose here some new rules for their nomenclature. This proposed nomenclature includes the name of species with 2 lowercase letters such as hs (Homo sapiens), mm (Mus musculus) and rn (Rattus norvegicus); Dj standing for DnaJ; the name of types with A, B, and C, which were previously classified as type I, II, and III according to the domain structure of the homologs; and finally Arabic numerals according to the chronological order of registration of the sequence data into the **database**.

L10 ANSWER 17 OF 47 MEDLINE
 ACCESSION NUMBER: 2001025016 MEDLINE
 DOCUMENT NUMBER: 20507688 PubMed ID: 11053263
 TITLE: Characterization of gene expression in human trabecular meshwork using single-pass sequencing of 1060 clones.
 AUTHOR: Gonzalez P; Epstein D L; Borrás T
 CORPORATE SOURCE: Department of Ophthalmology, Duke University Medical Center, Durham, North Carolina, USA.
 CONTRACT NUMBER: EY01894 (NEI)
 EY11906 (NEI)
 SOURCE: INVESTIGATIVE OPHTHALMOLOGY AND VISUAL SCIENCE, (2000 Nov) 41 (12) 3678-93.
 Journal code: 7703701. ISSN: 0146-0404.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-BE439390; GENBANK-BE440238
 ENTRY MONTH: 200011
 ENTRY DATE: Entered STN: 20010322
 Last Updated on STN: 20010322
 Entered Medline: 20001114

AB PURPOSE: To study the gene **expression** profile of the human trabecular meshwork (HTM). METHODS: A polymerase chain reaction (PCR)-amplified **cdna** library was constructed using RNA from the TM of a 67-year-old normal, perfused human eye. A total of 1060 clones were randomly selected for sequencing of one end. These sequences were searched against nonredundant **GenBank** and dbEST **databases** for similarity comparison by using a FASTA file and the BLASTcl3 program. Relative **expression** patterns of those clones that matched other **expressed** sequence tags (**ESTs**) were determined using the National Center for Biotechnology Information (NCBI) Unique Human Gene Sequence Collection (UniGene) **database**. RESULTS: Of the 1060 clones analyzed, 519 (48.9%) had sequences identical with known genes, 125 (11.8%) matched **ESTs**, and 189 (17.8%) did not match any **database** sequences. Of the remaining clones, 31 (3%) corresponded to mitochondrial transcripts and 196 (18.5%) to repetitive and noninformative sequences. It is notable that some of the genes highly represented in this library are not ubiquitously **expressed** in other tissues, which suggests a potentially important role in the HTM. As evidence for the presence of true novel genes in the library, one of the clones was fully sequenced. This clone comprised a complete open reading frame of 966 nucleotides, and its deduced amino acid sequence corresponded to a **protein** 33% similar to the MAS-related G-**protein**-coupled receptor. CONCLUSIONS: The identification of the more highly **expressed** genes in HTM and the

discovery of novel genes **expressed** in this tissue provides basic information for further research on the physiology of the TM and for the identification of glaucoma candidate genes.

L10 ANSWER 18 OF 47 MEDLINE
ACCESSION NUMBER: 2000467360 MEDLINE
DOCUMENT NUMBER: 20473755 PubMed ID: 11015613
TITLE: Large-scale analysis of gene expression changes during acute and chronic exposure to [Delta]9-THC in rats.
AUTHOR: Kittler J T; Grigorenko E V; Clayton C; Zhuang S Y; Bunday S C; Trower M M; Wallace D; Hampson R; Deadwyler S
CORPORATE SOURCE: University College of London, WC1E6BT London, UK.
SOURCE: PHYSIOLOGICAL GENOMICS, (2000 Sep 8) 3 (3) 175-85.
Journal code: 100894125. ISSN: 1094-8341.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200103
ENTRY DATE: Entered STN: 20010404
Last Updated on STN: 20010404
Entered Medline: 20010308

AB Large-scale **cdna** microarrays were employed to assess transient changes in gene **expression** levels following acute and chronic exposure to cannabinoids in rats. A total of 24,456 **cdna** clones were randomly selected from a rat brain **cdna** library, amplified by PCR, and arrayed at high density to investigate differential gene **expression** profiles following acute (24 h), intermediate (7 days), and chronic (21 days) exposure to Delta(9)-tetrahydrocannabinol (Delta(9)-THC), the psychoactive ingredient of marijuana. Hippocampal **mRNA** probes labeled with (33)P obtained from both vehicle and Delta(9)-THC-treated animals were hybridized with identical **cdna** microarrays. Results revealed a total of 49 different genes altered by Delta(9)-THC exposure; of these, 28 were identified, 10 had homologies to **expressed** sequence tags (**ESTs**), and 11 had no homology to known sequences in the **GenBank database**. Chronic or acute cannabinoid receptor activation altered **expression** of several genes (i.e., prostaglandin D synthase, calmodulin) involved in biochemical cascades of cannabinoid synthesis or cannabinoid effector systems. Other genes [i.e., neural cell adhesion molecule (NCAM), myelin basic **protein**], whose relation to cannabinoid system function was not immediately obvious, were also significantly altered.

Verification

of the changes obtained with the large-scale screen was determined by RNA dot blots in different groups of animals treated the same as those in the large-scale screen. Results are discussed in terms of the different types of genes affected at different times during chronic Delta(9)-THC exposure.

L10 ANSWER 19 OF 47 MEDLINE
ACCESSION NUMBER: 2000456215 MEDLINE
DOCUMENT NUMBER: 20392318 PubMed ID: 10932001
TITLE: Molecular cloning of a novel gene located on chromosome 3p25.3 and an analysis of its expression in nasopharyngeal carcinoma.
AUTHOR: Xie Y; Deng L; Jiang N; Zhan F; Cao L; Qiu Y; Tang X; Li G
CORPORATE SOURCE: Cancer Research Institute, Hunan Medical University, Changsha, Hunan, P. R. China.
SOURCE: CHUNG-HUA I HSUEH I CHUAN HSUEH TSA CHIH, (2000 Aug) 17 (4) 225-8.

JOURNAL code: 9425197. ISSN: 1003-9406.
PUB. COUNTRY: China
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: Chinese
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200009
ENTRY DATE: Entered STN: 20001005
Last Updated on STN: 20001005
Entered Medline: 20000925

AB OBJECTIVE: To obtain the novel genes associated with human nasopharyngeal carcinoma(NPC) on chromosome 3p24-26. METHODS: Twenty epithelial-derived **expressed** sequence tags(**EST**) were selected from chromosome 3p24-26 where loss of heterozygosity(LOH) frequently occurs in NPC tissues. Primers were designed based on the sequences of these **ESTs**. RT-PCR was used to amplify their corresponding **cDNA** fragments from NPC cell line HNE1 and primary cultures of normal nasopharyngeal epithelial cells. The differential **expression** of two **ESTs**, T93093 and R41598, was confirmed by Northern blot. Then, **expression** of **EST** T93093 was further detected in 7 normal nasopharyngeal and 19 NPC biopsies. **cDNA** library screening was used to get its full **cDNA** sequence and the sequence of this novel gene was analyzed by bioinformatics. RESULTS: Thirteen **ESTs**(T62511, N39155, N68660, R61275, T95314, R06143, H52697, H66521, AA128685, AA284537, N52379, AA054180, and H98090) showed the similar **expression** level and 5 **ESTs**(R00732, R07573, R98052, H91759, H17566) showed no **expression** in both types of cells. **EST** T93093 was down-**expressed**, whereas **EST** R41598 up-**expressed** in NPC HNE1 cells. The **EST** T93093 was also found to be down-**expressed** in 26.3%(5/19) of NPC biopsies. The full length **cDNA** of this gene was obtained and named NAG-7, which is located at chromosome 3p25.3. Its 1677 bp full length **cDNA** has a potential open reading frame(ORF) predicting a 94 amino acid **protein** with a molecular weight of 11023.87 Dalton. Bioinformatics analysis of the NAG-7 gene shows that it is a transmembrane **protein** containing a **protein** kinase C(PKC) phosphorylation site and a myristyl site. It has no significant homology to any reported genes in **database** of **GenBank** (AF086709). CONCLUSION: NAG-7 is a novel gene down-**expressed** in NPC, which may be involved in the development of NPC.

L10 ANSWER 20 OF 47 MEDLINE
ACCESSION NUMBER: 2000334233 MEDLINE
DOCUMENT NUMBER: 20334233 PubMed ID: 10873568
TITLE: Characterization of novel and identified genes in guinea pig organ of corti.
AUTHOR: Oshima T; Nakajima T; Wada H; Ikeda K; Takasaka T
CORPORATE SOURCE: Department of Otorhinolaryngology, Tohoku University School
of Medicine, 1-1 Seiryomachi, Aoba-ku, Sendai, 980-8574, Japan.. oshima@orl.med.tohoku.ac.jp
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2000 Jun 24) 273 (1) 84-9.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AU081352; GENBANK-AU081353; GENBANK-AU081354;
GENBANK-AU081355; GENBANK-AU081356; GENBANK-AU081357;
GENBANK-AU081358; GENBANK-AU081359; GENBANK-AU081360;
GENBANK-AU081361; GENBANK-AU081362; GENBANK-AU081363;

GENBANK-AU081364; GENBANK-AU081365; GENBANK-AU081366;
GENBANK-AU081367; GENBANK-AU081368; GENBANK-AU081369;
GENBANK-AU081370; GENBANK-AU081371; GENBANK-AU081372;
GENBANK-AU081373; GENBANK-AU081374; GENBANK-AU081375;
GENBANK-AU081376; GENBANK-AU081377; GENBANK-AU081378;
GENBANK-AU081379; GENBANK-AU081380; GENBANK-AU081381; +

ENTRY MONTH:

200007

ENTRY DATE:

Entered STN: 20000810

Last Updated on STN: 20000810

Entered Medline: 20000727

AB A number of **proteins** are **expressed** in the organ of Corti and are considered to be responsible for hearing. However, most of them have not been identified. Therefore, to achieve a better understanding of the genetic factors influencing these traits, the first step is to characterize the genes **expressed** in the organ of Corti. In the present study, a **cDNA** library was constructed from the guinea pig organ of Corti. After sequencing isolated clones, 196 **expressed** sequence tags (**ESTs**) were identified with FASTA analysis: 65 **ESTs** showed significant sequence homology to previously identified genes in guinea pig, human or other species, and

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ESTs showed no significant matches to sequences already present in the DNA **database** DDBJ/GenBank/EMBL. A variety of matching sequences, some of which were known to be cochlea-specific, were found through FASTA analysis of the 65 clones. RT-PCR with a panel of 10 different tissue **mRNA** revealed the restricted **expression** of 13 unknown clones. The results of our analysis allowed the establishment of a list of genes **expressed** in the guinea pig organ of Corti.

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L10 ANSWER 21 OF 47 MEDLINE

ACCESSION NUMBER: 2000247250 MEDLINE

DOCUMENT NUMBER: 20247250 PubMed ID: 10783258

TITLE: Molecular cloning of a novel NF2/ERM/4.1 superfamily gene, eh2, that is expressed in high-metastatic K1735 murine melanoma cells.

AUTHOR: Shimizu K; Nagamachi Y; Tani M; Kimura K; Shiroishi T; Wakana S; Yokota J

CORPORATE SOURCE: Biology Division, National Cancer Center Research Institute, 1-1, Tsukiji 5-chome, Chuo-ku, Tokyo, 104-0045, Japan.

SOURCE: GENOMICS, (2000 Apr 15) 65 (2) 113-20.

Journal code: 8800135. ISSN: 0888-7543.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AB032179; GENBANK-AB032366

ENTRY MONTH: 200007

ENTRY DATE: Entered STN: 20000728

Last Updated on STN: 20000728

Entered Medline: 20000720

AB We have cloned a novel gene, Ehm2, that is **expressed** in high-metastatic but not in low-metastatic K-1735 murine melanoma cells. The Ehm2 gene encodes a **protein** of 527 amino acid residues, showing up to 41% amino acid identity with the FERM domain of NF2/ERM/4.1 superfamily **proteins**, which have the function of connecting cell surface transmembrane **proteins** to cytoskeletal molecules. The Ehm2 gene was mapped to chromosome 4 and was **expressed** in the liver, lung, kidney, and testis and in 7- to 17-day embryos. The highest

level of homology was observed with NBL4, which is a new subfamily **protein** of the NF2/ERM/4.1 superfamily. A human homologue of the mouse Ehm2 gene, showing significant homology (83% identity), was identified in the genomic DNA and **EST databases**. Furthermore, seven rat **EST** clones and one pig **EST** clone in the **GenBank EST database** were identified as having 83-92% sequence homology with the **cDNA** sequence of the mouse Ehm2 gene. Thus, Ehm2 is a highly conserved gene that encodes a novel member of the NF2/ERM/4.1 superfamily **proteins**.
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L10 ANSWER 22 OF 47 MEDLINE
 ACCESSION NUMBER: 2000163500 MEDLINE
 DOCUMENT NUMBER: 20163500 PubMed ID: 10701565
 TITLE: Analysis of messages expressed by Echinostoma paraensei miracidia and sporocysts, obtained by random EST sequencing.
 AUTHOR: Adema C M; Leonard P M; DeJong R J; Day H L; Edwards D J; Burgett G; Hertel L A; Loker E S
 CORPORATE SOURCE: Department of Biology, University of New Mexico, Albuquerque 87131, USA.
 CONTRACT NUMBER: AI24340 (NIAID)
 SOURCE: JOURNAL OF PARASITOLOGY, (2000 Feb) 86 (1) 60-5.
 Journal code: 7803124. ISSN: 0022-3395.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200003
 ENTRY DATE: Entered STN: 20000327
 Last Updated on STN: 20000327
 Entered Medline: 20000313

AB A lambdaZAP **Express cDNA** library was constructed with **mRNA** obtained from immature miracidia within eggs, hatched miracidia, and sporocysts of Echinostoma paraensei. This **cDNA** library was amplified and 213 **expressed** sequence tag (**EST**) sequences (averaging 466 nucleotides in length) were obtained. The mean percentage of unresolved bases within the **EST** sequences was 0.4%, ranging from 0 to 4.6%. The 213 **ESTs** represent 151 unique messages. BLAST (version 2.0.8) analysis disclosed that 64 unique E. paraensei messages (42.4%) had significant similarities (BLAST score < or =e-5), at deduced amino acid or nucleotide levels, with known sequences in the nonredundant **GenBank databases** or the dbEST **database** (NCBI). The remainder, 57.6% of the unique **EST**-encoded messages, scored nonsignificant hits. Most of the E. paraensei messages that could be assigned a cellular role based on sequence similarities were involved in gene/**protein expression**. Several **ESTs** scored highest similarities with sequences obtained from trematode species. A total of 22,560 nucleotides present in open reading frames from **ESTs** that aligned with known sequences was used to determine codon usage for E. paraensei. Analysis of a subset of eight **ESTs** that contained full-length open reading frames did not reveal a bias in codon usage. Also, **EST** sequences were found to contain 3' untranslated regions with an average length of 69.9 +/- 88.4 nucleotides (n = 46). The **EST** sequences were submitted to **GenBank/dbEST**, adding to the 51 available Echinostoma-derived sequences, to provide reference information for both phylogenetic analysis and study of general trematode biology.

L10 ANSWER 23 OF 47 MEDLINE
 ACCESSION NUMBER: 1999453298 MEDLINE
 DOCUMENT NUMBER: 99453298 PubMed ID: 10521661
 TITLE: Developmental expression of specific genes detected in high-quality cDNA libraries from single human preimplantation embryos.
 AUTHOR: Adjaye J; Bolton V; Monk M
 CORPORATE SOURCE: Molecular Embryology Unit, Institute of Child Health, 30 Guilford Street, London, UK.. j.adjaye@ich.ucl.ac.uk
 SOURCE: GENE, (1999 Sep 17) 237 (2) 373-83.
 Journal code: 7706761. ISSN: 0378-1119.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199911
 ENTRY DATE: Entered STN: 20000111
 Last Updated on STN: 20000111
 Entered Medline: 19991108

AB We describe an improved highly sensitive method for generating **cDNA** libraries containing a high proportion of **cDNAs** enriched with 5'-coding sequences from single human preimplantation embryos and a 10 week old whole fetus. The embryonic **mRNA** was isolated using oligo-(dT) linked to magnetic beads. First-strand **cDNA** synthesis was carried out directly on the bound **mRNA**, followed by PCR designed to amplify the **cDNA** molecules synthesized in their entirety. The complexities of the libraries are between 10(5) and 10(6) independent clones. The average **cDNA** size is 1.0 kb, and the size range is 0.5-3.0 kb. PCR analysis of the embryonic libraries for specific genes has revealed transcripts for genes known to be transcribed in preimplantation stages, such as the imprinted gene SNRPN, developmental genes WNT11, HOX, OCT-1 and the embryonic

OCT-4, cytoskeletal genes keratin-18 and beta-actin, the cell cycle gene C-MOS, and housekeeping genes GAPDH and HPRT. Sequencing of random clones showed the presence of a variety of sequences, such as human chorionic gonadotrophin, ubiquitin, TFIIA, guanine nucleotide-binding **protein** (beta-subunit), annexin I, a gene encoding a kinesin-like **protein**, and TWIST, which encodes a basic helix-loop-helix (bHLH) transcription factor implicated in Saethre-Chotzen syndrome

(characterized by craniofacial and limb anomalies). Approximately 40% of these randomly analysed clones were full length. In addition to **cDNAs** matching known **ESTs** (Expressed Sequence Tags) in the **GenBank** and dbEST databases, novel sequences were detected at a frequency of 16% of randomly picked clones. The libraries are a valuable resource, providing longer **cDNAs** representing genes **expressed** during human preimplantation development.

L10 ANSWER 24 OF 47 MEDLINE
 ACCESSION NUMBER: 1999263238 MEDLINE
 DOCUMENT NUMBER: 99263238 PubMed ID: 10330131
 TITLE: Inventory of high-abundance mRNAs in skeletal muscle of normal men.
 AUTHOR: Welle S; Bhatt K; Thornton C A
 CORPORATE SOURCE: University of Rochester, Rochester, New York 14642 USA.. swelle@ican.net
 CONTRACT NUMBER: AG-10463 (NIA)
 AG-13070 (NIA)
 RR-00044 (NCRR)
 SOURCE: GENOME RESEARCH, (1999 May) 9 (5) 506-13.

Journal code: 9518021. ISSN: 1088-9051.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199906
ENTRY DATE: Entered STN: 19990712
Last Updated on STN: 19990712
Entered Medline: 19990624

AB G42875rial analysis of gene **expression** (SAGE) method was used to generate a catalog of 53,875 short (14 base) **expressed** sequence tags from polyadenylated RNA obtained from vastus lateralis muscle of healthy young men. Over 12,000 unique tags were detected. The frequency of

occurrence of each tag reflects the relative abundance of the corresponding **mRNA**. The **mRNA** species that were detected 10 or more times, each comprising $\geq 0.02\%$ of the **mRNA** population, accounted for 64% of the **mRNA** mass but $< 10\%$ of the total number of **mRNA** species detected. Almost all of the abundant tags matched **mRNA** or **EST** sequences cataloged in **GenBank**. Mitochondrial transcripts accounted for approximately 20% of the polyadenylated RNA. Transcripts encoding **proteins** of the myofibrils were the most abundant nuclear-encoded **mRNAs**. Transcripts encoding ribosomal **proteins**, and those encoding **proteins** involved in energy metabolism, also were very abundant. The **database** can be used as a reference for investigations of alterations in gene **expression** associated with conditions that influence muscle function, such as muscular dystrophies, aging, and exercise.

L10 ANSWER 25 OF 47 MEDLINE

ACCESSION NUMBER: 1999156852 MEDLINE
DOCUMENT NUMBER: 99156852 PubMed ID: 10036181
TITLE: Discovery of three novel orphan G-protein-coupled receptors.
AUTHOR: Marchese A; Sawzdargo M; Nguyen T; Cheng R; Heng H H; Nowak
CORPORATE SOURCE: T; Im D S; Lynch K R; George S R; O'dowd B F
Department of Pharmacology, Department of Medicine,
University of Toronto, Medical Sciences Building, Toronto,
Ontario, M5S 1A8, Canada.
SOURCE: GENOMICS, (1999 Feb 15) 56 (1) 12-21.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF118265; GENBANK-AF118266; GENBANK-AF118670
ENTRY MONTH: 199905
ENTRY DATE: Entered STN: 19990517
Last Updated on STN: 20000303
Entered Medline: 19990505

AB We have discovered three novel human genes, GPR34, GPR44, and GPR45, encoding family A G-**protein**-coupled receptors (GPCRs). The receptor encoded by GPR34 is most similar to the P2Y receptor subfamily, while the receptor encoded by GPR44 is most similar to chemoattractant receptors. The receptor encoded by GPR45 is the mammalian orthologue of a putative lysophosphatidic acid receptor from *Xenopus laevis*. Partial sequence of GPR34 was discovered during a search of the **GenBank database** of **expressed** sequence tags (**ESTs**). This sequence information was used both to isolate the full-length

translational open reading frame from a human genomic library and to assemble a contig from additional GPR34 **EST cDNAs**. Northern blot and in situ hybridization analyses revealed GPR34 **mRNA** transcripts in several human and rat brain regions. Also, we used polymerase chain reaction (PCR) to amplify human genomic DNA using degenerate oligonucleotides designed from sequences encoding transmembrane domains 3 and 7 of opioid and somatostatin receptors. Two PCR products partially encoding novel GPCRs, named GPR44 and GPR45, were discovered and used to isolate the full-length translational open reading frames from a human genomic library. Both GPR44 and GPR45 are **expressed** in the central nervous system and periphery. For chromosomal localization, fluorescence in situ hybridization analysis was performed to assign GPR34 to chromosomes 4p12 and Xp11. 3, GPR44 to chromosome 11q12-q13.3, and GPR45 to chromosome 2q11. 1-q12.

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L10 ANSWER 26 OF 47 MEDLINE
 ACCESSION NUMBER: 1999121000 MEDLINE
 DOCUMENT NUMBER: 99121000 PubMed ID: 9922225
 TITLE: Isolation of a gene product expressed by a subpopulation of human lung fibroblasts by differential display.
 AUTHOR: Lurton J; Rose T M; Raghu G; Narayanan A S
 CORPORATE SOURCE: Department of Medicine, School of Medicine, University of Washington, Seattle 98195, USA.
 CONTRACT NUMBER: DE39584 (NIDCR)
 SOURCE: AMERICAN JOURNAL OF RESPIRATORY CELL AND MOLECULAR BIOLOGY,
 (1999 Feb) 20 (2) 327-31.
 Journal code: 8917225. ISSN: 1044-1549.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF115384
 ENTRY MONTH: 199903
 ENTRY DATE: Entered STN: 19990324
 Last Updated on STN: 20000303
 Entered Medline: 19990311

AB Fibroblasts are the major cell type responsible for synthesizing matrix constituents in lung and other connective tissues. Evidence indicates that fibroblasts are heterogeneous, and that subpopulations with some distinct properties are clonally selected and expanded in fibrotic diseases. However, few distinct markers capable of demonstrating the presence of fibroblast subpopulations in tissues have been isolated so far. With the objective of identifying **proteins** that could detect fibroblast subpopulations, we compared the messenger RNA (**mRNA**) **expression** of two cultured human lung fibroblast subpopulations by differential display. Total RNA was obtained, complementary DNA (**cDNA**) was synthesized, and the polymerase chain reaction (PCR) products obtained with several primer pairs were compared. One 724-bp product, which was strongly **expressed** by one human lung fibroblast subpopulation, was identified and cloned. This product was poorly **expressed** by the other lung fibroblast subpopulation. The **mRNA** for the gene encoding this product was not detectable in human smooth-muscle cells, endothelial cells, or epithelial cells, although it was present in dermal fibroblasts. The **mRNA** was detected in normal and fibrotic human lungs. Search of the National Center

for Biotechnology (NCBI) **GenBank** DNA database with the sequence obtained from this clone revealed no significant matches. However, a search of the NCBI database of **expressed** sequence tags (dbEST) revealed five different human **expressed** sequence tag (**EST**) clones corresponding to the LR8 **cDNA** sequence. Six additional mouse and one pig **EST** clones were identified that showed significant similarity to the human fibroblast **cDNA**. Composites of the entire coding sequences for the human fibroblast gene product and the mouse homologue were assembled from the respective overlapping **EST** sequences. The open reading frame identified for each composite sequence predicted **protein** products of 270 and 263 amino acids for the human and mouse sequences, respectively, which were 52% identical, with three gaps. At the amino acid level, no significant sequence similarity was detected with any other sequences in exhaustive searches of the NCBI DNA and **protein** databases or the Blocks databases. A PCR product with predicted length and sequence was obtained by using a sense primer upstream to LR8 and an antisense primer within LR8. Our results indicate that this differentially displayed product represents a previously undescribed **protein** that could be useful for distinguishing fibroblasts, and possibly fibroblast subpopulations, from other cell types in lungs and other tissues.

L10 ANSWER 27 OF 47 MEDLINE
ACCESSION NUMBER: 1999097352 MEDLINE
DOCUMENT NUMBER: 99097352 PubMed ID: 9878255
TITLE: Molecular cloning of a gene on chromosome 19q12 coding for a novel intracellular protein: analysis of expression in human and mouse tissues and in human tumor cells, particularly Reed-Sternberg cells in Hodgkin disease.
AUTHOR: Van Leuven F; Torrekens S; Moechars D; Hilliker C; Buellens
CORPORATE SOURCE: M; Bollen M; Delabie J
Experimental Genetics Group, Center for Human Genetics, Flemish Institute for Biotechnology, Department of Biochemistry, K.U. Leuven, Campus Gasthuisberg, Louvain, B-3000, Belgium.. FREDVL@MED.KULEUVEN.AC.BE
SOURCE: GENOMICS, (1998 Dec 15) 54 (3) 511-20.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF091095; GENBANK-AF091096
ENTRY MONTH: 199902
ENTRY DATE: Entered STN: 19990311
Last Updated on STN: 19990311
Entered Medline: 19990223

AB A novel **protein**, named NNX3, was molecularly characterized by cloning its **cDNA**, and its gene was mapped to chromosome 19q12. The equivalent mouse **cDNA** and gene were also cloned to allow us to analyze **expression** in murine in addition to human cells and tissues. Human and mouse NNX3 genes are composed of nine exons coding for **proteins** that are unrelated to any known **protein**. Signal **peptides** and hydrophobic domains are absent, corroborating their localization in the cytoplasm in transfected Cos cells. In Western blotting and immunoprecipitation, human NNX3 appeared as a doublet of Mr 64K-66K, while mouse NNX3 was a 70-kDa **protein**, both apparently much larger than the predicted 50 kDa, due in part to a stretch of 16-18

acidic residues hinging two nearly equally sized domains. In addition, phosphorylation of serine residues was demonstrated. Putative nuclear targeting signals were predicted, but **NNX3 protein** and two truncated versions remained localized in the cytoplasm of transfected Cos cells. **NNX3** was **expressed** in embryonic and adult mouse tissues, particularly in brain, muscle, and lung. The **expression** of human **NNX3** was most notable in human skeletal muscle and in ganglion cells and was also evident in human tumors and derived cell lines. This was confirmed by entries appearing in the **GenBank EST database** during the later phase of this study, representing partial **NNX3 cDNA** isolated from diverse neoplastic and developing tissues. Surprisingly, **NNX3** was immunochemically detected in Reed-Sternberg cells of Hodgkin disease, in parallel with restin, a cytoplasmic **protein** we previously characterized (J. Delabie et al., 1993, Leuk. Lymphoma 12, 21-26). The cloning and comprehensive molecular analysis of **NNX3** as presented will form the basis for elucidating its function and, conversely, will constitute a marker for Reed-Sternberg cells in Hodgkin disease.
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L10 ANSWER 28 OF 47 MEDLINE
 ACCESSION NUMBER: 1998433873 MEDLINE
 DOCUMENT NUMBER: 98433873 PubMed ID: 9762909
 TITLE: cDNA cloning of Brassica napus malonyl-CoA:ACP transacylase
 (MCAT) (fab D) and complementation of an E. coli MCAT mutant.
 AUTHOR: Simon J W; Slabas A R
 CORPORATE SOURCE: Department of Biological Sciences, University of Durham, Science Laboratories, UK.. j.w.simon@durham.ac.uk
 SOURCE: FEBS LETTERS, (1998 Sep 18) 435 (2-3) 204-6.
 Journal code: 0155157. ISSN: 0014-5793.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AJ007046
 ENTRY MONTH: 199810
 ENTRY DATE: Entered STN: 19981029
 Last Updated on STN: 19981029
 Entered Medline: 19981022

AB The **GenBank database** was searched using the E. coli malonyl CoA:ACP transacylase (MCAT) sequence, for plant **protein/cDNA** sequences corresponding to MCAT, a component of plant fatty acid synthetase (FAS), for which the plant **cDNA** has not been isolated. A 272-bp Zea mays **EST** sequence (**GenBank** accession number: AA030706) was identified which has strong homology to the E. coli MCAT. A PCR derived **cDNA** probe from Zea mays was used to screen a Brassica napus (rape) **cDNA** library. This resulted in the isolation of a 1200-bp **cDNA** clone which encodes an open reading frame corresponding to a **protein** of 351 amino acids. The **protein** shows 47% homology to the E. coli MCAT amino acid sequence in the coding region for the mature **protein**. **Expression** of a plasmid (pMCATrap2) containing the plant **cDNA** sequence in Fab D89, an E. coli mutant, in MCAT activity restores growth demonstrating functional complementation and direct function of the cloned **cDNA**. This is the first functional evidence supporting the identification of a plant **cDNA** for MCAT.

L10 ANSWER 29 OF 47 MEDLINE
 ACCESSION NUMBER: 1998248992 MEDLINE

DOCUMENT NUMBER: 98248992 PubMed ID: 9587421
 TITLE: Identification of a novel human glutathione S-transferase using bioinformatics.
 AUTHOR: Liu S; Stoesz S P; Pickett C B
 CORPORATE SOURCE: Schering-Plough Research Institute, Kenilworth, New Jersey 07033, USA.
 SOURCE: ARCHIVES OF BIOCHEMISTRY AND BIOPHYSICS, (1998 Apr 15) 352 (2) 306-13.
 Journal code: 0372430. ISSN: 0003-9861.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF025887
 ENTRY MONTH: 199806
 ENTRY DATE: Entered STN: 19980611
 Last Updated on STN: 19980611
 Entered Medline: 19980603

AB In searching the **expressed** sequence tag (**EST**) data-base of **GenBank** with coding sequences of 11 known human glutathione S-transferases in conjunction with bioinformatic analysis, we have identified five **ESTs** that encode a new human glutathione S-transferase (GST) designated GST A4. The **cDNA** clone (I.M.A.G.E. Consortium **cDNA** Clone ID 515157) had an insert length of 1279 bp and contains an open reading frame of 666 bp, which encodes a **protein** of 222 amino acid residues. The GST A4 **protein** is identical in length to human GST A1 and A2 and is 54% identical to human GST A1 and A2. Sequence comparison with other human GSTs suggests that it is a new GST belonging to the alpha class GSTs. Northern blot analysis and **EST database** searches have demonstrated that the GST A4 **mRNA** is **expressed** at a high level in brain, placenta, and skeletal muscle and much lower in lung and liver. Analysis of the sequence tagged site (STS) **database** indicated that the GST A4 gene is located on chromosome 6. This STS represents a previously unidentified transcript further confirming the novelty of the new sequence.

L10 ANSWER 30 OF 47 MEDLINE
 ACCESSION NUMBER: 1998126432 MEDLINE
 DOCUMENT NUMBER: 98126432 PubMed ID: 9465292
 TITLE: An expressed-sequence-tag database of the human prostate: sequence analysis of 1168 cDNA clones.
 AUTHOR: Nelson P S; Ng W L; Schummer M; True L D; Liu A Y; Bumgarner R E; Ferguson C; Dimak A; Hood L
 CORPORATE SOURCE: Department of Molecular Biotechnology, University of Washington, Seattle 98195, USA.. psnels@u.washington.edu
 SOURCE: GENOMICS, (1998 Jan 1) 47 (1) 12-25.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AA447269; GENBANK-AA447270; GENBANK-AA447271;
 GENBANK-AA447272; GENBANK-AA447273; GENBANK-AA447274;
 GENBANK-AA447275; GENBANK-AA447276; GENBANK-AA447277;
 GENBANK-AA447278; GENBANK-AA447279; GENBANK-AA447280;
 GENBANK-AA447281; GENBANK-AA447282; GENBANK-AA447283;
 GENBANK-AA447284; GENBANK-AA447285; GENBANK-AA447286;
 GENBANK-AA447287; GENBANK-AA447288; GENBANK-AA447289;
 GENBANK-AA447290; GENBANK-AA447291; GENBANK-AA447292;
 GENBANK-AA447293; GENBANK-AA447294; GENBANK-AA447295;

ENTRY MONTH: GENBANK-AA447296; GENBANK-AA447297; GENBANK-AA447298; +
199804
ENTRY DATE: Entered STN: 19980430
Last Updated on STN: 19980430
Entered Medline: 19980420

AB The human prostate is a complex glandular organ with functional development under hormonal regulation. Diseases of the prostate result in significant morbidity and mortality in the form of benign prostatic hypertrophy and prostate adenocarcinoma. The characterization of the molecular framework of the human prostate at the level of **expressed** genes will facilitate the understanding of normal and pathological prostate biology. The purposes of this study were to acquire an initial assessment of the qualitative and quantitative diversity of gene **expression** in the normal human prostate and to determine the extent that genes with prostate-restricted **expression** can be assessed using an **expressed** sequence tag approach. We have constructed a directional **cDNA** library from normal adult human prostate tissue and partially sequenced the 5' end of 1168 randomly selected **cDNA** clones, resulting in more than 400 kb of DNA sequence. Homology searches of the sequenced **cDNAs** against the **GenBank** and dbEST **databases** revealed that 43% of the sequences are identical to human genes whose functions are known, 5% are similar but not identical to known genes in humans or lower organisms, 5% match the mitochondrial genome, 9% are composed of interspersed DNA repeats, 30% are homologous to sequences in the dbEST **database** without a described function, and 6% are novel sequences. A total of 780 distinct species were identified. In addition to the 74 novel transcripts,
4 genes, prostate-specific antigen (PSA), prostate secretory **protein** (PSP), prostate acid phosphatase (PAP), and human glandular kallikrein 2 (HK2), have no homologous sequences in the **databases** that originate from sources other than prostate and thus may represent genes with prostate-restricted **expression**. Sequences matching PSA, PSP, and PAP each accounted for > 1% of the total **ESTs** and represent highly abundant transcripts, correlating with the abundance of these **proteins** in the prostate gland. No novel transcripts were represented by more than one **EST** and thus are **expressed** at levels much lower than the known prostate-specific genes.

L10 ANSWER 31 OF 47 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:129805 BIOSIS
DOCUMENT NUMBER: PREV200200129805
TITLE: Notch signaling pathway modifier Lunatic Fringe gene is upregulated by retinoic acid during granulocytic differentiation in APL.
AUTHOR(S): Park, Dorothy J. (1); Vuong, Peter T. (1); Koeffler, H. Phillip (1)
CORPORATE SOURCE: (1) Hematology/Oncology, Cedars-Sinai Medical Center, Los Angeles, CA USA
SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 1, pp. 89a.
<http://www.bloodjournal.org/>. print.
Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 1 Orlando, Florida, USA December 07-11,
2001
ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English
AB Retinoids and their nuclear receptors play an important role in the

regulation of cellular differentiation. In acute promyelocytic leukemia (APL), chromosomal translocations involving retinoic acid receptor alpha (RARalpha) and its various aberrant fusion partners, such as PML and PLZF, play a causative role in pathogenesis of the disease, presumably by repressing downstream target genes. PML/RARalpha is also responsible for the in vitro and in vivo sensitivity to cell differentiation mediated by retinoic acid (RA). Using a PCR-based cDNA subtractive hybridization method, we have cloned a RA-regulated transcript 11.20. 11.20 was strongly upregulated by retinoic acid in a time-dependent manner in the APL cell line NB4 find the retinoid-responsive AML cell line HL60. Retinoid-dependent induction of 11.20 mRNA expression occurred independently of new protein synthesis. Similar pattern of expression was observed in normal CD34+ cells that were induced to differentiate into the granulocytic lineage by cytokines. DNA sequences from the partial cDNA encoding the 3' untranslated region of our clone and corresponding ESTs in the dbEST database at NCBI were used in the homology search using GenBank Blast search. Blast search identified a genomic clone CTD-231213 (GenBank Accession number AC012351) from human chromosome 7, and the genomic sequence (136,000 to 147,000) of this clone was used to predict a gene utilizing GrailEXP v3.0 via internet. GrailEXP predicted a putative gene encompassing a 7 kb genomic fragment. This gene was predicted to have 8 exons (1077 base pair, 358 amino acids), and it matched with a partial coding sequence of a human Drosophila Lunatic Fringe gene homologue and complete coding sequence of murine Lunatic Fringe gene. Members of the notch signaling pathway play critical roles in the determination of cell fate and maintenance of progenitors in many developmental systems including myeloid differentiation. Lunatic Fringe belongs to the family of notch signaling modifiers along with Radical and Manic Fringe genes. Therefore, retinoid-dependent induction of Lunatic Fringe gene expression in APL may play an important role in the granulocytic differentiation process.

L10 ANSWER 32 OF 47 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 2002:129475 BIOSIS
 DOCUMENT NUMBER: PREV200200129475
 TITLE: Identification of a new human gene that codes for a potential cytoskeletal protein belonging to a new sudfamily of Rho-GAP proteins.
 AUTHOR(S): Basseres, Daniela S. (1); Tizzei, Edna R. V. (1); Costa, Fernando F. (1); Saad, Sara T. O. (1)
 CORPORATE SOURCE: (1) Hematology and Hemotherapy Center, State University of Campinas, Campinas, SP Brazil
 SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 1, pp. 11a-12a. <http://www.bloodjournal.org/>. print.
 Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 1 Orlando, Florida, USA December 07-11, 2001
 ISSN: 0006-4971.
 DOCUMENT TYPE: Conference
 LANGUAGE: English
 AB Until recently, cytoskeletal proteins were thought to provide solely a mechanical support to the cell plasma membrane. Recent studies have revealed, however, that cytoskeletal proteins are involved in the regulation of major cell functions, such as cell signalling, protein trafficking, formation of specialized membrane domains,

activity modulation of ion channels, membrane pumps and receptors, control

of cell proliferation and transcription activity, among others.

Therefore,

identification of new human cytoskeletal **proteins** is crucial for improved understanding of cell function, since they are major players in signal transduction pathways. Searching the ORESTES database, we found the **expressed** sequence tag (EST)

PM3-LT0032-231299-001-h11 that demonstrated similarity to the pleckstrin homology (PH) domain of the cytoskeletal **protein** beta-spectrin.

The PH domain is thought to be involved in the recruitment of

cytoskeletal

proteins to the submembrane region of the cell. This **EST**

was also highly similar to KIAA1424 (GenBank AB037845), a 4655pb partial **cDNA** found in human brain. Northern analysis of this gene revealed a **mRNA** band of approximately 7.5Kb

expressed in many tissues, including peripheral blood leukocytes.

A more abundant **expression** was observed in brain and muscle.

RT-PCR analysis confirmed that this gene is **expressed** in

hematopoietic stem cells before and after induction of erythroid

differentiation with erythropoietin, with a lower **expression** in

the later steps of differentiation. It is also **expressed** in bone

marrow, tonsils and in the leukocytes of leukemia patients. In an attempt

to obtain the full-length sequence of this partial **cDNA**, we

employed similarity searches against the human genome database

at NCBI and used the genomic sequences obtained to search for new

ESTs in the 5' region, which could belong to the same transcript.

PCR and sequencing of human brain **cDNA** were used to validate the

inclusion of new sequences into the transcript. We also performed rapid

amplification of **cDNA** ends (RACE) in order to obtain the 5'end

sequence. The **cDNA** sequence is 7134pb long and potentially codes

for a 1957 aminoacid **protein** containing a PH, a Rho-GAP and a

PDZ domain. Rho-GAP domains activate the GTPase activity of small GTPases

of the Rho family, stimulating the formation of the inactive GDP-bound

form of these GTPases. PDZ domains are thought to mediate **protein**

-protein interactions. Clearly, this **protein** is not a

new member of the beta-spectrin family, but could represent a new class

of

cytoskeletal **proteins** involved in GTPase signalling. This

protein could also bind GTP/ATP itself through a P-loop present

inside the PDZ domain. Computer generated genomic analysis of this new

gene suggests that it lies on chromosome 10 and that it is composed of 25

exons. Rho-GAP **proteins** downregulate small GTPases of the Rho

family, which function as molecular switches that regulate diverse

cellular processes such as actin cytoskeleton organization and cell

proliferation. An abnormal **expression** of **proteins** in

the Rho-GTPase cascade could lead to neoplastic transformation,

particularly causing tumor invasion and metastasis. The fact that this

new

Rho-GAP **protein** is widely **expressed** reflects the

potential importance of its function. Immunolocalization studies are

currently being performed in order to better understand the role of this

protein. Finally, we have identified a new widely

expressed gene coding for a potential cytoskeletal **protein**

involved in a major signal transduction pathway.

L10 ANSWER 33 OF 47 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:526231 BIOSIS

DOCUMENT NUMBER: PREV200100526231

TITLE: Random sequencing of cDNAs and identification of mRNAs.

AUTHOR(S): Anderson, James V. (1); Horvath, David P.

CORPORATE SOURCE: (1) Biosciences Research Laboratory, Plant Science Research, U.S. Department of Agriculture, Agricultural Research Service, 1605 Albrecht Boulevard, Fargo, ND, 58105: andersjv@fargo.ars.usda.gov USA
SOURCE: Weed Science, (September October, 2001) Vol. 49, No. 5, pp.

590-597. print.
ISSN: 0043-1745.

DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

AB As a first step toward developing a genomics-based research program to study growth and development of underground adventitious shoot buds of leafy spurge, we initiated a leafy spurge **expressed** sequence tag (**EST**) **database**. From the approximately 2,000 clones randomly isolated from a **cDNA** library made from a population containing growth-induced underground adventitious shoot buds, we have obtained **ESTs** for 1,105 **cDNAs**. Approximately 29% of the leafy spurge **EST database** consists of **expressed** genes of unknown identity (hypothetical **proteins**), and 10% represents ribosomal **proteins**. The remaining 60% of the **database** is composed of **expressed** genes that show BLASTX sequence identity scores of gtoreq80 with known **GenBank** accessions. Clones showing sequence identity to a Histone H3, a gibberellic acid-responsive gene, Tubulin, and a light-harvesting chlorophyll a/b-binding **protein** were shown to be differentially **expressed** in underground adventitious shoot buds of leafy spurge after breaking of dormancy. RNA encoding a putative cyclin-dependent **protein** kinase (CDK)-activating kinase, a gene associated with cell division, and Scarecrow-like 7, a gene involved in GA signaling, were present at similar levels in dormant and growth-induced underground adventitious shoot buds. These data show how even a small **EST database** can be used to develop a genomics-based research program that will help us identify genes responsive to or involved in the mechanisms controlling underground adventitious shoot bud growth and development.

L10 ANSWER 34 OF 47 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:514713 BIOSIS
DOCUMENT NUMBER: PREV200100514713
TITLE: Analysis of the filarial parasite *Brugia malayi* adult male stage EST clusters for novel gene identification.
AUTHOR(S): Kamal, Ibrahim H. (1); Ganatra, Mehul B. (1); Foster, Jeremy M. (1); Moran, Laurie S. (1); Ware, Jennifer L. (1);
Guiliano, David; Blaxter, Mark L.; Helmy, Hanan; Slatk, Barton E. (1); Ramzy, Reda M.
CORPORATE SOURCE: (1) New England Biolabs, Inc., Beverly, MA USA
SOURCE: International Genome Sequencing and Analysis Conference, (2000) Vol. 12, pp. 70-71. print.
Meeting Info.: 12th International Genome Sequencing and Analysis Conference Miami Beach, Florida, USA September 12-15, 2000
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English
AB The current **database** of *Brugia malayi* (a filarial nematode responsible for lymphatic elephantiasis) contains DNA sequences of more than 22,000 **expressed** sequence tags (**ESTs**) providing a resource for identifying new genes and determining their functions. The
B.

malayi adult male **cdna** library was selected for detailed analysis. A total of 1611 **ESTs** from B. malayi adult male stage were identified, clustered by a sequence similarity algorithm and assembled into 1356 separate clusters. All the sequences have been submitted to dbEST/**GenBank**. These clusters of the Filarial **database** version 2.0 (FilDB v. 2.0) were analyzed using BLAST search for the identification of novel genes. Comparison of these clusters with **GenBank database** identified 151 clusters hitting the free living nematode Caenorhabditis elegans, 90 clusters hitting other organisms and 704 as novel genes which have no significant similarities in the **database**. The remaining 411 clusters, (30%) are not included in these analyses since they are shorter than 200 bp in length and contain more than 10% Ns (aNybase). Members of many gene families, including cytoskeletal house keeping **proteins**, GTB-binding **proteins**, and house keeping enzymes were identified. Other identified genes include RAS-related signaling **protein**, calcium activated potassium channel **protein**, aspartyl and cysteine proteases, sex determining gene (her-1) and major sperm **protein**. About 50% of the clusters that hit the C. elegans **database** have similarity to hypothetical or predicted **proteins**. Among those novel genes (52%) there is a set of potentially Brugia specific targets for immunotherapy and drug development. The variety and redundancy of **ESTs** in this study suggest that the **cdna** library reflects in vivo gene **expression**. A large scale **EST** effort should uncover many new genes and provide information about genes involved in the biochemical pathways of the nematode. As this approach is expanded to the analysis of **ESTs** from other B. malayi stages, other genes involved in development and/or pathogenicity are likely to be revealed.

L110 ANSWER 35 OF 47 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 2001:492683 BIOSIS
 DOCUMENT NUMBER: PREV200100492683
 TITLE: Cloning of a novel mouse Gabarapl2 cDNA and its characterization.
 AUTHOR(S): Chen, Zheng (1); Xin, Yu-Rong; Jiang, Ying; Jiang, Ju-Xiang
 CORPORATE SOURCE: (1) School of Life Science, Suzhou University, Suzhou, 215006: zhengchen_99@yahoo.com, xinyu@umdnj.edu China
 SOURCE: Acta Pharmacologica Sinica, (August, 2001) Vol. 22, No. 8, pp. 751-755. print.
 ISSN: 0253-9756.
 DOCUMENT TYPE: Article
 LANGUAGE: English
 SUMMARY LANGUAGE: Chinese; English
 AB AIM: To clone a novel mouse GABAA-receptor-associated **protein** like 2 (Gabarapl2) gene, and to analysis its primary function. METHODS: With the aid of computer, the human GABARAPL2 **cdna** was used as information probe to search mouse **EST database** of **GenBank** for mouse homolog. A series of overlapping **EST** were found and assembled into an **EST** contig using Genetics Computer Group (GCG) ASSEMBLY program. The existence of the gene was then identified by experiment. Northern blotting was performed to hybridize (alpha-32P) dATP labeled probe with **mRNA** of 11 different mouse tissues that had been transferred to the nylon membrane. RESULTS: The novel gene was deposited in **GenBank** under Accession No AF190644. Its **cdna** contained an intact open reading frame and a canonical

polyadenylation signal AATAAA followed by polyA. The deduced **protein** was completely identical to that of human GABARAPL2, and was termed Gabarapl2 by Mouse Gene Nomenclature Committee. The putative **protein** of Gabarapl2 has a calculated molecular weight of 13 700 and an isoelectric point of 8.56. It was also predicted to contain two **protein** kinase C phosphorylation sites and one tyrosine kinase phosphorylation site. Northern hybridization showed that Gabarapl2 was **expressed** as a single 1.35 kb transcript, with high levels in brain, thymus, lung, heart, kidney, and liver, and low in pancreas, testis, small intestine, colon, and stomach. CONCLUSION: A novel mouse Gabarapl2 gene was cloned and identified.

L10 ANSWER 36 OF 47 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:290628 BIOSIS

DOCUMENT NUMBER: PREV200100290628

TITLE: Using lab on-line to clone and identify the esophageal cancer related gene 4.

AUTHOR(S): Bi Mei-Xia; Han Wei-Dong; Lu Shi-Xin (1)

CORPORATE SOURCE: (1) Cancer Institute (Hospital), Chinese Academy of Medical

Sciences, Peking Union Medical College, Beijing, 100021: shlu@public.bta.net.cn China

SOURCE: Shengwu Huaxue yu Shengwu Wuli Xuebao, (May, 2001) Vol. 33,

No. 3, pp. 257-261. print.

ISSN: 0582-9879.

DOCUMENT TYPE: Article

LANGUAGE: Chinese

SUMMARY LANGUAGE: Chinese; English

AB Using Internet as platform, **databases** as materials and software as tools to assemble a lab on-line is revolutionizing in bioscience research. The major works of lab on-line are cloning, identification, localization of genes, and the structural and functional analysis of **proteins**. In this report, the esophageal cancer related gene 4 (ECRG-4) (accession number: AF325503) was successfully isolated. The 97

bp

ECRG-4 **EST** was initially used to fish the human **EST** **databases**. Five pieces of **ESTs** showed strong homology to it, and they were assembled to one 772 bp **cdna** sequence by DNASTAR software. Then the 447 bp full open reading frame of ECRG-4 was determined by ORF FINDER to encode 148 amino acids. Sequence of ECRG-4

did

not reveal remarkable similarity to the known sequences in a homology analysis with the public **database** of **GenBank**, showing that it is a new gene. Homology analysis of **protein** coding by ECRG-4 showed a 31% homology with mouse IgG V region. ECRG-4 gene is **expressed** in normal esophagus, bladder and brain tissues, but its **expression** was significantly down-regulated in prostate tumors and tumor cell lines. ECRG-4 gene was located in 2q14.1-14.3 by HTGS and STS, and was conformed by radiation hybrid (RH) method. We propose that this purely lab on-line cloning approach can be used by modestly sized laboratories to rapidly and accurately characterize human genes without wasting too much money and time.

L10 ANSWER 37 OF 47 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:288231 BIOSIS

DOCUMENT NUMBER: PREV200100288231

TITLE: Molecular cloning of NELIN, a putative human cytoskeleton regulation gene.

AUTHOR(S): Zhao Yong; Wei Ying-Jie; Cao Hui-Qing; Ding Jin-Feng (1)

CORPORATE SOURCE: (1) Molecular Medicine Center for Cardiovascular Diseases,

SOURCE: Fu Wai Heart Hospital and Cardiovascular Institute, Peking Union Medical College and Chinese Academy of Medical Sciences, Beijing, 100037: jinfengd@yahoo.com China
Shengwu Huaxue yu Shengwu Wuli Xuebao, (2001) Vol. 33, No. 1, pp. 19-24. print.
ISSN: 0582-9879.

DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: Chinese; English

AB For searching cardiovascular-associated genes and investigating their **expression** profiles, human adult heart and aorta **cDNA** libraries were constructed, and a novel gene from adult heart **cDNA** library was isolated based on large-scale **ESTs** (**expressed** sequence tags) sequencing (**GenBank** accession number AF114264). The 2 736 bp clone contains one 1 344 bp open reading frame extending from 412 to 1 755. We named it NELIN (nexilin-like **protein**) because it shares high similarity with the rat nexilin. NELIN was **expression**-restricted in heart, skeletal muscle, artery and vein by Northern blot and RT-PCR analyses, and mapped to chromosome 1p31-1p32 by **database** analyses. Based on domain structure, NELIN could regulate the formations of stress fibers, focal adhesion and its signaling complex, and even participates in the signal transduction in FAs(focal adhesions).

L10 ANSWER 38 OF 47 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:76253 BIOSIS
DOCUMENT NUMBER: PREV200100076253
TITLE: Characterization of a novel subgroup of putative seven transmembrane receptors.
AUTHOR(S): Soderberg, C. (1); Lind, P.
CORPORATE SOURCE: (1) Pharmacia Corp., Uppsala Sweden
SOURCE: Society for Neuroscience Abstracts, (2000) Vol. 26, No. 1-2, pp. Abstract No.-140.2. print.
Meeting Info.: 30th Annual Meeting of the Society of Neuroscience New Orleans, LA, USA November 04-09, 2000
Society for Neuroscience
. ISSN: 0190-5295.

DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

AB One of the largest **protein** superfamilies is the one of G-**protein**-coupled receptors (GPCRs). The main characteristics of this large group of receptors is the presence of seven transmembrane α -helices, and that they signal through heterotrimeric intracellular G **proteins**. This family is highly diversified with regards to the natural ligands ranging from glycoprotein hormones, through an array of bioactive peptodes, lipid derivatives, monoamines, and ions. Based on structural relations the receptors have been divided into three subfamilies of which the largest is the one of rhodopsin-like receptors. In this study, suppression subtractive hybridization (SSH), a PCR-based **cDNA** subtraction method, was used to perform subtraction of male rat hypothalamus vs. rat brain (excl. hypothalamus). The differentially **expressed cDNA** was cloned and 157 clones were sequenced and used as query sequences in BLAST searches. One clone, B06, showed homology to human TM7SF1 (transmembrane 7 superfamily member 1, **Genbank** AF027826), a recently identified putative seven-pass transmembrane **protein** showing weak homology to previously known members of the GPCR superfamily (Spangenberg et al). Searching with the sequence in **EST databases** revealed the existence of two homologues of TM7SF1, which we have denoted TM7SF2 and TM7SF3. RACE-PCR (Rapid Amplification of **cDNA** Ends) of 5'- and 3'-ends

of **cdna** was used to obtain full-length clones of the receptors from mouse and rat. **Expression** of TM7SF2 mRNA is mainly located to the brain and testis unlike TM7SF1, which is highly **expressed** in the kidney and heart and only weakly in brain and placenta (Spangenberg et al). Spangenberg, C., Winterpacht, A., Zabel, B.U., and Lobbert, R.W., (1998) Genomics 48;178-185

L10 ANSWER 39 OF 47 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1998:6246 BIOSIS

DOCUMENT NUMBER: PREV19980006246

TITLE: Expressed sequence tags of citrus fruit during rapid cell development phase.

AUTHOR(S): Hisada, Sunao; Akihama, Tomoya; Endo, Tomoko; Moriguchi, Takaya (1); Omura, Mitsuo

CORPORATE SOURCE: (1) Dep. Citriculture, Natl. Inst. Fruit Tree Sci., Okitsu,

SOURCE: Shimizu, Shizuoka 424-02 Japan
Journal of the American Society for Horticultural Science, (Nov., 1997) Vol. 122, No. 6, pp. 808-812.
ISSN: 0003-1062.

DOCUMENT TYPE: Article

LANGUAGE: English

AB A **cdna** library was constructed from satsuma mandarin (Citrus unshiu Marc.) fruit tissues during the rapid cell enlargement phase. A total of 950 individual **cdna** clones was partially sequenced and compared with **GenBank databases** for characterizing the gene repertoire **expressed** during this developmental phase. Among these, 426 **cdna** clones (44.8%) showed sequence identity with previously characterized genes with optimized (OPT) scores of gtoreq200, while 524 clones (55.2%) resulted in low OPT scores (<200) and did not show any significant sequence identity with previously published genes. Based on nucleotide sequence, most clones with OPT scores of gtoreq200 were assumed to be transcription-, translation-, cell-wall-metabolism-, and stress-response-related genes. Other clones showed homology with published sequences related to housekeeping and stress-response-related genes, including metallothionein-like **proteins**, late-embryogenesis-abundant (LEA) **proteins**, and heat-shock **proteins**. These results suggested that Citrus fruit during rapid cell enlargement were metabolically active and expanding in response to biotic and abiotic stress. For clones with low nucleotide sequence homology, the recurrence was evaluated by aligning nucleotide sequences

of each clone and generating contig maps. **Expressed** sequence tags (**ESTs**) of 162 clones with OPT scores <200 have not been reported for any other organism. Collectively, randomly sequenced **cdna** clones described in this study provided information on types of genes **expressed** during the rapid cell enlargement phase in Citrus fruit. These genes should be used as candidates for Citrus genome mapping projects.

L10 ANSWER 40 OF 47 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1994:400086 BIOSIS

DOCUMENT NUMBER: PREV199497413086

TITLE: Cloning and characterization of pig muscle cDNAs by an expressed sequence tag approach.

AUTHOR(S): Tuggle, C. K.; Schmitz, C. B.

CORPORATE SOURCE: Dep. Anim. Sci., Iowa State Univ., Ames, IA 50011 USA

SOURCE: Animal Biotechnology, (1994) Vol. 5, No. 1, pp. 1-13.
ISSN: 1049-5398.

DOCUMENT TYPE: Article

LANGUAGE: English

AB To provide additional unique marker sequences for genome mapping, we have cloned and partially sequenced 14 pig skeletal muscle **cDNAs**, representing 11 independent genes. Random selection from an adult skeletal muscle **cDNA** library, coupled with dot blot hybridization of the **cDNA** clones with complex probes representing muscle and non-muscle gene **expression**, was used to identify putative muscle-specific **cDNAs**. These **cDNAs** were then partially sequenced and the resulting primary structural information was used to screen the **Genbank**/European Molecular Biology Laboratory (EMBL) and **Protein** Information Resource (PIR) **databases**. Pig **cDNAs** with significant similarity to alpha-actin, alpha-7-integrin, alpha-actinin2, myosin binding **protein** H, and myosin light chain kinase were identified. Northern analysis of alpha-actinin2 showed the **expression** pattern of this pig gene closely matched that reported for human alpha-actinin2. Six **cDNAs** had no significant **database** match indicating that these genes have not been sequenced in other species. These new pig **ESTs** can be physically and genetically mapped for use in comparative genome mapping, and will be useful in the genetic and biochemical analysis of muscle.

L10 ANSWER 41 OF 47 LIFESCI COPYRIGHT 2002 CSA

ACCESSION NUMBER: 2000:61361 LIFESCI

TITLE: A cDNA sequence of phosphopyruvate hydratase (enolase) from

AUTHOR: Black Tiger Prawn, *Penaeus monodon*
Boonchuoy, C.; Boonyawan, B.; Panyim, S.; Sonthayanon, B.*
CORPORATE SOURCE: Institute of Molecular Biology and Genetics, Mahidol University, Salaya Campus, Phutthamonthon 4 Rd., Phutthamonthon District, Nakhon Pathom 73170, Thailand; E-mail: scbst@mahidol.ac.th

SOURCE: Asia-Pacific Journal of Molecular Biology and Biotechnology

[Asia-Pacific J. Mol. Biol. Biotechnol.], (1999) 6(00) vol. 7, no. 1, pp. 89-94.
ISSN: 0128-7451.

DOCUMENT TYPE: Journal

FILE SEGMENT: Q4

LANGUAGE: English

SUMMARY LANGUAGE: English

AB A sequence determination was performed on a 1.86 kb **cDNA** clone designated as PMM020. The clone was among a set of random **cDNA** clones isolated from an abdominal muscle **cDNA** library of Black Tiger Prawn which had been partially sequenced for **expressed** sequence tags (5'-**EST**) markers. Earlier **database** query via a BLAST program indicated that a partial DNA sequence from this clone matched enolase sequences from other eukaryotic organisms. DNA sequencing was thus performed on subcloned DNA fragments from PMM020 and an 1861 bp of combined sequence was found. A tract of poly (A) was found at the 3' side beyond position 1861 of the sequence, which indicated that the 3'

end

of the transcript was intact. An open reading frame for 434 amino acids was found starting from the predicted translation initiation codon (ATG) at nucleotide position 24 and ending at a termination codon (TAA) at position 1327. The predicted **protein** molecular weight was 47 kDa. An amino acid motif specific to enolase, DDLTVTNPK, was found at residue positions 320-328. Upon comparing with an enolase **cDNA** sequence from *Xenopus laevis*; the overall nucleotide sequence identity between the two sequences was 62.0% while the identity within the open reading frame was 69.4% and the calculated **protein** sequence

identity was 72.5%. When compared to those of other eukaryotes, the calculated amino acid sequence identities of 77.6% (*Drosophila melanogaster*), 63.1% (yeast, *Saccharomyces cerevisiae*), 72.7% (chicken, *Gallus gallus*), 71.3% (mouse, *Mus musculus*) were found. The high percent identity for both nucleotide and predicted **protein** sequences, together with the expected length of the polypeptide chain, identified the cloned sequence as phosphopyruvate hydratase (**GenBank** accession no. AF100985).

L10 ANSWER 42 OF 47 LIFESCI COPYRIGHT 2002 CSA
ACCESSION NUMBER: 1999:110119 LIFESCI
TITLE: Assignment of human proliferation associated p100 gene (C20orf1) to human chromosome band 20q11.2 by in situ hybridization
AUTHOR: Zhang, Y.; Heidebrecht, H.-J.; Rott, A.; Schlegelberger, B.; Parwaresch, R.
CORPORATE SOURCE: Department of Hematopathology, University of Kiel, Michaelisstr. 11, 24105 Kiel, Germany; E-mail: hheidebrecht@path.uni-kiel.de
SOURCE: Cytogenetics and Cell Genetics [Cytogenet. Cell Genet.], (19990000) vol. 84, no. 3-4, pp. 182-183. ISSN: 0301-0171.
DOCUMENT TYPE: Journal
FILE SEGMENT: G
LANGUAGE: English

AB p100 is a new nuclear proliferation associated **protein** whose **expression** is restricted to cell cycle phases S, G sub(2), and M. The gene encoding the p100 **protein** was recently cloned from a HeLa **cDNA** library by PCR using primers deduced from sequences of the p100 **protein** (unpublished observation). This gene shares no significant homology with any characterized genes in the **Genbank database** and has been assigned the approved symbol C20orf1 for chromosome 20 open reading fragment 1. In this study C20orf1 was assigned to human chromosome band 20q11.2 by fluorescence in situ hybridization (FISH). One **EST** marker, AA134490, which shares complete homology (406 bases) with the C20orf1 gene, has been mapped at 49-50 cM on chromosome 20, thus confirming the chromosome assignment of C20orf1 by FISH. The retinoblastoma like 1 gene (RBL1) and protooncogene SRC are found in the vicinity of C20orf1. Topoisomerase (DNA) I (TOP1) has been assigned to 20q12 arrow right q13.1. Very recently, STK15 (alias BTAK), a centromere-associated serine/threonine kinase, was localized to 20q13 and shown to be amplified and overexpressed in different human tumors.

L10 ANSWER 43 OF 47 LIFESCI COPYRIGHT 2002 CSA
ACCESSION NUMBER: 1999:17786 LIFESCI
TITLE: Identification and mapping of a novel human gene, HRMT1L1, homologous to the rat protein arginine N-methyltransferase 1 (PRMT1) gene
AUTHOR: Katsanis, N.; Yaspo, M.-L.; Fisher, E.M.C.*
CORPORATE SOURCE: Neurogenetics Unit, Imperial Coll. Sch. Med. at St. Mary's, Norfolk Place, London W2 1PG, UK
SOURCE: MAMM. GENOME, (19970700) vol. 8, no. 7, pp. 526-529. ISSN: 0938-8990.
DOCUMENT TYPE: Journal
FILE SEGMENT: G
LANGUAGE: English

AB Human chromosome (Chr) 21 is the smallest and one of the most intensely studied autosomes. It has served as a paradigm for the Human Genome Project, being the first chromosome for which a detailed genetic and a

high-resolution physical map have been produced (6th International Workshop on Chromosome 21, Cold Spring Harbor, 1996). Having accomplished the initial goals of the Genome Project, the next aim is to describe the complete sequence and the full complement of genes residing on the chromosome. Although 700-1000 genes are predicted to map to Chr 21, less than 10% of these have been identified to date (Genome Database, Version 6.0, November 1996). We are enriching the transcription map of

21q

by a combination of methods, such as **expressed** sequence tag (**EST**) **database** searching and **cDNA** selection. As a result of two independent approaches, we have been able to identify various novel transcripts. Here we report the isolation of a human

homolog

(HRMT1L1) of the rat **protein** arginine N-methyltransferase 1 gene (PRMT1, **Genbank** accession number U60882, Lin et al. 1996), its fine mapping on Chr 21, and its **expression** pattern. (DBO)

L10 ANSWER 44 OF 47 LIFESCI COPYRIGHT 2002 CSA

ACCESSION NUMBER: 97:62796 LIFESCI

TITLE: DRES search engine: Of flies, men and ESTs

AUTHOR: Guffanti, A.; Banfi, S.; Simon, G.; Ballabio, A.; Borsani, G.

CORPORATE SOURCE: Telethon Inst. Genet. and Med. (Tigem), San Raffaele Biomedical Science Park, Via Olgettina 58, 20132 Milano, Italy

SOURCE: TRENDS GENET., (1997) vol. 13, no. 2, pp. 79-80. ISSN: 0168-9525.

DOCUMENT TYPE: Journal

TREATMENT CODE: General Review

FILE SEGMENT: G; Z

LANGUAGE: English

SUMMARY LANGUAGE: English

AB Gene identification based on cross-species comparisons has primarily relied on experimental approaches, including hybridization of libraries with DNA probes or antibodies, and PCR using degenerate oligonucleotides. These techniques are often difficult and time-consuming, especially when the evolutionary distance between the two species is very high, as with *Drosophila* and humans. Furthermore, it is difficult to apply these approaches systematically in order to identify a significant number of homolog genes in different species. Computer-based similarity searching represents a new weapon in the arsenal of gene identification techniques. Its effectiveness relies on the availability of a significant number of sequences for the query and target organisms. Among model organisms, the fruit fly *Drosophila melanogaster* represents a powerful source of information due to the high number of well-characterized mutants displaying interesting and diverse phenotypes. More than 10 000 genes, 3800 **proteins** and 35 000 alleles are known in *Drosophila*. This information has been deposited in FlyBase, a comprehensive **database** containing information on the genetics and molecular biology of this organism. A rapidly growing number of **expressed** sequence tags (**ESTs**) are being generated by biotechnology companies and public consortia, from a large variety of tissue sources

and

organisms. As of November 1996, more than 500 000 human **ESTs**, which correspond to a significant percentage of all human genes, have

been

deposited in the **EST** division of **GenBank** (dbEST). We have applied the power of *Drosophila* genetics to the vast resource of human **cDNAs** represented in dbEST to identify novel human genes of high biological interest. We previously identified 66 human **cDNAs** showing significant homology to *Drosophila* mutant genes by

screening dbEST with keywords using the 'text string' option. Each **EST** clone was given a progressive DRES (Drosophila-related **expressed** sequence) number and its map position was determined using fluorescence in situ hybridization (FISH) and radiation hybrid mapping. The results of this first effort are available in table form on the DRES homepage. These **cDNAs** represent a valuable tool for the identification of human disease genes by the positional candidate approach.

L10 ANSWER 45 OF 47 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI
ACCESSION NUMBER: 1999-12578 BIOTECHDS

TITLE: New collectin protein of human origin and DNA encoding it;
for the treatment of bacterium and virus infection

AUTHOR: Wakamiya N
PATENT ASSIGNEE: Fuso-Pharm.
LOCATION: Osaka, Japan.
PATENT INFO: WO 9937767 29 Jul 1999
APPLICATION INFO: WO 1998-JP3328 24 Jul 1998
PRIORITY INFO: JP 1998-11281 23 Jan 1998
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 1999-458691 [38]

AN 1999-12578 BIOTECHDS

AB A collectin **protein** (277 amino acids) and its encoding **polynucleotide** of human origin, is new. The collectin is an agent for the treatment of bacteria and virus infections, especially in the human body. In an example, a consensus sequence derived from human collectins was used to search the **GenBank expressed** sequence tag (**EST**) **database** for homology. A sequence (R29493) is identified and primers devised from this for amplification

of

a human fetal lung **cDNA** library by polymerase chain reaction (PCR). The amplification product was used to screen the library and a **cDNA** fragment obtained encoding the new collectin **protein**. Northern blot analysis showed that the **protein** was **expressed** specifically in lung tissue, but not in other tissue such as heart, brain, liver, kidney or pancreas. (58pp)

L10 ANSWER 46 OF 47 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI
ACCESSION NUMBER: 1999-01454 BIOTECHDS

TITLE: Nucleic acid encoding delta-sarcoglycan polypeptide;
recombinant protein production via vector expression in
host cell for Duchenne muscular dystrophy therapy

AUTHOR: Campbell K P; Jung D; Duclos F; Straub V; McPherson J
PATENT ASSIGNEE: Univ.Washington-St.Louis; Univ.Iowa-Res.Found.
LOCATION: St. Louis, MO, USA; Iowa City, IA, USA.
PATENT INFO: US 5837537 17 Nov 1998
APPLICATION INFO: US 1996-7197758 25 Sep 1996
PRIORITY INFO: US 1996-719758 25 Sep 1996
DOCUMENT TYPE: Patent
LANGUAGE: English
OTHER SOURCE: WPI: 1999-023460 [02]

AN 1999-01454 BIOTECHDS

AB A nucleic acid (1,110 bp) encoding delta-sarcoglycan **protein** (256 amino acids) is new. Also claimed are a DNA **expression** construct containing the above and prokaryotic and eukaryotic cells transformed with the construct. Recombinant delta-sarcoglycan can be used to produce antibodies that can be used to detect reduced delta-sarcoglycan levels associated with Duchenne muscular dystrophy.

In

an example, a trypsin (EC-3.4.21.4) digest of purified rabbit skeletal

muscle dystrophin-glycoprotein complex was fractionated by reverse-phase HPLC and the **peptides** were sequenced and compared to known gamma-sarcoglycan **protein** sequence. **Peptide** sequences not found in the gamma-sarcoglycan **protein** sequence were used to search the **GenBank database** of **expressed** sequence tags (**EST**). An **EST** encoding one of the **peptide** fragments was identified and isolated from a normalised human placenta **cDNA** library. The clone from which the **EST** was generated was sequenced to identify a 1.1kb **cDNA** sequence with a 768 bp open reading frame encoding a **protein** of 256 amino acids. (14pp)

L10 ANSWER 47 OF 47 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI
ACCESSION NUMBER: 1995-14478 BIOTECHDS

TITLE: The determination of differential gene expression patterns in

prostate carcinoma utilizing a high through-put cDNA sequencing approach;
high throughput cDNA sequencing and expressed sequence

tag

cDNA library screening (conference abstract)

AUTHOR: Nelson P S; Huang G M; Ng W L; Yu J; Farkas J; Peterson E; Liang H A; Chen L; Hood L

CORPORATE SOURCE: Univ.Washington-Seattle

LOCATION: Department of Molecular Biotechnology, University of Washington, Seattle, WA 98195, USA.

SOURCE: FASEB J.; (1995) 9, 4, A834

CODEN: FAJOEC

ISSN: 0892-6638

Experimental Biology 95, Atlanta, Georgia, 9-13 April, 1995.

DOCUMENT TYPE: Journal

LANGUAGE: English

AN 1995-14478 BIOTECHDS

AB A normal human prostate tissue **cDNA** library was constructed and 1,200 unique clones were subjected to single pass partial DNA sequencing yielding a normal prostate **expressed** sequence tag (**EST**) **database**. The sequences were compared to sequence data from DNA and **protein databases** and to a human bone marrow **EST library database**. Sequence homology showed that 40% of the prostate **ESTs** matched known genes, and 60% were new sequences. There was very little overlap between the human bone marrow **EST database** and the human prostate **EST database** with only 1% of the new **cDNAs** exhibiting similarity. Characterization of the prostate **EST** library was performed using nucleic acid hybridization to determine differential

gene

expression. 80 Clones from the normal prostate library were chosen. The relative **expression** of these clones was determined using a dot blot hybridization method with polymerase chain reaction generated probes from normal prostate, 2 prostate adenocarcinomas and 1 prostate carcinoma cell line, DU145. Of these, 12/42 **Genbank** match clones and 5/31 no **Genbank** match clones had differential **expression**. **ESTs** may be used as markers for prostate differentiation. (0 ref)

=> log h

COST IN U.S. DOLLARS

SINCE FILE
ENTRY

TOTAL
SESSION

FULL ESTIMATED COST

251.53

251.74

SESSION WILL BE HELD FOR 60 MINUTES
STN INTERNATIONAL SESSION SUSPENDED AT 20:01:20 ON 08 JUL 2002

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LOGINID:ssspta1600kxc

PASSWORD:

* * * * * RECONNECTED TO STN INTERNATIONAL * * * * *
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AT 20:11:19 ON 08 JUL 2002

FILE 'MEDLINE' ENTERED AT 20:11:19 ON 08 JUL 2002
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COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	251.53	251.74

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
19:04:09
ON 08 JUL 2002

L1 13496 S EST
L2 34 S L1(S) (NO#(W) CORRELAT?)
L3 21 DUP REM L2 (13 DUPLICATES REMOVED)
L4 3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5 1972 S L4(S) (PROTEIN OR PEPTIDE)
L6 1748 S L5(S) (EXPRESS?)
L7 775 S L6(S) DATABASE#
L8 355 DUP REM L7 (420 DUPLICATES REMOVED)
L9 96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN)
L10 47 S L8(S) GENBANK

=> s l8(s) (heart or bone or brain)
L11 87 L8(S) (HEART OR BONE OR BRAIN)

=> s l11 or l9
L12 137 L11 OR L9

=> s l12 and (no#(w) express?)
4 FILES SEARCHED...
L13 1 L12 AND (NO#(W) EXPRESS?)

=> d ibib abs tot

L13 ANSWER 1 OF 1 MEDLINE
ACCESSION NUMBER: 2001653629 MEDLINE
DOCUMENT NUMBER: 21560218 PubMed ID: 11703281
TITLE: Keratin K6irs is specific to the inner root sheath of hair
follicles in mice and humans.

AUTHOR: Porter R M; Corden L D; Lunny D P; Smith F J; Lane E B; McLean W H
 CORPORATE SOURCE: CRC Cell Structure Research Group, School of Life Sciences,
 SOURCE: University of Dundee, Dundee DD1 4HN, UK.
 BRITISH JOURNAL OF DERMATOLOGY, (2001 Oct) 145 (4) 558-68.
 Journal code: 0004041. ISSN: 0007-0963.
 PUB. COUNTRY: England: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AA354256
 ENTRY MONTH: 200112
 ENTRY DATE: Entered STN: 20011115
 Last Updated on STN: 20020123
 Entered Medline: 20011210

AB BACKGROUND: Keratins are a multigene family of intermediate filament **proteins** that are differentially **expressed** in specific epithelial tissues. To date, no type II keratins specific for the inner root sheath of the human hair follicle have been identified. OBJECTIVES: To characterize a novel type II keratin in mice and humans. METHODS: Gene sequences were aligned and compared by BLAST analysis. Genomic DNA and **mRNA** sequences were amplified by polymerase chain reaction (PCR) and confirmed by direct sequencing. Gene **expression** was analysed by reverse transcription (RT)-PCR in mouse and human tissues. A rabbit polyclonal antiserum was raised against a C-terminal **peptide** derived from the mouse K6irs **protein**. **Protein expression** in murine tissues was examined by immunoblotting and immunofluorescence. RESULTS: Analysis of human **expressed** sequence tag (**EST**) data generated by the Human Genome Project revealed a fragment of a novel cytokeratin **mRNA** with characteristic amino acid substitutions in the 2B domain. No further

human

ESTs were found in the **database**; however, the complete human gene was identified in the draft genome sequence and several mouse **ESTs** were identified, allowing assembly of the murine **mRNA**. Both species' **mRNA** sequences and the human gene were confirmed experimentally by PCR and direct sequencing. The human gene spans more than 16 kb of genomic DNA and is located in the type II keratin cluster

on

chromosome 12q. A comprehensive immunohistochemical survey of **expression** in the adult mouse by immunofluorescence revealed that this novel keratin is **expressed** only in the inner root sheath of the hair follicle. Immunoblotting of murine epidermal keratin extracts revealed that this **protein** is specific to the anagen phase of the hair cycle, as one would expect of an inner root sheath marker. In humans, **expression** of this keratin was confirmed by RT-PCR using **mRNA** derived from plucked anagen hairs and epidermal biopsy material. By this means, strong **expression** was detected in human hair follicles from scalp and eyebrow. **Expression** was also readily detected in human palmoplantar epidermis; however, **no expression** was detected in face **skin** despite the presence of fine hairs histologically. CONCLUSIONS: This new keratin, designated K6irs, is a valuable histological marker for the inner root sheath of hair follicles in mice and humans. In addition, this keratin represents a new candidate gene for inherited structural hair defects

such

as loose anagen syndrome.

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
19:04:09
ON 08 JUL 2002

L1 13496 S EST
L2 34 S L1(S) (NO#(W) CORRELAT?)
L3 21 DUP REM L2 (13 DUPLICATES REMOVED)
L4 3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5 1972 S L4(S) (PROTEIN OR PEPTIDE)
L6 1748 S L5(S) (EXPRESS?)
L7 775 S L6(S) DATABASE#
L8 355 DUP REM L7 (420 DUPLICATES REMOVED)
L9 96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
L10 47 S L8(S) GENBANK
L11 87 S L8(S) (HEART OR BONE OR BRAIN)
L12 137 S L11 OR L9
L13 1 S L12 AND (NO#(W) EXPRESS?)

=> s l12(s) (transcri?)
L14 67 L12(S) (TRANSCRI?)

=> d ibib abs tot

L14 ANSWER 1 OF 67 MEDLINE
ACCESSION NUMBER: 2002326077 IN-PROCESS
DOCUMENT NUMBER: 22064257 PubMed ID: 12069307
TITLE: Purification and identification of a tributyltin-binding
protein from serum of Japanese flounder, *Paralichthys
olivaceus*.
AUTHOR: Shimasaki Yohei; Oshima Yuji; Yokota Yoshiko; Kitano
Takeshi; Nakao Miki; Kawabata Shun-ichiro; Imada
Nobuyoshi;
CORPORATE SOURCE: Honjo Tsuneo
Laboratory of Marine Biochemistry, Graduate School of
Bioresource and Bioenvironmental Sciences, Kyushu
University, Fukuoka, Japan.
SOURCE: ENVIRONMENTAL TOXICOLOGY AND CHEMISTRY / SETAC, (2002 Jun)
21 (6) 1229-35.
Journal code: 8308958. ISSN: 0730-7268.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020619
Last Updated on STN: 20020619

AB Tributyltin (TBT) is an industrial chemical used as an antifoulant in
marine environments. Previously, we reported that TBT accumulates in the
serum or plasma of some fishes and is bound to a high molecular weight
compound in the serum of the Japanese flounder, *Paralichthys olivaceus*.

In this study, we succeeded in purifying the TBT-binding **protein**
(TBT-bp) from the serum of Japanese flounder by using gel filtration
chromatography, anion exchange chromatography, and polyacrylamide gel
electrophoresis, with a 2.6% yield and a 77-fold purification. The
molecular mass of TBT-bp was approximately 46.5 kDa on sodium dodecyl
sulfate-polyacrylamide gel electrophoresis, and its isoelectric point was
approximately 3.0 on isoelectric focusing-polyacrylamide gel
electrophoresis. The TBT-bp contained 42% N-glycan. The **cdna**
nucleotide sequence of TBT-bp was determined by reverse

transcription-polymerase chain reaction of Japanese flounder liver, and we deduced a sequence of 191 amino acids of mature TBT-bp. No sequence identical to the TBT-bp amino acid sequence was found within the SWISS-PROT (<http://www.nig.ac.jp/>) **protein database**; however, a lipocalin-like sequence pattern was observed. We concluded

that

the TBT-bp was a novel **protein** that has not yet been reported, although some DNA sequences from **expressed** sequence tags (**ESTs**) of Japanese flounder liver had a high identity. A high **expression** level of TBT-bp gene was found in the liver, but the gene was slightly detectable in the **kidney** and **brain**.

L14 ANSWER 2 OF 67 MEDLINE

ACCESSION NUMBER: 2002271428 IN-PROCESS

DOCUMENT NUMBER: 22006440 PubMed ID: 12012232

TITLE: Gene expression profiles in young adult Ciona intestinalis.

AUTHOR: Ogasawara Michio; Sasaki Akane; Metoki Hito; Shin-I Tadasu; Kohara Yuji; Satoh Nori; Satou Yutaka

CORPORATE SOURCE: Department of Zoology, Graduate School of Science, Kyoto University, Sakyo-ku, Kyoto 606-8502, Japan.

SOURCE: DEVELOPMENT GENES AND EVOLUTION, (2002 May) 212 (4) 173-85.

Journal code: 9613264. ISSN: 0949-944X.

PUB. COUNTRY: Germany: Germany, Federal Republic of Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals

ENTRY DATE: Entered STN: 20020516

Last Updated on STN: 20020516

AB Comparison of 12,230 **expressed** sequence tags (**ESTs**) of 3' ends of **cDNA** clones derived from young adults of Ciona intestinalis allowed us to categorize them into 976 independent clusters. When the 5'-end sequences of 10,400 **ESTs** of the 976 clusters were compared with the sequences in **databases**, 406 of the clusters showed significant matches ($P < E-15$) with reported **proteins** with defined functions, while 117 showed matches with putative **proteins** for which there is not enough information to categorize their function, and 453 had no significant sequence similarities to known **proteins**. The 406 clusters with sequence similarity to **proteins** with defined functions consisted of 304 clusters related to **proteins** with functions common to many kinds of cells, 73 related to **proteins** associated with cell-cell communication and 29 related to **transcription** factors. Spatial **expression** of all of the 976 clusters was examined by a newly improved whole-mount in situ hybridization method. A total of 430 clusters

did not show distinct in situ hybridization signals, while 122 clusters showed ubiquitous distribution of signals, and 253 clusters showed signals

in multiple tissues. The remaining 171 clusters showed signals specific to

a certain organ or tissue: 16 showed epidermis-specific **expression**, 3 were specific to the neural complex, 1 to **heart**, 6 to body-wall muscle, 94 to pharyngeal gill, 3 to esophagus, 26 to stomach, 1 to intestine and 21 to endostyle. Many of these organ-specific genes encode **proteins** with no sequence similarity to known **proteins**. The present analysis thus highlights characteristic gene **expression** profiles of Ciona young adults and provides not only molecular markers for organs and tissues but also **transcriptomic** information useful for further genomic analyses of this model organism.

L14 ANSWER 3 OF 67 MEDLINE
 ACCESSION NUMBER: 2002050047 MEDLINE
 DOCUMENT NUMBER: 21634684 PubMed ID: 11774267
 TITLE: Identification and characterization of 9D7, a novel human protein overexpressed in renal cell carcinoma.
 COMMENT: Erratum in: Int J Cancer 2002 Apr 20;98(6):956
 AUTHOR: Klade Christoph S; Dohnal Alexander; Furst Walter; Sommergruber Wolfgang; Heider Karl-Heinz; Gharwan Helen; Ratschek Manfred; Adolf Gunther R
 CORPORATE SOURCE: Boehringer Ingelheim Austria GmbH, Research and Development, Vienna, Austria.. cklade@intercell.co.at
 SOURCE: INTERNATIONAL JOURNAL OF CANCER, (2002 Jan 10) 97 (2) 217-24.
 Journal code: 0042124. ISSN: 0020-7136.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200201
 ENTRY DATE: Entered STN: 20020125
 Last Updated on STN: 20020502
 Entered Medline: 20020117

AB With the objective of discovering novel tumor-associated antigens of the cancer/**testis** type, we compared the **transcriptional** profiles of renal cell carcinoma (RCC) and non-tumorous **kidney** and further screened for genes **expressed** in RCC and **testis**, but not other normal tissues. In a first step, a representational difference analysis library consisting of approximately 1,900 RCC **cdna** clones was generated. Clones were then spotted onto filters and hybridized with **cdna** probes derived from a **testis**-specific **cdna** library, a pool of RCCs and a pool of 10 healthy normal tissues, respectively. Based on strong hybridization signals with both RCC and **testis**, but not normal tissue probes, 185 clones were sequenced and annotated. After **EST-database** comparison, 35 clones were selected for experimental analysis, including conventional and quantitative RT-PCR as well as Northern blotting. Clone 9D7 showed strong **mRNA expression** in RCC as well as in several other major tumor types. In normal tissues there was little or no **mRNA expression** with the exception of **heart**. 9D7 was cloned to full-size and found to represent a novel human gene containing 5 exons residing on chromosome 14. Alternative splicing within exon 1 generates 2 open-reading-frames consisting of 717 or 435 bp corresponding to predicted **proteins** of 239 or 145 amino acids. 9D7 shows high homology (227/239 amino acids or 95% identity) to a growth factor-inducible gene of *Rattus norvegicus* involved in apoptosis. In situ hybridization as well as immunohistochemical analysis using 9D7-specific antisera confirmed overexpression of 9D7 in RCCs as compared to normal **kidney** tissue.
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L14 ANSWER 4 OF 67 MEDLINE
 ACCESSION NUMBER: 2001653629 MEDLINE
 DOCUMENT NUMBER: 21560218 PubMed ID: 11703281
 TITLE: Keratin K6irs is specific to the inner root sheath of hair follicles in mice and humans.
 AUTHOR: Porter R M; Corden L D; Lunny D P; Smith F J; Lane E B; McLean W H

CORPORATE SOURCE: CRC Cell Structure Research Group, School of Life Sciences,
University of Dundee, Dundee DD1 4HN, UK.
SOURCE: BRITISH JOURNAL OF DERMATOLOGY, (2001 Oct) 145 (4) 558-68.
Journal code: 0004041. ISSN: 0007-0963.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AA354256
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20011115
Last Updated on STN: 20020123
Entered Medline: 20011210

AB BACKGROUND: Keratins are a multigene family of intermediate filament **proteins** that are differentially **expressed** in specific epithelial tissues. To date, no type II keratins specific for the inner root sheath of the human hair follicle have been identified. OBJECTIVES: To characterize a novel type II keratin in mice and humans. METHODS: Gene sequences were aligned and compared by BLAST analysis. Genomic DNA and **mRNA** sequences were amplified by polymerase chain reaction (PCR) and confirmed by direct sequencing. Gene **expression** was analysed by reverse **transcription** (RT)-PCR in mouse and human tissues. A rabbit polyclonal antiserum was raised against a C-terminal **peptide** derived from the mouse K6irs **protein**. **Protein expression** in murine tissues was examined by immunoblotting and immunofluorescence. RESULTS: Analysis of human **expressed** sequence tag (EST) data generated by the Human Genome Project revealed a fragment of a novel cytokeratin **mRNA** with characteristic amino acid substitutions in the 2B domain. No further human **ESTs** were found in the **database**; however, the complete human gene was identified in the draft genome sequence and several mouse **ESTs** were identified, allowing assembly of the murine **mRNA**. Both species' **mRNA** sequences and the human gene were confirmed experimentally by PCR and direct sequencing.

The human gene spans more than 16 kb of genomic DNA and is located in the type II keratin cluster on chromosome 12q. A comprehensive immunohistochemical survey of **expression** in the adult mouse by immunofluorescence revealed that this novel keratin is **expressed** only in the inner root sheath of the hair follicle. Immunoblotting of murine epidermal keratin extracts revealed that this **protein** is specific to the anagen phase of the hair cycle, as one would expect of an inner root sheath marker. In humans, **expression** of this keratin was confirmed by RT-PCR using **mRNA** derived from plucked anagen hairs and epidermal biopsy material. By this means, strong **expression** was detected in human hair follicles from scalp and eyebrow. **Expression** was also readily detected in human palmoplantar epidermis; however, no **expression** was detected in face **skin** despite the presence of fine hairs histologically. CONCLUSIONS: This new keratin, designated K6irs, is a valuable histological marker for the inner root sheath of hair follicles in mice and humans. In addition, this keratin represents a new candidate gene for inherited structural hair defects such as loose anagen syndrome.

L14 ANSWER 5 OF 67 MEDLINE
ACCESSION NUMBER: 2001648583 MEDLINE
DOCUMENT NUMBER: 21557683 PubMed ID: 11700951
TITLE: Cloning and identification of differentially expressed transcripts in primary culture of GABAergic neurons.

AUTHOR: Li Z; Li Q; Sun C X; Hertz L; Yu A C
 CORPORATE SOURCE: Brain Research Institute, Shanghai Research Center of Life Sciences, Chinese Academy of Sciences.
 SOURCE: NEUROCHEMICAL RESEARCH, (2001 Oct) 26 (10) 1101-5.
 Journal code: 7613461. ISSN: 0364-3190.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200205
 ENTRY DATE: Entered STN: 20011112
 Last Updated on STN: 20020503
 Entered Medline: 20020502

AB A RNA based arbitrarily primed polymerase chain reaction (RAP-PCR) was used to identify differentially **expressed transcripts** in primary cultures of cerebral cortical neurons prepared from E16 mouse cerebral cortex. The majority of neurons found in this culture preparation are known to be GABAergic. Different primer combinations were used, and the PCR products were separated on PAGE. Visualization by silver staining revealed a high resolution RNA fingerprint pattern with a total of about 200 **transcripts**. Six differentially **expressed** **cDNA** fragments were recovered, cloned and sequenced. The results of a NCBI **database** search showed that 6 clones were highly homologous to known genes and **expressed** sequence tags (**ESTs**), and that they were either up-regulated or down-regulated during development. Among these clones, Clone 3.1.7 shared 99% sequence homology to mouse Reelin, a neuronal migration and positioning related **protein**. Clone 4.6.2 shared 91% homology to Rat prepro **bone morphogenetic protein-3 mRNA**. Clone 6.10.2 had 90% homology to a novel orphan gene of calcium-independent alpha-latrotoxin receptor, which stimulates presynaptic neurotransmitter release. Northern blot analysis confirmed the up-regulated **expression** profile of Clone 6.10.2 in neuron from Day 2 to 7 during stages of differentiation and development.

L14 ANSWER 6 OF 67 MEDLINE

ACCESSION NUMBER: 2001543308 MEDLINE
 DOCUMENT NUMBER: 21475973 PubMed ID: 11591886
 TITLE: MRP8, a new member of ABC transporter superfamily, identified by EST database mining and gene prediction program, is highly expressed in breast cancer.
 AUTHOR: Bera T K; Lee S; Salvatore G; Lee B; Pastan I
 CORPORATE SOURCE: Laboratory of Molecular Biology, Division of Basic Sciences, National Cancer Institute, National Institutes of Health, Bethesda, Maryland 20892-4255, USA.
 SOURCE: MOLECULAR MEDICINE, (2001 Aug) 7 (8) 509-16.
 Journal code: 9501023. ISSN: 1076-1551.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200202
 ENTRY DATE: Entered STN: 20011010
 Last Updated on STN: 20020215
 Entered Medline: 20020214

AB BACKGROUND: With the completion of the human draft genome sequence, efforts are now devoted to identifying new genes. We have developed a computer-based strategy that utilizes the **EST database** to identify new genes that could be targets for the immunotherapy of cancer or could be involved in the multistep process of cancer. MATERIALS

AND METHODS: Utilizing our computer-based screening strategy, we identified a cluster of **expressed** sequence tags (**ESTs**) that are highly **expressed** in **breast** cancer. Northern blot and reverse **transcriptase** polymerase chain reaction (RT-PCR) analyses demonstrated the tissue specificity of the computer-generated cluster and comparison with the human genome sequence assisted in isolating a full-length **cDNA** clone. RESULTS: We identified a new gene that is highly **expressed** in **breast** cancer. This gene is **expressed** at moderate levels in normal **breast** and **testis** and at very low levels in liver, **brain**, and placenta. The gene has two major **transcripts** of 4.5 kb and 4.1 kb. The 4.5-kb **transcript** is very abundant in **breast** cancer, and has an open reading frame of 1382 amino acids. The predicted **protein** sequence of the 4.5-kb **transcript** reveals that it has high homology with MRP5, a member of multidrug resistant-associated **protein** family (MRP). There are seven reported members in the MRP family; we designate this gene as MRP8 (ABCC11). The 4.5-kb MRP8 **transcript** consists of 31 exons and is located in a genomic region of over 80.4 kb on chromosome 16q12.1. The smaller 4.1-kb **transcript** of MRP8 is found in **testis** and may initiate within intron 6 of the gene. CONCLUSION: The selective **expression** of MRP8 (ABCC11), a new member of ATP-binding cassette transporter superfamily could be a molecular target for the treatment of **breast** cancer.

L14 ANSWER 7 OF 67 MEDLINE
 ACCESSION NUMBER: 2001528245 MEDLINE
 DOCUMENT NUMBER: 21458557 PubMed ID: 11574155
 TITLE: Discovery and mapping of ten novel G protein-coupled receptor genes.
 AUTHOR: Lee D K; Nguyen T; Lynch K R; Cheng R; Vanti W B; Arkhitko O; Lewis T; Evans J F; George S R; O'Dowd B F
 CORPORATE SOURCE: Department of Pharmacology, University of Toronto, Toronto, Ontario, M5S 1A8, Canada.
 SOURCE: GENE, (2001 Sep 5) 275 (1) 83-91.
 Journal code: 7706761. ISSN: 0378-1119.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF411107; GENBANK-AF411108; GENBANK-AF411109; GENBANK-AF411110; GENBANK-AF411111; GENBANK-AF411112; GENBANK-AF411113; GENBANK-AF411114; GENBANK-AF411115; GENBANK-AF411116; GENBANK-AF411117
 ENTRY MONTH: 200112
 ENTRY DATE: Entered STN: 20011001
 Last Updated on STN: 20020122
 Entered Medline: 20011213
 AB We report the identification, cloning and tissue distributions of ten novel human genes encoding G **protein**-coupled receptors (GPCRs) GPR78, GPR80, GPR81, GPR82, GPR93, GPR94, GPR95, GPR101, GPR102, GPR103 and a pseudogene, psi GPR79. Each novel orphan GPCR (oGPCR) gene was discovered using customized searches of the GenBank high-throughput genomic sequences **database** with previously known GPCR-encoding sequences. The **expressed** genes can now be used in assays to determine endogenous and pharmacological ligands. GPR78 shared highest identity with the oGPCR gene GPR26 (56% identity in the transmembrane (TM) regions). psi GPR79 shared highest sequence identity with the P2Y(2) gene and contained a frame-shift truncating the encoded receptor in TM5,

demonstrating a pseudogene. GPR80 shared highest identity with the P2Y(1) gene (45% in the TM regions), while GPR81, GPR82 and GPR93 shared TM identities with the oGPCR genes HM74 (70%), GPR17 (30%) and P2Y(5) (40%), respectively. Two other novel GPCR genes, GPR94 and GPR95, encoded a subfamily with the genes encoding the UDP-glucose and P2Y(12) receptors (sharing >50% identities in the TM regions). GPR101 demonstrated only distant identities with other GPCR genes and GPR102 shared identities

with

GPR57, GPR58 and PNR (35-42% in the TM regions). GPR103 shared identities with the neuropeptide FF 2, neuropeptide Y2 and galanin GalR1 receptors (34-38% in the TM regions). Northern analyses revealed GPR78 **mRNA expression** in the pituitary and placenta and GPR81 **expression** in the pituitary. A search of the GenBank **databases** with the GPR82 sequence retrieved an identical sequence in an **expressed** sequence tag (**EST**) partially encoding GPR82 from human colonic tissue. The GPR93 sequence retrieved an identical, human **EST** sequence from human primary tonsil B-cells and an **EST** partially encoding mouse GPR93 from small intestinal tissue. GPR94 was **expressed** in the frontal cortex, caudate putamen and thalamus of **brain** while GPR95 was **expressed** in the human **prostate** and rat stomach and fetal tissues. GPR101 revealed **mRNA transcripts** in caudate putamen and hypothalamus. GPR103 **mRNA** signals were detected in the cortex, pituitary, thalamus, hypothalamus, basal forebrain, midbrain and pons.

L14 ANSWER 8 OF 67 MEDLINE
ACCESSION NUMBER: 2001493705 MEDLINE
DOCUMENT NUMBER: 21427669 PubMed ID: 11536302
TITLE: GDEP, a new gene differentially expressed in normal prostate and prostate cancer.
AUTHOR: Olsson P; Bera T K; Essand M; Kumar V; Duray P; Vincent J; Lee B; Pastan I
CORPORATE SOURCE: Laboratory of Molecular Biology, Division of Basic Sciences, National Cancer Institute, National Institutes of Health, Bethesda, Maryland 20892-4255, USA.
SOURCE: PROSTATE, (2001 Sep 15) 48 (4) 231-41.
JOURNAL CODE: 8101368. ISSN: 0270-4137.
PUB. COUNTRY: United States
JOURNAL; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200110
ENTRY DATE: Entered STN: 20010906
Last Updated on STN: 20011008
Entered Medline: 20011004
AB BACKGROUND: The **database** of human **expressed** sequence tags (dbEST) is a potential source for the identification of tissue specific genes. The **database** contains sequences that originate from **cdna** libraries from different tissues cell types and tumors. METHODS: Computer based analysis identified a cluster of sequence homologous **ESTs**, containing **ESTs** derived only from human **prostate cdna** libraries. The tissue specificity was examined by multiple tissue RNA dot blots and RT-PCR. The new RNA **transcript** was characterized using northern blot analysis, RACE-PCR, and a ribonuclease protection assay. RESULTS: We have identified a gene differentially **expressed** in **prostate** using **EST database** analysis and experimental studies. We name the gene GDEP for gene differentially **expressed** in **prostate**. The major GDEP **transcript** is about 520 bp

long. GDEP RNA was detected in nine **prostate** tissue samples, four normal and five cancer. **Expression in prostate** epithelial cells was established by in situ hybridization. Weak **expression** was detected in the **prostate** cancer cell line LNCaP. In vitro **transcription**/translation indicate that the RNA encodes a small 34 amino acid **protein**. The major **transcript** consists of two exons with one large intron (> 15 kb). The GDEP gene was mapped to chromosome 4q21.1 by radiation hybrid mapping.

CONCLUSIONS: Our data proves that tissue specific genes can be identified by **EST database** mining. The **prostate** specificity of GDEP **expression** indicates that GDEP may be useful in the diagnosis or treatment of **prostate** cancer. Published 2001 Wiley-Liss, Inc.

L14 ANSWER 9 OF 67 MEDLINE
ACCESSION NUMBER: 2001485446 MEDLINE
DOCUMENT NUMBER: 21418781 PubMed ID: 11527381
TITLE: Analysis of the mammalian talin2 gene TLN2.
AUTHOR: Monkley S J; Pritchard C A; Critchley D R
CORPORATE SOURCE: Department of Biochemistry, University of Leicester, University Road, Leicester, LE1 7RH, United Kingdom.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2001 Sep 7) 286 (5) 880-5.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200110
ENTRY DATE: Entered STN: 20010903
Last Updated on STN: 20011015
Entered Medline: 20011011

AB We have utilised genomic and **EST databases** to assemble the sequence of the human talin2 (TLN2) gene. Talin2 **protein** is similar in size and sequence to talin1 throughout its length (74% identity, 86% similarity). The major differences are in (i) the size of the genes, the TLN2 gene is >200 kb compared with approximately 30 kb for TLN1 due to a difference in intron size, although intron/exon boundaries, with the exception of two, are strictly conserved; (ii) the **expression** patterns, TLN1 gives rise to an approximately 8-kb **mRNA** which is observed in all tissues, whereas TLN2 gives rise to multiple **transcripts** with the highest levels in **heart**.
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L14 ANSWER 10 OF 67 MEDLINE
ACCESSION NUMBER: 2001325836 MEDLINE
DOCUMENT NUMBER: 21226134 PubMed ID: 11327696
TITLE: Cloning, mapping, genomic organization, and expression of mouse M-LP, a new member of the peroxisomal membrane protein Mpv17 domain family.
AUTHOR: Iida R; Yasuda T; Tsubota E; Matsuki T; Kishi K
CORPORATE SOURCE: Department of Forensic Medicine, Fukui Medical University, Matsuoka-cho, Fukui, 910-1193, Japan..
ireiko@fmsrsa.fukui-med.ac.jp
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2001 May 4) 283 (2) 292-6.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AI482564
ENTRY MONTH: 200106
ENTRY DATE: Entered STN: 20010611
Last Updated on STN: 20010611
Entered Medline: 20010607

AB We have identified a mouse full-length **cDNA** and gene encoding a novel **protein** (M-LP), based on an **expressed** sequence tag (**EST**) sequence (GenBank Accession No. AI482564) obtained by differential display screening of age-dependently **expressed** genes in mouse **kidney**. The ML-P gene is composed of three exons, ranges over 5 kb on mouse chromosome 16B1-B2 and is **expressed** as two **transcripts** (1455 and 3058 bp), both of which include the same open-reading frame encoding 194 amino acids. M-LP is **expressed** mainly in **kidney** and spleen and shows age-dependent **expression**. M-LP has sequence homologies and membrane topologies very similar to the Mpv17 **protein**, a peroxisomal **protein** involved in the development of early-onset glomerulosclerosis. Search of the **protein** domain family **database** (ProDom) revealed that M-LP is a new member of the Mpv17 domain family (PD008400).

L14 ANSWER 11 OF 67 MEDLINE
ACCESSION NUMBER: 2001292584 MEDLINE
DOCUMENT NUMBER: 21269186 PubMed ID: 11374908
TITLE: Isolation of novel heart-specific genes using the BodyMap database.
AUTHOR: Soejima H; Kawamoto S; Akai J; Miyoshi O; Arai Y; Morohka T; Matsuo S; Niikawa N; Kimura A; Okubo K; Mukai T
CORPORATE SOURCE: Department of Biochemistry, Saga Medical School, 5-1-1 Nabeshima, Saga, 849-8501, Japan.. soejimah@post.saga-med.ac.jp
SOURCE: GENOMICS, (2001 May 15) 74 (1) 115-20.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB042554; GENBANK-AB042555; GENBANK-AB042556;
GENBANK-AB042557; GENBANK-AB042558; GENBANK-AB044805;
GENBANK-AB044806; GENBANK-AB044807
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010827
Last Updated on STN: 20010827
Entered Medline: 20010823

AB Two novel **heart**-specific genes, C3orf3 (chromosome 3 open reading frame 3) and MMGL (myomegalin-like), were isolated using BodyMap, a gene **expression database** based on site-directed 3' **expressed** sequence tags (3'-**ESTs**) which were collected from nonbiased **cDNA** libraries of various tissues. The **cDNA** of C3orf3 was 1667 bp and was composed of 12 exons within a 10-kb-long genomic sequence. MMGL consisted of 8 exons within a genomic sequence of over 70 kb, leading to four alternatively spliced **transcripts**. Both genes were strongly **expressed** in **heart** and also in skeletal muscle. C3orf3 and MMGL were mapped to 3p22 and 1q1, respectively. Subcellular localizations of their putative **proteins** were determined as being in the cytoplasm for C3orf3 and in the cytoplasm and nucleus for MMGL. This study showed that BodyMap is
a
useful **database** for the isolation of tissue-specific genes.

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L14 ANSWER 12 OF 67 MEDLINE

ACCESSION NUMBER: 2001272086 MEDLINE

DOCUMENT NUMBER: 21238674 PubMed ID: 11340635

TITLE: PRAC: A novel small nuclear protein that is specifically expressed in human prostate and colon.

AUTHOR: Liu X F; Olsson P; Wolfgang C D; Bera T K; Duray P; Lee B; Pastan I

CORPORATE SOURCE: Laboratory of Molecular Biology, Division of Basic Sciences, National Cancer Institute, National Institutes of

Health, Bethesda, Maryland, USA.

SOURCE: PROSTATE, (2001 May 1) 47 (2) 125-31.

Journal code: 8101368. ISSN: 0270-4137.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200105

ENTRY DATE: Entered STN: 20010529

Last Updated on STN: 20010529

Entered Medline: 20010521

AB BACKGROUND: The **database** of human **Expressed** Sequence Tags (dbEST) provides a potential source for identification of tissue-specific genes. This **database** contains sequences that originate from **cDNA** libraries from particular tumors, organs or cell types. In this report, we have used the **EST database** to identify PRAC, a novel gene specifically **expressed** in human **Prostate**, **prostate** cancer, Rectum And distal Colon. METHODS: Using a computer based analysis, a cluster of sequence homologous **ESTs** was identified which contained **ESTs** derived only from human **prostate cDNA** libraries. The tissue specificity was examined by multiple tissue RNA dot blots and RT-PCR. The PRAC **transcript** and **protein** was identified using Northern blot analysis, RACE-PCR, primer extension, and western blot. RESULTS: PRAC encode a 382 nucleotide RNA found in **prostate**, rectum, distal colon, and in three **prostate** cancer cell lines; LNCaP, PC-3 and DU145. This **transcript** encodes a 6 kDa nuclear **protein**. The PRAC gene is located on chromosome 17 at position 17q21, about 4 kbp downstream

from the homeodomain Hoxb-13 gene. CONCLUSIONS: Our data proves that the **EST database** can be a useful tool for discovery of **prostate**-specific genes. The nuclear localization, identification of potential phosphorylation sites, and possible cotranscription with the Hoxb-13 gene suggest that PRAC may have a regulatory role in the nucleus. Copyright 2001 Wiley-Liss, Inc.

L14 ANSWER 13 OF 67 MEDLINE

ACCESSION NUMBER: 2001190983 MEDLINE

DOCUMENT NUMBER: 21024389 PubMed ID: 11149669

TITLE: Blood-brain barrier genomics.

AUTHOR: Li J Y; Boado R J; Pardridge W M

CORPORATE SOURCE: Department of Medicine, UCLA School of Medicine, Los Angeles, California 90095-1682, USA.

CONTRACT NUMBER: NS-38894 (NINDS)

SOURCE: JOURNAL OF CEREBRAL BLOOD FLOW AND METABOLISM, (2001 Jan) 21 (1) 61-8.

Journal code: 8112566. ISSN: 0271-678X.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF306546
ENTRY MONTH: 200104
ENTRY DATE: Entered STN: 20010410
Last Updated on STN: 20010410
Entered Medline: 20010405

AB The blood-brain barrier (BBB) is formed by the **brain** microvascular endothelium, and the unique transport properties of the BBB are derived from tissue-specific gene **expression** within this cell. The current studies developed a gene microarray approach specific for the BBB by purifying the initial **mRNA** from isolated rat **brain** capillaries to generate tester **cDNA**. A polymerase chain reaction-based subtraction cloning method, suppression subtractive hybridization (SSH), was used, and the BBB **cDNA** was subtracted with driver **cDNA** produced from **mRNA** isolated from rat liver and **kidney**. Screening 5% of the subtracted tester **cDNA** resulted in identification of 50 gene products and more than 80% of those were selectively **expressed** at the BBB; these included novel gene sequences not found in existing **databases**, **ESTs**, and known genes that were not known to be selectively **expressed** at the BBB. Genes in the latter category include tissue plasminogen activator, insulin-like growth factor-2, PC-3 gene product, myelin basic **protein**, regulator of G **protein** signaling 5, utrophin, IkappaB, connexin-45, the class I major histocompatibility complex, the rat homologue of the **transcription** factors hbrm or EZH1, and organic anion transporting polypeptide type 2. Knowledge of tissue-specific gene **expression** at the BBB could lead to new targets for **brain** drug delivery and could elucidate mechanisms of **brain** pathology at the microvascular level.

L14 ANSWER 14 OF 67 MEDLINE

ACCESSION NUMBER: 2001182568 MEDLINE
DOCUMENT NUMBER: 21100433 PubMed ID: 11167026
TITLE: Transcriptome analysis of channel catfish (*Ictalurus punctatus*): genes and expression profile from the brain.
AUTHOR: Ju Z; Karsi A; Kocabas A; Patterson A; Li P; Cao D; Dunham R; Liu Z
CORPORATE SOURCE: The Fish Molecular Genetics and Biotechnology Laboratory, 203 Swingle Hall, Department of Fisheries and Allied Aquacultures and Program of Cell and Molecular Biosciences, Auburn University, AL, Auburn 36849, USA.
SOURCE: GENE, (2000 Dec 31) 261 (2) 373-82.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200103
ENTRY DATE: Entered STN: 20010404
Last Updated on STN: 20010404
Entered Medline: 20010329

AB **Expressed** sequence tag (**EST**) analysis was conducted using a complementary DNA (**cDNA**) library made from the **brain mRNA** of channel catfish (*Ictalurus punctatus*). As part of our **transcriptome** analysis in catfish to develop molecular reagents for comparative functional genomics, here we report analysis of 1201 **brain cDNA** clones. Of the 1201 clones, 595 clones (49.5%) were identified as known genes by BLAST

searches and 606 clones (50.5%) as unknown genes. The 595 clones of known gene products represent **transcripts** of 251 genes. These known genes were categorized into 15 groups according to their biological functions. The largest group of known genes was the genes involved in translational machinery (21.4%) followed by mitochondrial genes (6.2%), structural genes (3.1%), genes homologous to sequences of unknown functions (2.3%), enzymes (2.7%), hormone and regulatory **proteins** (2.5%), genes involved in immune systems (2.1%), genes involved in sorting, transport, and metal metabolism (1.8%), **transcriptional** factors and DNA repair **proteins** (1.6%), proto-oncogenes (1.2%), lipid binding **proteins** (1.2%), stress-induced genes (0.7%), genes homologous to human genes involved in mental diseases (0.6%), and development or differentiation-related genes (0.3%). The number of genes represented by the 606 clones of unknown genes is not known at present, but the high percentage of clones showing no homology to any known genes in the GenBank **databases** may indicate that a great number of novel genes exist in teleost **brain**.

L14 ANSWER 15 OF 67 MEDLINE
 ACCESSION NUMBER: 2001076993 MEDLINE
 DOCUMENT NUMBER: 20510011 PubMed ID: 11054555
 TITLE: Human allantoicase gene: cDNA cloning, genomic organization and chromosome localization.
 AUTHOR: Vigetti D; Monetti C; Acquati F; Taramelli R; Bernardini G
 CORPORATE SOURCE: Dipartimento di Biologia Strutturale e Funzionale, Universita degli Studi dell'Insubria, Via J. H. Dunant 3, I-21100, Varese, Italy.
 SOURCE: GENE, (2000 Oct 3) 256 (1-2) 253-60.
 Journal code: 7706761. ISSN: 0378-1119.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF215924
 ENTRY MONTH: 200101
 ENTRY DATE: Entered STN: 20010322
 Last Updated on STN: 20010322
 Entered Medline: 20010111

AB Uric-acid-degrading enzymes (uricase, allantoinase, allantoicase, ureidoglycolate lyase and urease) were lost during vertebrate evolution and the causes for this loss are still unclear. We have recently cloned the first vertebrate allantoicase **cdna** from the amphibian *Xenopus laevis*. Surprisingly, we have found some mammalian **expressed** sequence tags (**ESTs**) that show high similarity with *Xenopus* allantoicase **cdna**. From a human fetal spleen **cdna** library and adult **kidney EST** clone, we have obtained a 1790 nucleotide long **cdna**. The 3' end of this sequence reveals a substantial high identity with the corresponding portion of *Xenopus* allantoicase **cdna**. In contrast, at the 5' end the human sequence diverges from that of *Xenopus*; since no continuous

open

reading frame can be found in this region, the hypothetical human **protein** appears truncated at its N-terminus. We proposed that such a **transcript** could be due to an incorrect splicing mechanism that introduces an intron portion at the 5' end of human **cdna**. Allantoicase **cdna** is **expressed** in adult **testis**, **prostate**, **kidney** and fetal spleen. By comparison with available genomic sequences deposited in **database**, we have determined that the human allantoicase gene consists of five exons and spans 8kb. We have also mapped the gene in chromosome 2.

L14 ANSWER 16 OF 67 MEDLINE

ACCESSION NUMBER: 2001058771 MEDLINE
DOCUMENT NUMBER: 20472053 PubMed ID: 11018261
TITLE: Isolation of a cDNA for a novel human RING finger protein gene, RNF18, by the virtual transcribed sequence (VTS) approach(1).
AUTHOR: Yoshikawa T; Seki N; Azuma T; Masuho Y; Muramatsu M; Miyajima N; Saito T
CORPORATE SOURCE: Biological Technology Laboratory, Helix Research Institute,
Kisarazu, Chiba, Japan.
SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (2000 Oct 2) 1493 (3) 349-55.
Journal code: 0217513. ISSN: 0006-3002.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB037682
ENTRY MONTH: 200012
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001222

AB We have recently developed a novel **database** system, designated as the virtual **transcribed** sequence (VTS) which efficiently extracts many genes from public human genome **databases**, and tested the feasibility of this novel computational approach (N. Miyajima, C. Burge, T. Saito, Biochem. Biophys. Res. Commun. 272 (2000) 801; <http://host45.maze.co.jp/vts/>). In this study, using the VTS approach, we isolated a **cDNA** for a novel human gene with RING finger motif (C(3)HC(4)), which is not deposited in public **EST databases**. The isolated **cDNA** clone is 2163 bp in length, and contains an open reading frame of 452 amino acids. We designated the novel gene as RNF18. A **database** search showed that the RNF18 gene had the moderate similarity to SS-A/Ro52 **protein**, which is a ribonucleoprotein reactive with autoantibodies in patients with Sjogren's syndrome and systemic lupus erythematosus. Tissue distribution analyses by Northern blot and RT-PCR methods demonstrated that the RNF18 messenger RNA was preferentially **expressed** in **testis**. The exon-intron boundaries of RNF18 gene were determined by aligning the **cDNA** sequence with the corresponding genome sequence. The isolated **cDNA** consists of eight exons that span about 11 kb of the genome DNA. The precise chromosomal location of the RNF18 gene was determined by PCR-based radiation hybrid mapping, and the gene was located to centromere region of chromosome 11 between markers NIB1900 and D11S1350. Taken together, the VTS approach should provide a novel **cDNA** cloning strategy for isolating unidentified genes, which are not found even in **EST databases** but are detectable computationally.

L14 ANSWER 17 OF 67 MEDLINE

ACCESSION NUMBER: 2001027226 MEDLINE
DOCUMENT NUMBER: 20490576 PubMed ID: 11035752
TITLE: Identification of tgh-2, a filarial nematode homolog of Caenorhabditis elegans daf-7 and human transforming growth factor beta, expressed in microfilarial and adult stages of Brugia malayi.
AUTHOR: Gomez-Escobar N; Gregory W F; Maizels R M
CORPORATE SOURCE: Institute of Cell, Animal and Population Biology,

Kingdom. University of Edinburgh, Edinburgh EH9 3JT, United
SOURCE: INFECTION AND IMMUNITY, (2000 Nov) 68 (11) 6402-10.
Journal code: 0246127. ISSN: 0019-9567.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF104016
ENTRY MONTH: 200011
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001115

AB A novel member of the transforming growth factor beta (TGF-beta) family has been identified in the filarial nematode parasite *Brugia malayi* by searching the recently developed **Expressed** Sequence Tag (**EST**) database produced by the Filarial Genome Project. Designated tgh-2, this new gene shows most similarity to a key product regulating dauer larva formation in *Caenorhabditis elegans* (DAF-7) and to the human down-modulatory cytokine TGF-beta. Homology to DAF-7 extends throughout the length of the 349-amino-acid (aa) **protein**, which is divided into an N-terminal 237 aa, including a putative signal sequence, a 4-aa basic cleavage site, and a 108-aa C-terminal active domain. Similarity to human TGF-beta is restricted to the C-terminal domain, over which there is a 32% identity between TGH-2 and TGF-beta1, including every cysteine residue. **Expression** of tgh-2 **mRNA** has been measured over the filarial life cycle. It is maximal in the microfilarial stage, with lower levels of activity around the time of molting within the mammal, but continues to be **expressed** by mature adult male and female parasites. **Expression** in both the microfilaria, which is in a state of arrested development, and the adult, which is terminally differentiated, indicates that tgh-2 may play a role other than purely developmental. This is consistent with our observation that TGH-2 is secreted by adult worms in vitro. Recombinant TGH-2 **expressed** in baculovirus shows a low level of binding to TGF-beta-receptor bearing mink lung epithelial cells (MELCs), which is partially inhibited (16 to 39%) with human TGF-beta, and activates plasminogen activator inhibitor-1 **transcription** in MELCs, a marker for TGF-beta-mediated transduction. Further tests will be required to establish whether the major role of *B. malayi* TGH-2 (Bm-TGH-2) is to modulate the host immune response via the TGF-beta pathway.

L14 ANSWER 18 OF 67 MEDLINE
ACCESSION NUMBER: 2001012409 MEDLINE
DOCUMENT NUMBER: 20461778 PubMed ID: 10858550
TITLE: Cloning, expression and functional characterization of rat napsin.
AUTHOR: Schauer-Vukasinovic V; Wright M B; Breu V; Giller T
CORPORATE SOURCE: F. Hoffmann-La Roche Ltd., Pharma Division, Preclinical Research, Grenzacherstrasse 124, CH-4070 Basel, Switzerland.
SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (2000 Jun 21) 1492 (1) 207-10.
Journal code: 0217513. ISSN: 0006-3002.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200010
ENTRY DATE: Entered STN: 20010322

Last Updated on STN: 20010322

Entered Medline: 20001031

AB A full-length **cDNA** clone coding for rat napsin was identified by homology search of the ZooSeq rat **EST database** (Incyte). Northern blot analysis revealed high **expression** of napsin **mRNA transcripts** in **kidney**, **lung** and spleen. Western blot analysis showed that rat napsin is **expressed** in **kidney** as a 50-kDa, highly glycosylated, monomeric **protein**. Lysates prepared from human embryonic **kidney** cells (HEK293) transfected with rat napsin showed increased enzymatic activity which was inhibited by pepstatin.

L14 ANSWER 19 OF 67

MEDLINE

ACCESSION NUMBER: 2000412228 MEDLINE

DOCUMENT NUMBER: 20314386 PubMed ID: 10854696

TITLE: Mouse receptor-activity-modifying proteins 1, -2 and -3: amino acid sequence, expression and function.

AUTHOR: Husmann K; Sexton P M; Fischer J A; Born W

CORPORATE SOURCE: Research Laboratory for Calcium Metabolism, Departments of Orthopaedic Surgery and Medicine, Zurich, Switzerland.. khusmann@balgrist.unizh.ch

SOURCE: MOLECULAR AND CELLULAR ENDOCRINOLOGY, (2000 Apr 25) 162 (1-2) 35-43.

Journal code: 7500844. ISSN: 0303-7207.

PUB. COUNTRY: Ireland

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200008

ENTRY DATE: Entered STN: 20000907

Last Updated on STN: 20000907

Entered Medline: 20000828

AB The calcitonin receptor-like receptor (CRLR) requires novel receptor-activity-modifying **proteins** (RAMPs) for its function as an adrenomedullin (ADM) or a calcitonin (CT) gene-related **peptide** (CGRP) receptor. Here, mouse **cDNA** clones representing **expressed** sequence tags (**ESTs**) in the GenEMBL **database** have been identified. They encode for **proteins** with 70, 68 and 84% amino acid sequence identity with respect to human RAMP1, -2 and -3. On Northern blot analysis of polyA(+) RNA mouse RAMP1 (mRAMP1) encoding **mRNA** with an apparent size of 0.8 kb was predominantly observed in embryonic and adult **brain** and **lung** and in adult skeletal muscle. Mouse RAMP2 encoding 0.8 and 1.2 kb **mRNA** were recognized in all tissues analyzed with the highest levels in embryonic **brain**, **lung** and gut and in adult **heart**, **lung**, skeletal muscle and **brain**. A single 1.2 kb mRAMP3 encoding **transcript** was mainly **expressed** in embryonic and adult **brain**. In COS-7 cells co-**expressing** rat CRLR (rCRLR) and mRAMP1, [125I]halphacGRP binding was inhibited by ralphacGRP(8-37), ralphacGRP and rbetaCGRP with IC(50) of 1.4+/-0.5, 4.5+/-0.6 and 7+/-0.3 nM, respectively. CyclicAMP accumulation was maximally stimulated tenfold by rbetaCGRP and ralphacGRP with EC(50) of 0.65+/-0.67 and 0.86+/-0.6 nM. In the same cells co-**expressing** rCRLR and mRAMP2, binding of [125I]rADM was displaced by rADM and rADM(20-50) with IC(50) of 1.9+/-0.5 and 3.4+/-1.4 nM, respectively, and a maximal sevenfold stimulation of cAMP accumulation

was

observed with rADM with an EC(50) of 0.82+/-0.85 nM. In the cells co-**expressing** rCRLR and mRAMP3, [125I]halphacGRP binding was inhibited by ralphacGRP(8-37), rbetaCGRP, ralphacGRP, rADM and rADM(20-50)

with IC(50) between 4 and 22 nM. cAMP accumulation was stimulated by rADM with an EC(50) of 5.1+/-2.7 nM that was 12-fold and 11-fold lower than that of ralphaCGRP and rbetaCGRP. In conclusion, mouse RAMP1, -2 and -3 exhibit high amino acid sequence homology to the corresponding human RAMPs. Co-expression of rCRLR with mRAMP1, -2 or -3 in COS-7 cells revealed distinct CGRP-, ADM- or ADM/CGRP receptors.

L14 ANSWER 20 OF 67 MEDLINE

ACCESSION NUMBER: 2000410298 MEDLINE
DOCUMENT NUMBER: 20399702 PubMed ID: 10945605
TITLE: Cancer gene discovery using digital differential display.
AUTHOR: Scheurle D; DeYoung M P; Binninger D M; Page H; Jahanzeb M;
Narayanan R
CORPORATE SOURCE: Department of Biology, Florida Atlantic University, Boca Raton 33431, USA.
SOURCE: CANCER RESEARCH, (2000 Aug 1) 60 (15) 4037-43.
Journal code: 2984705R. ISSN: 0008-5472.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200008
ENTRY DATE: Entered STN: 20000907
Last Updated on STN: 20000907
Entered Medline: 20000831

AB The Cancer Gene Anatomy Project **database** of the National Cancer Institute has thousands of **expressed** sequences, both known and novel, in the form of **expressed** sequence tags (**ESTs**). These **ESTs**, derived from diverse normal and tumor **cDNA** libraries, offer an attractive starting point for cancer gene discovery. Using a data-mining tool called Digital Differential Display (DDD) from the Cancer Gene Anatomy Project **database**, **ESTs** from six different solid tumor types (**breast**, colon, lung, **ovary**, pancreas, and **prostate**) were analyzed for differential **expression**. An electronic **expression** profile and chromosomal map position of these hits were generated from the Unigene **database**. The hits were categorized into major classes of genes including ribosomal **proteins**, enzymes, cell surface molecules, secretory **proteins**, adhesion molecules, and immunoglobulins and were found to be differentially **expressed** in these tumorderived libraries. Genes known to be up-regulated in **prostate**, **breast**, and pancreatic carcinomas were discovered by DDD, demonstrating the utility of this technique. Two hundred known genes and 500 novel sequences were discovered to be differentially **expressed** in these select tumor-derived libraries. Test genes were validated for **expression** specificity by reverse **transcription**-PCR, providing a proof of concept for gene discovery by DDD. A comprehensive **database** of hits can be accessed at <http://www.fau.edu/cmabb/publications/cancergenesis.htm>. This solid tumor DDD **database** should facilitate target identification for cancer diagnostics and therapeutics.

L14 ANSWER 21 OF 67 MEDLINE

ACCESSION NUMBER: 2000409153 MEDLINE
DOCUMENT NUMBER: 20239719 PubMed ID: 10775800
TITLE: Identification of human estrogen-inducible transcripts that
potentially mediate the apoptotic response in breast cancer.

AUTHOR: Szelei J; Soto A M; Geck P; Desronvil M; Prechtl N V;
 Weill
 B C; Sonnenschein C
 CORPORATE SOURCE: Department of Anatomy and Cell Biology, Tufts University
 School of Medicine, 136 Harrison Avenue, Boston, MA 02111,
 USA.
 CONTRACT NUMBER: AG13807 (NIA)
 CA13410 (NCI)
 CA55574 (NCI)
 +
 SOURCE: JOURNAL OF STEROID BIOCHEMISTRY AND MOLECULAR BIOLOGY,
 (2000 Mar) 72 (3-4) 89-102.
 Journal code: 9015483. ISSN: 0960-0760.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200008
 ENTRY DATE: Entered STN: 20000907
 Last Updated on STN: 20000907
 Entered Medline: 20000825

AB Hormone manipulation has been used for several decades with the purpose
 of inducing **breast** cancer regression. On the one hand, hormone
 ablation and antiestrogen administration were used on the rationale that
 estrogens induce proliferation of their target cells. Before the advent
 of the antiestrogen tamoxifen, on the other hand, the estrogen agonist DES
 was used to obtain clinical remissions. The rationale for the use of
 diethylstilbestrol (DES) was totally empirical. In fact, the efficacy of
 both treatments was comparable. A mechanistic explanation for
 estrogen-induced regression is urgently needed in order to provide a
 rationale for its use in therapeutic fields, and to develop markers to
 identify this phenotype in order to recognize responsive tumors. In this
 report, we use E8CASS cells (a MCF7 variant) as a model to study
 estrogen-mediated regression. The proliferation rate of E8CASS cells is
 decreased by estrogens. In order to isolate **mRNA** sequences
 induced by estradiol, a subtracted library was prepared from E8CASS cells
 grown in the presence and absence of estrogens. Twenty nine
 differentially **expressed** unique sequences were found. Seven of them were
 homologous to known genes, 12 of them were homologous to **expressed**
 sequence tags (**EST**), and 10 sequences had no homologues in the
databases. The two sequences showing the highest induction by
 estradiol (E9 and E43) were chosen for further analysis. The sequence of
 the E43 coding region has 96% homology to the bovine actin2 gene and 100%
 identity to bovine actin2 **protein**, and it is homologous to the
 human actin-related **protein** 3 (Arp3). It has been suggested that
 Arp3 is involved in actin nucleation. The phenotype of E8CASS cells is
 clearly affected by estrogen treatment. It is likely that E43 may be
 involved in these morphological changes. The E9 **cDNA** is a
 putative zinc-finger **protein** of the PHD family of
transcriptional transactivators. A member of this family, Requiem,
 is involved in apoptosis. The E9 **mRNA** is highly
expressed in E8CASS cells treated with estrogens, a treatment
 which results in decreased proliferation rate and increased DNA
 degradation. This correlation suggests that E9 may be a mediator of
 estrogen-induced regression of **breast** cancer.

DOCUMENT NUMBER: 20334634 PubMed ID: 10874211
 TITLE: Isolation and characterization of human NBL4, a gene involved in the beta-catenin/tcf signaling pathway.
 AUTHOR: Ishiguro H; Furukawa Y; Daigo Y; Miyoshi Y; Nagasawa Y; Nishiwaki T; Kawasoe T; Fujita M; Satoh S; Miwa N; Fujii Y;
 Nakamura Y
 CORPORATE SOURCE: Laboratory of Molecular Medicine, Human Genome Center, Institute of Medical Science, The University of Tokyo, Minato-ku, Tokyo 108-8639, Japan.
 SOURCE: JAPANESE JOURNAL OF CANCER RESEARCH, (2000 Jun) 91 (6) 597-603.
 Journal code: 8509412. ISSN: 0910-5050.
 PUB. COUNTRY: Japan
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AB030240; GENBANK-D30788; GENBANK-U13673
 ENTRY MONTH: 200008
 ENTRY DATE: Entered STN: 20000901
 Last Updated on STN: 20000922
 Entered Medline: 20000818

AB beta-Catenin, a key regulator of cellular proliferation, is often mutated in various types of human cancer. To investigate cellular responses related to the beta-catenin signaling pathway, we applied a differential display method using mouse cells transfected with an activated form of mutant beta-catenin. This analysis and subsequent northern-blot hybridization confirmed that **expression** of a murine gene encoding NBL4 (novel band 4.1-like **protein** 4) was up-regulated by activation of beta-catenin. To examine a possible role of NBL4 in cancer, we isolated the human homologue of the murine NBL4 gene by matching mNBL4 against the human **EST** (**expressed** sequence tag) **database** followed by 5' rapid amplification of **cdna** ends (5'RACE). The **cdna** of hNBL4 encoded a **protein** of 598 amino acids that shared 87% identity in amino acid sequence with murine NBL4 and 71% with zebrafish NBL4. A 2.2-kb hNBL4 **transcript** was **expressed** in all human tissues examined with high levels of **expression** in **brain**, liver, thymus and peripheral blood leukocytes and low levels of **expression** in **heart**, **kidney**, **testis** and colon. We determined its chromosomal localization at 5q22 by fluorescence in situ hybridization. **Expression** of hNBL4 was significantly reduced when beta-catenin was depleted in SW480 cells, a human cancer cell line that constitutionally accumulates beta-catenin. The results support the view that NBL4 is an important component of the beta-catenin / Tcf pathway and is probably related to determination of cell polarity or proliferation.

L14 ANSWER 23 OF 67 MEDLINE
 ACCESSION NUMBER: 2000231760 MEDLINE
 DOCUMENT NUMBER: 20231760 PubMed ID: 10767556
 TITLE: cdna cloning of acyl-CoA desaturase homologs in the silkworm, Bombyx mori.
 AUTHOR: Yoshiga T; Okano K; Mita K; Shimada T; Matsumoto S
 CORPORATE SOURCE: Laboratory of Molecular Entomology and Baculovirology, RIKEN, Hirosawa 2-1, Wako, Saitama, Japan.
 SOURCE: GENE, (2000 Apr 4) 246 (1-2) 339-45.
 Journal code: 7706761. ISSN: 0378-1119.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF157627; GENBANK-AF182405; GENBANK-AF182406
ENTRY MONTH: 200005
ENTRY DATE: Entered STN: 20000613
Last Updated on STN: 20000613
Entered Medline: 20000531

AB We have isolated two acyl-CoA desaturase clones from a pheromone gland **cDNA** library by using the **EST (expressed sequence tag) database** of *Bombyx mori*. The putative acyl-CoA desaturases encoded by the clones *desat 1* (2029bp) and *desat 2* (2341bp) have 98% identity, and both **proteins** show 61% identities to *Trichoplusia ni* acyl-CoA Delta(11) desaturase. The deduced amino acid sequences conserve well the histidine clusters that are catalytically essential for acyl-CoA desaturase activity. Northern blot and RT-PCR analyses revealed that both **transcripts** of *desat 1* and *desat 2* were **expressed** predominantly in the pheromone gland. Both **transcripts** detected 3days before adult eclosion dramatically increased a day before adult eclosion, keeping the **mRNA** levels high even after eclosion. These results, combined with the fact that Delta(11) and Delta(10, 12) desaturation of palmitate is a key step to synthesize pheromone in *B. mori*, suggest that the desaturases encoded by *desat 1* and *desat 2* are involved in either or both of the desaturation steps in the pheromone biosynthetic pathway of *B. mori*. The **mRNA** levels of *desat 1* and *desat 2* were not affected by decapitation or injection of the pheromone biosynthesis activating neuropeptide (PBAN) into the adult female moth, suggesting that the **transcription** of *desat 1* and *desat 2* is not regulated by PBAN. In addition to the clones in the pheromone gland, eight other clones encoding the same Delta(9) desaturase homolog were found in an embryonic **cDNA** library by searching from the **EST database** of *B. mori*. The deduced amino acid sequence from one of the clones (*desat 3*) shows 79% identity to *T. ni* Delta(9) desaturase but only 52% identity to the desaturases in the pheromone gland of *B. mori*. Northern blot analysis showed that the **mRNA** corresponding to the *desat 3* was detected in the **ovary** and fat body, but not in the pheromone gland. Abundance of the Delta(9) desaturase clones (eight out of the 762 randomly sequenced clones) in the library prepared from diapause-destined embryos (40h after oviposition) suggests that the Delta(9) desaturase encoded by *desat 3* plays an important role in embryonic development in *B. mori*.

L14 ANSWER 24 OF 67 MEDLINE
ACCESSION NUMBER: 2000163069 MEDLINE
DOCUMENT NUMBER: 20163069 PubMed ID: 10697961
TITLE: cDNA cloning, expression profile, and genomic structure of human and mouse RNF10/Rnf 10 genes, encoding a novel RING finger protein.
AUTHOR: Seki N; Hattori A; Sugano S; Muramatsu M; Saito T
CORPORATE SOURCE: National Institute of Radiological Sciences, Chiba, Japan.
SOURCE: JOURNAL OF HUMAN GENETICS, (2000) 45 (1) 38-42.
Journal code: 9808008. ISSN: 1434-5161.
PUB. COUNTRY: Japan
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB026621; GENBANK-AB027196
ENTRY MONTH: 200004
ENTRY DATE: Entered STN: 20000427
Last Updated on STN: 20000427

Entered Medline: 20000418

AB RING finger (C3HC4-type zinc finger) is a variant zinc finger motif present in a new family of **proteins** including **transcription** regulators. A new member of the RING finger **protein** family was identified through a mouse **expressed** sequence tag (**EST**) **database** search, and its full-length **cDNA** was isolated from a mouse **brain** full length-enriched **cDNA** library. The gene was designated as Rnf10, for RING finger **protein** 10. The **cDNA** clone consists of 3110 nucleotides and encodes an open reading frame (ORF) of an 804-amino acid **protein**. A **database** search revealed that human KIAA0262 **protein** (accession number, D87451) has strong homology to mouse Rnf10. To confirm that mouse Rnf10 is the homolog or an isolog

of

human KIAA0262, a human RNF10 **cDNA** was cloned in our hands from a fetal **brain cDNA** pool. The newly isolated **cDNA** contained an ORF for 811 amino acids which had almost identical structure to mouse Rnf10 **protein**, indicating that the human ORF codes for RNF10 **protein**. This finding was also supported by comparative chromosome mapping in which both genes were localized in a conserved linkage homology region between mouse and human. Comparison of the RNF10 and KIAA0262 **proteins** revealed that both were **transcribed** from the same gene and that the longer RNF10 ORF would be the authentic form. The complete genomic organization of RNF10 was determined to consist of 17 exons spanning at least 40kb in the genome.

L14 ANSWER 25 OF 67 MEDLINE
ACCESSION NUMBER: 2000130111 MEDLINE
DOCUMENT NUMBER: 20130111 PubMed ID: 10662542
TITLE: Identification and characterization of BPTF, a novel bromodomain transcription factor.
AUTHOR: Jones M H; Hamana N; Shimane M
CORPORATE SOURCE: Chugai Research Institute for Molecular Medicine, 153-2 Nagai, Niihari, Ibaraki, 300-4101, Japan.
SOURCE: GENOMICS, (2000 Jan 1) 63 (1) 35-9.
JOURNAL code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB032251
ENTRY MONTH: 200004
ENTRY DATE: Entered STN: 20000421
Last Updated on STN: 20000421
Entered Medline: 20000411

AB The bromodomain is a 110-amino-acid conserved structural region associated

with **proteins** that regulate signal-dependent, nonbasal **transcription**. The bromodomain can regulate histone acetyl transferase activity and interacts specifically with acetylated lysine residues. A key role for bromodomain **proteins** in maintaining normal proliferation is indicated by the implication of several bromodomain **proteins** in cancer, with four of these identified at translocation breakpoints. We searched **EST databases** for novel bromodomain genes. The sequence from one **EST** was used to initiate generation of a full-length clone from a **testis cDNA** library. The completed sequence encodes a predicted **protein** of 2781 amino acids, which, in addition to the bromodomain, harbors further motifs characteristic of a **transcriptional** coactivator: two PHD fingers and an extensive

glutamine-rich acidic domain. There are several other regions that are conserved with the *Caenorhabditis elegans* putative **protein** F26H11, which may be functionally homologous. The novel gene, called BPTF, is **expressed** in all tissues examined as a 10.5-kb **transcript**. The **protein** has extensive identity with the smaller FAC1 **protein**, suggesting that the two either are derived from the same locus or are synonymous. BPTF has been mapped to 17q23. Functional domains found within BPTF are consistent with a role for this **protein** in hormonally regulated, chromatin-mediated regulation of **transcription**.
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L14 ANSWER 26 OF 67 MEDLINE
 ACCESSION NUMBER: 2000123885 MEDLINE
 DOCUMENT NUMBER: 20123885 PubMed ID: 10631317
 TITLE: Caveolin-1 isoforms are encoded by distinct mRNAs. Identification Of mouse caveolin-1 mRNA variants caused by alternative transcription initiation and splicing.
 AUTHOR: Kogo H; Fujimoto T
 CORPORATE SOURCE: Department of Anatomy and Molecular Cell Biology, Nagoya University School of Medicine, Showa-ku, Nagoya, Japan.. hkogo@med.nagoya-u.ac.jp
 SOURCE: FEBS LETTERS, (2000 Jan 14) 465 (2-3) 119-23. Journal code: 0155157. ISSN: 0014-5793.
 PUB. COUNTRY: Netherlands
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200002
 ENTRY DATE: Entered STN: 20000309
 Last Updated on STN: 20000309
 Entered Medline: 20000218

AB By searching the **EST database** with the known **cDNA** sequence encoding alpha-caveolin-1 (full-length: FL), we found a variant having a hitherto unknown sequence in place of the first exon (5'-end variant: 5'V). The **expression** level of 5'V **mRNA** was equivalent to that of FL **mRNA**. The entire sequences of FL and 5'V **mRNA** were determined by 3'- and 5'-RACE analysis; their sizes were 2484 bp and 2533 bp, respectively, and the sequences were identical except for the region of the first exon. By Northern blotting, FL and 5'V **mRNAs** showed the same tissue distribution, and were intensely **expressed** in the lung, heart, and skeletal muscle. Analyzing the **protein** production from these **mRNAs** using green fluorescent **protein** as a tag, we found FL **mRNA** to produce the alpha-isoform predominantly, but to form little beta-isoform. The production of the beta-isoform from 5'V **mRNA** was also demonstrated. By sequence analysis of the first intron of the caveolin-1 gene, a TATA box was found at 28 bp upstream of the **transcription** initiation site for 5'V **mRNA**. This is the first demonstration of caveolin-1 **mRNA** variants generated by alternative **transcription** initiation, and it indicates that the two isoforms of caveolin-1 are produced from two distinct **mRNAs**.

L14 ANSWER 27 OF 67 MEDLINE
 ACCESSION NUMBER: 2000077667 MEDLINE
 DOCUMENT NUMBER: 20077667 PubMed ID: 10612420
 TITLE: Structure and distribution of rat menin mRNA.
 AUTHOR: Maruyama K; Tsukada T; Hosono T; Ohkura N; Kishi M; Honda M; Nara-Ashizawa N; Nagasaki K; Yamaguchi K

CORPORATE SOURCE: Growth Factor Division, National Cancer Center Research
Institute, Tokyo, Japan.. kmaruyam@gan2.res.ncc.go.jp
SOURCE: MOLECULAR AND CELLULAR ENDOCRINOLOGY, (1999 Oct 25) 156
(1-2) 25-33.
Journal code: 7500844. ISSN: 0303-7207.
PUB. COUNTRY: Ireland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB023400; GENBANK-AB023401
ENTRY MONTH: 200001
ENTRY DATE: Entered STN: 20000124
Last Updated on STN: 20000124
Entered Medline: 20000113

AB Menin is a **protein** product of a tumor suppressor gene MEN1,
mutations of which are responsible for multiple endocrine neoplasia type
1, an autosomal dominant familial cancer syndrome. We isolated rat menin
cdna clones from a fetal rat **brain cdna**
library. We also determined the nucleotide sequence of the **protein**
coding region of mouse menin **cdna**, which was partly registered
in the **expressed** sequence tag (**EST**) **database**
. Deduced amino acid sequences of rat and mouse menin are highly
homologous to human menin. All of the previously reported
disease-associated missense mutations and single amino acid deletions

were
observed at the residues that are conserved among these three species.

Rat
immune
MEN1 **transcripts** were detected not only in the endocrine tissues
but also in the tissues of the nervous, digestive, reproductive and
systems. The MEN1 **transcripts** were abundantly **expressed**
in the developing rat **brain** on day 14-18 of gestation.
Immunoblotting and immunocytochemical analysis of the COS-7 cells
transfected with a rat menin-**expression** vector revealed that the
translated product has a molecular mass of approximately 70 kDa, and is
localized mainly in the nucleus. These findings are consistent with those
reported on human menin.

L14 ANSWER 28 OF 67 MEDLINE

ACCESSION NUMBER: 2000012750 MEDLINE
DOCUMENT NUMBER: 20012750 PubMed ID: 10544010
TITLE: Identification and gene structure of a novel human
PLZF-related transcription factor gene, TZFP.
AUTHOR: Lin W; Lai C H; Tang C J; Huang C J; Tang T K
CORPORATE SOURCE: Institute of Biomedical Sciences, Academia Sinica, Taipei,
115, Taiwan.. wenlin@ibms.sinica.edu.tw
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1999
Nov 2) 264 (3) 789-95.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF130255
ENTRY MONTH: 199912
ENTRY DATE: Entered STN: 20000113
Last Updated on STN: 20000113
Entered Medline: 19991222

AB A novel **cdna** clone was identified through yeast two-hybrid
experiments. Following cross-examination between the **cdna**
clones, **EST** clones, and the cosmid clone, we could digitally

assemble a new zinc finger **transcription** factor gene. This predicted gene has a **cDNA** size of about 1960 bp and is translated into a 487-amino-acid **protein**. According to **database** analysis, this gene contains three C2H2 zinc finger motifs and is highly related to human PLZF (promyelocytic leukemia zinc finger **protein**). The full-length coding region of the gene was isolated, and its sequences were confirmed by DNA sequencing. Interestingly, one splicing variant lacking exon III was also identified. Northern blot analysis revealed that this gene is mainly **expressed** in human **testis**. In conclusion, we have identified a new member of the PLZF zinc finger **protein** family, the **testis** zinc finger **protein** (TZFP), which is mainly **expressed** in **testis** tissue.

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L14 ANSWER 29 OF 67 MEDLINE
 ACCESSION NUMBER: 1999453299 MEDLINE
 DOCUMENT NUMBER: 99453299 PubMed ID: 10521662
 TITLE: A complex population of RNAs exists in human ejaculate spermatozoa: implications for understanding molecular aspects of spermiogenesis.
 AUTHOR: Miller D; Briggs D; Snowden H; Hamlington J; Rollinson S; Lilford R; Krawetz S A
 CORPORATE SOURCE: Centre for Reproduction Growth and Development, University of Leeds' Division of Obstetrics and Gynaecology, Level D, Clarendon Wing, Leeds General Infirmary, Belmont Grove, Leeds, UK.. d.miller@leeds.ac.uk
 CONTRACT NUMBER: HD36512 (NICHD)
 SOURCE: GENE, (1999 Sep 17) 237 (2) 385-92.
 Journal code: 7706761. ISSN: 0378-1119.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199911
 ENTRY DATE: Entered STN: 20000111
 Last Updated on STN: 20000111
 Entered Medline: 19991108

AB The presence of **mRNAs** in human ejaculate spermatozoa is well established, yet little is known of the representation or function of these **transcripts**. To address these issues, the complexity of spermatozoal RNA was examined. As expected, **testis-expressed mRNAs** were detected by RT-PCR in mature human spermatozoa. Interestingly, when a **testis cDNA** library was probed with total spermatozoal RNA, less than 2% of plaques gave a strong hybridization signal, suggesting a rather unique sperm-derived population. To further define the sequence distribution, 18 strongly hybridizing clones were selected at random for end-sequence analysis. Twelve matched unique sequences in the **EST**, STS and NR **databases**, whereas five showed no similarity to any of the sequences in the **databases**. In addition, one clone belonged to the SINE repetitive element family. As demonstrated by sequencing randomly primed cloned inserts, short (SINE/MER) or long (LINE/ORF2) interspersed repeat-like sequences are also contained as part of the spermatozoal RNA fraction. It is now evident that human spermatozoa contain a rich repertoire of both known and unknown **protein**-encoding and non-coding RNAs. This provides a unique opportunity to identify and investigate the many genes responsible for the structure and function/dysfunction of the male gamete using spermatozoal RNA as the template.

L14 ANSWER 30 OF 67 MEDLINE
 ACCESSION NUMBER: 1999389722 MEDLINE
 DOCUMENT NUMBER: 99389722 PubMed ID: 10458907
 TITLE: Novel human and mouse homologs of *Saccharomyces cerevisiae* DNA polymerase eta.
 AUTHOR: McDonald J P; Rapic-Otrin V; Epstein J A; Broughton B C; Wang X; Lehmann A R; Wolgemuth D J; Woodgate R
 CORPORATE SOURCE: Section on DNA Replication, Repair and Mutagenesis, National Institute of Child Health and Human Development, Bethesda, Maryland, 20892-2725, USA.
 CONTRACT NUMBER: RO1HD34915 (NICHD)
 SOURCE: GENOMICS, (1999 Aug 15) 60 (1) 20-30.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals; Space Life Sciences
 OTHER SOURCE: GENBANK-AF140501; GENBANK-AF151691
 ENTRY MONTH: 199909
 ENTRY DATE: Entered STN: 19991012
 Last Updated on STN: 20020124
 Entered Medline: 19990930

AB The *Saccharomyces cerevisiae* RAD30 gene encodes a novel eukaryotic DNA polymerase, pol eta that is able to replicate across cis-syn cyclobutane pyrimidine dimers both accurately and efficiently. Very recently, a human homolog of RAD30 was identified, mutations in which result in the sunlight-sensitive, cancer-prone, Xeroderma pigmentosum variant group phenotype. We report here the cloning and localization of a second human homolog of RAD30. Interestingly, RAD30B is localized on chromosome 18q21.1 in a region that is often implicated in the etiology of many human cancers. The mouse homolog (Rad30b) is located on chromosome 18E2. The human RAD30B and mouse Rad30b **mRNA transcripts**, like many repair **proteins**, are highly **expressed** in the **testis**. In situ hybridization analysis indicates that **expression** of mouse Rad30b occurs predominantly in postmeiotic round spermatids. **Database** searches revealed genomic and **EST** sequences from other eukaryotes such as *Aspergillus nidulans*, *Schizosaccharomyces pombe*, *Brugia malayi*, *Caenorhabditis elegans*, *Trypanosoma cruzi*, *Arabidopsis thaliana*, and *Drosophila melanogaster* that also encode putative homologs of RAD30, thereby suggesting that Rad30-dependent translesion DNA synthesis is conserved within the eukaryotic kingdom.
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L14 ANSWER 31 OF 67 MEDLINE
 ACCESSION NUMBER: 1999375318 MEDLINE
 DOCUMENT NUMBER: 99375318 PubMed ID: 10444326
 TITLE: Endogenous retroviruses provide the primary polyadenylation signal for two new human genes (HHLA2 and HHLA3).
 AUTHOR: Mager D L; Hunter D G; Schertzer M; Freeman J D
 CORPORATE SOURCE: British Columbia Cancer Agency and Department of Medical Genetics, University of British Columbia, Vancouver, British Columbia, Canada.. dixie@interchange.ubc.ca
 SOURCE: GENOMICS, (1999 Aug 1) 59 (3) 255-63.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English

FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF126162; GENBANK-AF126163; GENBANK-AF126164
ENTRY MONTH: 199911
ENTRY DATE: Entered STN: 20000113
Last Updated on STN: 20000113
Entered Medline: 19991130

AB By screening the **expressed** sequence tag (**EST**) **database**, we identified **transcripts** of two new human genes that are polyadenylated within a long terminal repeat (LTR) of the HERV-H endogenous retrovirus family. The first gene, termed HHLA2, is represented by two **EST** clones and one **cDNA** clone, all of which have a polyadenylated LTR as their 3' end. The gene has an open reading frame (ORF) of 414 amino acids with three immunoglobulin-like domains and is **expressed** primarily in intestinal tissues, **kidney**, and **lung**. Seven small **EST** clones from several different tissues were found for the second gene, termed HHLA3.

As with HHLA2, all HHLA3 **ESTs** utilized a HERV-H LTR as the polyadenylation signal. Three types of alternatively spliced HHLA3 **transcripts** that could encode **proteins** of 76, 121, or 153 amino acids were detected. Interestingly, the ORF for two of these **transcripts** continues into the LTR. For both HHLA2 and 3, no major human **transcripts** that utilized a non-LTR polyadenylation signal were detected. Analysis of RNA from baboon, which lacks the LTRs at these genomic loci, showed that the baboon HHLA2 and 3 genes use other polyadenylation signals. This study demonstrates that ancient retroviral insertions have assumed gene regulatory functions during the course of human evolution.
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L14 ANSWER 32 OF 67 MEDLINE
ACCESSION NUMBER: 1999326706 MEDLINE
DOCUMENT NUMBER: 99326706 PubMed ID: 10396028
TITLE: A novel human GnRH receptor homolog gene: abundant and wide
tissue distribution of the antisense transcript.
AUTHOR: Millar R; Conklin D; Lofton-Day C; Hutchinson E; Troskie B;
Illing N; Sealton S C; Hapgood J
CORPORATE SOURCE: MRC Molecular Reproductive Endocrinology Research Unit,
University of Cape Town Medical School, Observatory 7925,
South Africa.
SOURCE: JOURNAL OF ENDOCRINOLOGY, (1999 Jul) 162 (1) 117-26.
Journal code: 0375363. ISSN: 0022-0795.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199909
ENTRY DATE: Entered STN: 19991005
Last Updated on STN: 19991005
Entered Medline: 19990920

AB Gonadotropin releasing hormone (GnRH) regulates the reproductive system through a specific G-**protein**-coupled receptor (GPCR) in pituitary gonadotropes. The existence of two (or more) forms of GnRH in most vertebrates suggested the existence of GnRH receptor subtypes (I and II). Using sequence information for extracellular loop 3 of a putative Type II GnRH receptor from a reptile species, we have looked for a Type

II GnRH receptor gene in the human genome **EST** (**expressed** sequence tag) **database**. A homolog was identified which has 45%

and 41% amino acid identity with exons 2 and 3 of the known human GnRH pituitary receptor (designated Type I) and much lower homology with all other GPCRs. A total of 27 contiguous **ESTs** was found and comprised a continuous sequence of 1642 nucleotides. The **EST** sequences were confirmed in the cloned human gene and in PCR products of **cDNA** from several tissues. All **EST transcripts** detected were in the antisense orientation with respect to the novel GnRH receptor sequence and were highly **expressed** in a wide range of human **brain** and peripheral tissues. PCR of **cDNA** from a wide range of tissues revealed that intronic sequence equivalent to intron

2 of the Type I GnRH receptor was retained. The failure to splice out putative intron sequences in **transcripts** which spanned exon-intron boundaries is expected in antisense **transcripts**, as candidate donor and acceptor sites were only present in the gene when **transcribed** in the orientation encoding the GnRH receptor homolog. No **transcripts** extended 5' to the sequence corresponding to intron 2 of the Type I GnRH as the antisense **transcripts** terminated in poly A due to the presence of a polyadenylation signal sequence in the putative intron 2 when **transcribed** in the antisense orientation. These findings suggest that a Type II GnRH

receptor gene has arisen during vertebrate evolution and is also present in the human. However, the receptor may have become vestigial in the human, possibly due to the abundant and universal tissue **transcription** of the opposite DNA strand to produce antisense RNA.

L14 ANSWER 33 OF 67 MEDLINE
ACCESSION NUMBER: 1999156852 MEDLINE
DOCUMENT NUMBER: 99156852 PubMed ID: 10036181
TITLE: Discovery of three novel orphan G-protein-coupled receptors.
AUTHOR: Marchese A; Sawzdargo M; Nguyen T; Cheng R; Heng H H; Nowak
CORPORATE SOURCE: T; Im D S; Lynch K R; George S R; O'dowd B F
Department of Pharmacology, Department of Medicine,
University of Toronto, Medical Sciences Building, Toronto,
Ontario, M5S 1A8, Canada.
SOURCE: GENOMICS, (1999 Feb 15) 56 (1) 12-21.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF118265; GENBANK-AF118266; GENBANK-AF118670
ENTRY MONTH: 199905
ENTRY DATE: Entered STN: 19990517
Last Updated on STN: 20000303
Entered Medline: 19990505

AB We have discovered three novel human genes, GPR34, GPR44, and GPR45, encoding family A G-protein-coupled receptors (GPCRs). The receptor encoded by GPR34 is most similar to the P2Y receptor subfamily, while the receptor encoded by GPR44 is most similar to chemoattractant receptors. The receptor encoded by GPR45 is the mammalian orthologue of a putative lysophosphatidic acid receptor from *Xenopus laevis*. Partial sequence of GPR34 was discovered during a search of the GenBank database of **expressed** sequence tags (**ESTs**). This sequence information was used both to isolate the full-length translational open reading frame from a human genomic library and to assemble a contig from additional GPR34 **EST cDNAs**. Northern blot and in situ hybridization analyses revealed GPR34

mRNA transcripts in several human and rat **brain** regions. Also, we used polymerase chain reaction (PCR) to amplify human genomic DNA using degenerate oligonucleotides designed from sequences encoding transmembrane domains 3 and 7 of opioid and somatostatin receptors. Two PCR products partially encoding novel GPCRs, named GPR44 and GPR45, were discovered and used to isolate the full-length translational open reading frames from a human genomic library. Both

GPR44

and GPR45 are **expressed** in the central nervous system and periphery. For chromosomal localization, fluorescence in situ hybridization analysis was performed to assign GPR34 to chromosomes 4p12 and Xp11. 3, GPR44 to chromosome 11q12-q13.3, and GPR45 to chromosome 2q11. 1-q12.

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L14 ANSWER 34 OF 67 MEDLINE

ACCESSION NUMBER: 1999132385 MEDLINE

DOCUMENT NUMBER: 99132385 PubMed ID: 9931487

TITLE: Identification and cloning of three novel human G protein-coupled receptor genes GPR52, PsiGPR53 and GPR55: GPR55 is extensively expressed in human brain.

AUTHOR: Sawzdargo M; Nguyen T; Lee D K; Lynch K R; Cheng R; Heng H H; George S R; O'Dowd B F

CORPORATE SOURCE: Department of Pharmacology, University of Toronto, Medical Sciences Building, Toronto, Ontario, Canada, USA.

SOURCE: BRAIN RESEARCH. MOLECULAR BRAIN RESEARCH, (1999 Feb 5) 64 (2) 193-8.

Journal code: 8908640. ISSN: 0169-328X.

PUB. COUNTRY: Netherlands

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AF096784; GENBANK-AF096785; GENBANK-AF096786;

GENBANK-AF100789

ENTRY MONTH: 199903

ENTRY DATE: Entered STN: 19990326

Last Updated on STN: 20000303

Entered Medline: 19990312

AB The G **protein**-coupled receptor (GPCR) family share a structural motif of seven transmembrane segments with large numbers of conserved residues in those regions. Here, we report the identification and cloning of two novel human intronless GPCR genes, GPR52, GPR55 and a pseudogene PsiGPR53. GPR55 was identified from the **expressed** sequence tags (**EST**) **database** whereas GPR52 and pseudogene PsiGPR53 originated from the high throughput genome (HTG) **database**. A partial **cDNA** clone obtained from the IMAGE Consortium of GPR55 was used to screen a human genomic library to acquire the full length gene. GPR52 and PsiGPR53 were amplified from human genomic DNA using primers based on the HTG sequences. GPR55 and GPR52 encode receptors of 319 and 361 amino acids, respectively. GPR55 gene was mapped to chromosome

2q37, using fluorescence in situ hybridization (FISH), and its **mRNA transcripts** have been detected in the caudate nucleus and putamen, but not in five other **brain** regions. Human receptors showing the highest amino acid identity to GPR55 include P2Y5 (29%), GPR23 (30%), GPR35 (27%) and CCR4 (23%). GPR52 gene localized to chromosome 1q24 shares the highest identity with GPR21 (71%), histamine

H2

(27%) and 5-HT4 (26%) human receptors. PsiGPR53 is a pseudogene mapped to chromosome 6p21 that demonstrates the highest similarity to the MRG

(35%),

MAS (28%) and C5a (24%) human receptor genes.
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L14 ANSWER 35 OF 67 MEDLINE

ACCESSION NUMBER: 1998342085 MEDLINE
DOCUMENT NUMBER: 98342085 PubMed ID: 9675132
TITLE: JH8, a gene highly homologous to the mouse jerky gene,
maps
to the region for childhood absence epilepsy on 8q24.
COMMENT: Erratum in: Biochem Biophys Res Commun 1998 Sep
18;250(2):536
AUTHOR: Morita R; Miyazaki E; Fong C Y; Chen X N; Korenberg J R;
Delgado-Escueta A V; Yamakawa K
CORPORATE SOURCE: Brain Science Institute, The Institute of Physical and
Chemical Research (RIKEN), 2-1 Hirosawa, Wako-shi,
Saitama,
351-0198, Japan.
CONTRACT NUMBER: 5P01-NS21908 (NINDS)
PO1 HD17449 (NICHD)
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1998
Jul 20) 248 (2) 307-14.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF072467; GENBANK-AF072468; GENBANK-AF072469
ENTRY MONTH: 199808
ENTRY DATE: Entered STN: 19980903
Last Updated on STN: 20000303
Entered Medline: 19980827

AB Insertional inactivation of the jerky gene in transgenic mice resulted
epileptic seizures, suggesting that the jerky gene was responsible for
mouse epilepsy. To isolate a human homologue of the jerky gene, we
screened an **Expressed Sequence Tag (EST)**
database using the **cdna** sequence of the mouse jerky gene
and identified several **EST** clones which contained homologous
sequences to mouse jerky gene. Using a clone which showed highest
homology
as a probe, we isolated **cdna** clones from a human fetal
brain cdna library. Sequence analysis of these clones
named JH8 (jerky homologue of Human on chromosome 8) indicated that it
encoded a putative **protein** with 520 amino acid residues. The JH8
gene has 77% identity to the mouse jerky gene at the DNA level, and its
protein has 76% identity and 84% similarity to the mouse
protein at the amino acid level. Northern blot analysis showed
that the JH8 gene is **expressed** ubiquitously with a major
transcript of about 9.5 kb in size. Fluorescence in situ
Hybridization (FISH) analysis and radiation hybrid panel mapping revealed
that the JH8 gene was located on chromosome band 8q24.3 in a region that
was syntenic to mouse chromosome 15, the mapping site of the mouse jerky
gene. Childhood Absence Epilepsy (CAE), one type of Idiopathic
Generalized
Epilepsy (IGE), has been mapped to chromosome 8q24.3 by linkage analysis.
These results suggest that JH8 is a strong candidate gene for CAE.
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L14 ANSWER 36 OF 67 MEDLINE

ACCESSION NUMBER: 1998248992 MEDLINE
DOCUMENT NUMBER: 98248992 PubMed ID: 9587421
TITLE: Identification of a novel human glutathione S-transferase

using bioinformatics.

AUTHOR: Liu S; Stoesz S P; Pickett C B
 CORPORATE SOURCE: Schering-Plough Research Institute, Kenilworth, New Jersey
 07033, USA.
 SOURCE: ARCHIVES OF BIOCHEMISTRY AND BIOPHYSICS, (1998 Apr 15) 352
 (2) 306-13.
 Journal code: 0372430. ISSN: 0003-9861.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF025887
 ENTRY MONTH: 199806
 ENTRY DATE: Entered STN: 19980611
 Last Updated on STN: 19980611
 Entered Medline: 19980603

AB In searching the **expressed** sequence tag (**EST**) data-base of GenBank with coding sequences of 11 known human glutathione S-transferases in conjunction with bioinformatic analysis, we have identified five **ESTs** that encode a new human glutathione S-transferase (GST) designated GST A4. The **cdna** clone (I.M.A.G.E. Consortium **cdna** Clone ID 515157) had an insert length of 1279 bp and contains an open reading frame of 666 bp, which encodes a **protein** of 222 amino acid residues. The GST A4 **protein** is identical in length to human GST A1 and A2 and is 54% identical to human GST A1 and A2. Sequence comparison with other human GSTs suggests that it is a new GST belonging to the alpha class GSTs. Northern blot analysis and **EST database** searches have demonstrated that the GST A4 **mRNA** is **expressed** at a high level in **brain**, placenta, and skeletal muscle and much lower in **lung** and liver. Analysis of the sequence tagged site (STS) **database** indicated that the GST A4 gene is located on chromosome 6. This STS represents a previously unidentified **transcript** further confirming the novelty of the new sequence.

L14 ANSWER 37 OF 67 MEDLINE
 ACCESSION NUMBER: 1998234549 MEDLINE
 DOCUMENT NUMBER: 98234549 PubMed ID: 9570954
 TITLE: Identification, characterization, and genetic mapping of Rad51d, a new mouse and human RAD51/RecA-related gene.
 AUTHOR: Pittman D L; Weinberg L R; Schimenti J C
 CORPORATE SOURCE: Jackson Laboratory, Bar Harbor, Maine 04609, USA.
 CONTRACT NUMBER: CA34196 (NCI)
 GM45415 (NIGMS)
 HD07065 (NICHD)

SOURCE: GENOMICS, (1998 Apr 1) 49 (1) 103-11.
 Journal code: 8800135. ISSN: 0888-7543.

PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF034955; GENBANK-AF034956
 ENTRY MONTH: 199806
 ENTRY DATE: Entered STN: 19980708
 Last Updated on STN: 19980708
 Entered Medline: 19980625

AB Homologous DNA recombination occurs in all organisms and is important for repair of DNA damage during mitosis. One of the critical genes for DNA repair and meiotic recombination in yeast is RAD51, and homologs of RAD51 have been identified in several species, including mouse and human. Here

we describe a new RAD51-related mammalian gene, named Rad51d, identified by searching the **EST database** with the yeast RAD55 and human RAD51B/REC2 genes. A full-length 1.5-kb mouse **cDNA** clone that encodes a predicted 329-amino-acid **protein** was isolated. Rad51d **mRNA** was present in every mouse tissue examined. Four different **transcript** sizes were detected, one of which was specific to **testis**. Human **cDNA** clones that predicted 71% amino acid identity to the mouse **protein** were also isolated. Interestingly, the sequences of these human clones and of RT-PCR-derived products provided evidence for alternative splicing. These **mRNAs** are predicted to encode **proteins** that are truncated relative to the mouse and lack the ATP-binding motif characteristic of RecA-related **proteins**. Using an interspecific backcross mapping panel, Rad51d was mapped to mouse Chromosome 11, 48.5 cM from the centromere. By radiation hybrid mapping, the human ortholog RAD51D was mapped to chromosome 17q11, which is a region syntenic to mouse Chromosome 11. Due to its **expression** pattern and sequence similarity to other RAD51 family members, it is likely that Rad51d is part of a complex of **proteins** required for DNA repair and meiotic recombination.

L14 ANSWER 38 OF 67 MEDLINE

ACCESSION NUMBER: 1998234542 MEDLINE

DOCUMENT NUMBER: 98234542 PubMed ID: 9570947

TITLE: Divergently transcribed overlapping genes expressed in liver and kidney and located in the 11p15.5 imprinted domain.

AUTHOR: Cooper P R; Smilinich N J; Day C D; Nowak N J; Reid L H; Pearsall R S; Reece M; Prawitt D; Landers J; Housman D E; Winterpacht A; Zabel B U; Pelletier J; Weissman B E; Shows T B; Higgins M J

CORPORATE SOURCE: Department of Human Genetics, Roswell Park Cancer Institute, Buffalo, New York 14263, USA.

CONTRACT NUMBER: CA63176 (NCI)
CA63333 (NCI)
HG00333 (NHGRI)

SOURCE: GENOMICS, (1998 Apr 1) 49 (1) 38-51.
Journal code: 8800135. ISSN: 0888-7543.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AC001228; GENBANK-AF087428

ENTRY MONTH: 199806

ENTRY DATE: Entered STN: 19980708

Last Updated on STN: 20000512

Entered Medline: 19980625

AB Human chromosomal band 11p15.5 has been shown to contain genes involved in

the development of several pediatric and adult tumors and in Beckwith-Wiedemann syndrome (BWS). Overlapping P1 artificial chromosome clones from this region have been used as templates for genomic sequencing

in an effort to identify candidate genes for these disorders. PowerBLAST identified several matches with **expressed** sequence tags (**ESTs**) from fetal **brain** and liver **cDNA** libraries. Northern blot analysis indicated that two of the genes identified by these **ESTs** encode **transcripts** of 1-1.5 kb with predominant **expression** in fetal and adult liver and **kidney**. With RT-PCR and RACE, full-length **transcripts** were isolated for these two genes, with the largest open reading frames encoding putative **proteins** of 253 and 424 amino acids.

Database comparison of the predicted amino acid sequence of the larger **transcript** indicated homology to integral membrane organic cation transporters; hence, we designate this gene ORCTL2 (organic cation transporter-like 2). An **expressed** sequence polymorphism provided evidence that the ORCTL2 gene exhibits "leaky" imprinting in both human fetal **kidney** and human fetal liver. The mouse orthologue (Orctl2) was identified, and a similar polymorphism was used to demonstrate maternal-specific **expression** of this gene in fetal liver from interspecific F1 mice. The predicted **protein** of the smaller gene showed no significant similarity in the **database**. Northern and RACE analyses suggest that this gene may have multiple **transcription** start sites. Determination of the genomic structure in humans indicated that the 5'-end of this **transcript** overlaps in divergent orientation with the first two exons of ORCTL2, suggesting a possible role for antisense regulation of one gene by the other. We, therefore, provisionally name this second **transcript** ORCTL2S (ORCTL2-antisense). The **expression** patterns of these genes and the imprinted **expression** of ORCTL2 are suggestive of a possible role in the development of Wilms tumor (WT) and hepatoblastoma. Although SSCP analysis of 62 WT samples and 10 BWS patients did not result in the identification of any mutations in ORCTL2 or ORCTL2S, it will be important to examine their **expression** pattern in tumors and BWS patients, since epigenetic alteration at these loci may play a role in the etiology of these diseases.

L14 ANSWER 39 OF 67 MEDLINE
 ACCESSION NUMBER: 1998201609 MEDLINE
 DOCUMENT NUMBER: 98201609 PubMed ID: 9524256
 TITLE: A novel 52 kDa protein induces apoptosis and concurrently activates c-Jun N-terminal kinase 1 (JNK1) in mouse C3H10T1/2 fibroblasts.
 AUTHOR: Sun L; Liu Y; Fremont M; Schwarz S; Siegmann M; Matthies R;
 Jost J P
 CORPORATE SOURCE: Friedrich Miescher Institute, Basel, Switzerland.
 SOURCE: GENE, (1998 Feb 27) 208 (2) 157-66.
 Journal code: 7706761. ISSN: 0378-1119.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF029071
 ENTRY MONTH: 199805
 ENTRY DATE: Entered STN: 19980514
 Last Updated on STN: 20000303
 Entered Medline: 19980504

AB A 52 kDa **protein** (p52) was purified from chicken embryos and its corresponding **cDNA** was cloned. The p52 **cDNA** is 1768 bp long and has an open reading frame of 465 amino acids. The sequence of the p52 **cDNA** shows significant homology with mouse and human **cDNAs** from the **EST database**, so do the deduced amino acid sequences, indicating the existence of human and mouse homologues of p52. Northern blot hybridization showed that the p52 **mRNA** was **expressed** in a wide range of embryonic and adult tissues. There was more p52 **mRNA** in embryonic **heart** and liver than in the **brain** or muscle. The adult **testis** had the highest level of p52 **mRNA**, whereas adult

liver had the lowest. **Expression** of p52 in mouse C3H10T1/2 fibroblasts caused apoptotic cell death, upregulation of **transcription** factor c-Jun and activation of c-Jun N-terminal kinase 1 (JNK1). In addition, **expression** of Bcl-2, but not of the dominant negative mutant JNK1, can block the p52-mediated apoptosis. These results indicate that p52 may represent a new cell-death **protein** inducing apoptosis and activating JNK1 through different pathways.

L14 ANSWER 40 OF 67 MEDLINE

ACCESSION NUMBER: 1998158621 MEDLINE

DOCUMENT NUMBER: 98158621 PubMed ID: 9490669

TITLE: Molecular cloning of translocation t(1;14)(q21;q32) defines

a novel gene (BCL9) at chromosome 1q21.

AUTHOR: Willis T G; Zalcberg I R; Coignet L J; Wlodarska I; Stul M;

Jadayel D M; Bastard C; Treleaven J G; Catovsky D; Silva M L; Dyer M J

CORPORATE SOURCE: Academic Department of Haematology and Cytogenetics, Institute of Cancer Research, Haddow Laboratories, Sutton, Surrey, UK.

SOURCE: BLOOD, (1998 Mar 15) 91 (6) 1873-81.
Journal code: 7603509. ISSN: 0006-4971.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals

ENTRY MONTH: 199804

ENTRY DATE: Entered STN: 19980416
Last Updated on STN: 19980416
Entered Medline: 19980409

AB Abnormalities of chromosome 1q21 are common in B-cell malignancies and have been associated with a poor response to therapy. The nature of the involved gene(s) on chromosome 1q21 remains unknown. A cell line (CEMO-1) has recently been established from a patient with precursor-B-cell acute lymphoblastic leukemia (ALL), which exhibited a t(1;14)(q21;q32). To identify the gene involved in this translocation, we have cloned both rearranged IGHJ alleles using long-distance inverse polymerase chain reaction (LDI-PCR). Two IGHJ fragments were amplified from CEMO-1 DNA and sequenced. One allele showed novel sequences upstream of JH5 with no homology to either IGH or any other sequences on the **databases**. Using a single-copy Xho I fragment immediately 5' of JH5, PAC clones were isolated and mapped to chromosome 1q21 on normal metaphases by fluorescence in situ hybridization (FISH), confirming that this allele represented the t(1;14)(q21;q32) breakpoint. Sequence analysis of the

1q21

Xho I fragment showed identity with an **expressed** sequence tag (**EST**), and this probe was therefore used to probe Northern blots. Two **transcripts** of 6.3 kb and 4.2 kb **expressed** at low level in **mRNA** from all tissues were detected: a third **transcript** of 1.6 kb was **expressed** only in thymus, spleen, and small intestine. Full-length BCL9 **cDNA** clones were obtained from a normal human fetal **brain cDNA** library supplemented by 5' and 3' RACE. Sequence analysis predicted a **protein** of 1394 amino acids containing 18% proline, 11% glycine, 11% serine, and 6% methionine, but no recognizable **protein** motifs or significant homologies to any other known **proteins**. The CEMO-1 1q21 breakpoint fell within the 3' UTR of the BCL9 gene. Low-level **expression** of BCL9 was detected in Epstein-Barr virus-transformed normal B cells by Northern blot; in contrast, abundant

BCL9 **expression** was observed in CEMO-1, indicating that deregulated **expression** of this gene was one pathological consequence of the translocation. Screening of a panel of 39 B-cell malignancies with 1q abnormalities by Southern blot showed one additional case with a breakpoint in the 3' UTR of BCL9, indicating that this was a recurrent breakpoint. FISH analysis using an 850-kb YAC spanning BCL9 identified a further case with t(1;22)(q21;q11) causing juxtaposition of BCL9 to the IGLambda locus. Other breakpoints were heterogeneous, falling both centromeric (10 cases) and telomeric (10 cases) of the BCL9 gene. These data suggest that BCL9 may be the target of translocation in some B-cell malignancies with abnormalities of 1q21 and that deregulated BCL9 **expression** may be important in their pathogenesis.

L14 ANSWER 41 OF 67 MEDLINE

ACCESSION NUMBER: 1998149982 MEDLINE
DOCUMENT NUMBER: 98149982 PubMed ID: 9480748
TITLE: **FACL4**, a new gene encoding long-chain acyl-CoA synthetase 4, is deleted in a family with Alport syndrome, elliptocytosis, and mental retardation.
AUTHOR: Piccini M; Vitelli F; Bruttini M; Pober B R; Jonsson J J; Villanova M; Zollo M; Borsani G; Ballabio A; Renieri A
CORPORATE SOURCE: Genetica Medica, Policlinco le Scotte, 53100 Siena, Italy.
SOURCE: GENOMICS, (1998 Feb 1) 47 (3) 350-8.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-Y12777; GENBANK-Y13058
ENTRY MONTH: 199804
ENTRY DATE: Entered STN: 19980416
Last Updated on STN: 19980416
Entered Medline: 19980408

AB We observed a family in which two boys were diagnosed with Alport syndrome, elliptocytosis, and mental retardation and carried a large deletion of the Xq22.3-q23 region, encompassing the COL4A5 gene. This suggests the possibility of a new contiguous gene syndrome. In an attempt to characterize the genes contributing to this complex phenotype, we have isolated a gene encoding a new long-chain acyl-CoA synthetase (**FACL4** or **LACS4**) from the region deleted in these patients. Among several **ESTs** identified by searching the human gene map **database** maintained at the National Center for Biotechnology Information, using the map position as a query, only one was deleted in the patients. RACE products containing the entire ORF were subsequently generated. Northern blot analysis showed a 5-kb **mRNA expressed** in several tissues except for liver and lung. **Brain** shows a longer **transcript**, possibly reflecting the use of a **brain-specific** upstream ATG start codon. **FACL4** encodes a predicted **protein** product of 670 amino acids (711 in **brain**), with a remarkable level of conservation compared to the rat acyl-CoA synthetases **ACS4** and **brain-specific ACS3 protein** sequences. We are investigating the possibility that the absence of this enzyme may play a role in the development of mental retardation or other signs associated with Alport syndrome in the family.
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L14 ANSWER 42 OF 67 MEDLINE

ACCESSION NUMBER: 1998136197 MEDLINE
DOCUMENT NUMBER: 98136197 PubMed ID: 9469824

TITLE: Isolation and characterization of RAD51C, a new human member of the RAD51 family of related genes.
 AUTHOR: Dosanjh M K; Collins D W; Fan W; Lennon G G; Albala J S; Shen Z; Schild D
 CORPORATE SOURCE: Life Sciences Division, Lawrence Berkeley National Laboratory, Berkeley, CA 94720, USA.
 CONTRACT NUMBER: ES08353 (NIEHS)
 GM30990 (NIGMS)
 SOURCE: NUCLEIC ACIDS RESEARCH, (1998 Mar 1) 26 (5) 1179-84.
 Journal code: 0411011. ISSN: 0305-1048.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF029669; GENBANK-AF029670
 ENTRY MONTH: 199804
 ENTRY DATE: Entered STN: 19980410
 Last Updated on STN: 19980410
 Entered Medline: 19980402

AB The yeast and human RAD51 genes encode strand-transfer **proteins** that are thought to be involved in both recombinational repair of DNA damage and meiotic recombination. In yeast, the Rad51 family of related **proteins** also includes Rad55, Rad57 and Dmc1. In mammalian cells, five genes in this family have been identified (HsRAD51, XRCC2, XRCC3, RAD51B/hREC2 and HsDMC1), and here we report the isolation of the sixth member, RAD51C. RAD51C was originally identified by a computer screen of the **EST database**. A full-length approximately 1.3 kb **cDNA** clone has been isolated that encodes a **protein** of 376 aa, having a 18-26% aa identity with other human Rad51 family members.
 RAD51C includes a previously mapped sequenced-tagged site location near the end of chromosome 17q. The RAD51C **transcript** is **expressed** in various human tissues, with highest level of **expression** in **testis**, followed by **heart** muscle, spleen and **prostate**. Yeast two-hybrid experiments indicate that the Rad51C **protein** binds to two other members of the Rad51 **protein** family (Xrcc3 and Rad51B) but not to itself. These findings suggest that Rad51C may function similarly to the yeast Rad55 or Rad57 **proteins**, rather than as a Rad51 functional homolog.

L14 ANSWER 43 OF 67 MEDLINE
 ACCESSION NUMBER: 1998126432 MEDLINE
 DOCUMENT NUMBER: 98126432 PubMed ID: 9465292
 TITLE: An expressed-sequence-tag database of the human prostate: sequence analysis of 1168 cDNA clones.
 AUTHOR: Nelson P S; Ng W L; Schummer M; True L D; Liu A Y; Bumgarner R E; Ferguson C; Dimak A; Hood L
 CORPORATE SOURCE: Department of Molecular Biotechnology, University of Washington, Seattle 98195, USA.. psnels@u.washington.edu
 SOURCE: GENOMICS, (1998 Jan 1) 47 (1) 12-25.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AA447269; GENBANK-AA447270; GENBANK-AA447271;
 GENBANK-AA447272; GENBANK-AA447273; GENBANK-AA447274;
 GENBANK-AA447275; GENBANK-AA447276; GENBANK-AA447277;
 GENBANK-AA447278; GENBANK-AA447279; GENBANK-AA447280;
 GENBANK-AA447281; GENBANK-AA447282; GENBANK-AA447283;

GENBANK-AA447284; GENBANK-AA447285; GENBANK-AA447286;
GENBANK-AA447287; GENBANK-AA447288; GENBANK-AA447289;
GENBANK-AA447290; GENBANK-AA447291; GENBANK-AA447292;
GENBANK-AA447293; GENBANK-AA447294; GENBANK-AA447295;
GENBANK-AA447296; GENBANK-AA447297; GENBANK-AA447298; +

ENTRY MONTH:

199804

ENTRY DATE:

Entered STN: 19980430

Last Updated on STN: 19980430

Entered Medline: 19980420

AB The human **prostate** is a complex glandular organ with functional development under hormonal regulation. Diseases of the **prostate** result in significant morbidity and mortality in the form of benign prostatic hypertrophy and **prostate** adenocarcinoma. The characterization of the molecular framework of the human **prostate** at the level of **expressed** genes will facilitate the understanding of normal and pathological **prostate** biology. The purposes of this study were to acquire an initial assessment of the qualitative and quantitative diversity of gene **expression** in the normal human **prostate** and to determine the extent that genes with **prostate**-restricted **expression** can be assessed using an **expressed** sequence tag approach. We have constructed a directional **cDNA** library from normal adult human **prostate** tissue and partially sequenced the 5' end of 1168 randomly selected **cDNA** clones, resulting in more than 400 kb of DNA sequence. Homology searches of the sequenced **cDNAs** against the GenBank and dbEST **databases** revealed that 43% of the sequences are identical to human genes whose functions are known, 5% are similar but not identical to known genes in humans or lower organisms, 5% match the mitochondrial genome, 9% are composed of interspersed DNA repeats, 30% are homologous to sequences in the dbEST **database** without a described function, and 6% are novel sequences. A total of 780 distinct species were identified. In addition to the 74 novel **transcripts**, 4 genes, **prostate**-specific antigen (PSA), **prostate** secretory protein (PSP), **prostate** acid phosphatase (PAP), and human glandular kallekrein 2 (HK2), have no homologous sequences in the **databases** that originate from sources other than **prostate** and thus may represent genes with **prostate**-restricted **expression**. Sequences matching PSA, PSP, and PAP each accounted for > 1% of the total **ESTs** and represent highly abundant **transcripts**, correlating with the abundance of these **proteins** in the **prostate** gland. No novel **transcripts** were represented by more than one **EST** and thus are **expressed** at levels much lower than the known **prostate**-specific genes.

L14 ANSWER 44 OF 67

MEDLINE

ACCESSION NUMBER: 1998121324 MEDLINE

DOCUMENT NUMBER: 98121324 PubMed ID: 9461426

TITLE: Molecular cloning and characterization of a highly conserved human 67-kDa laminin receptor pseudogene mapping to Xq21.3.

AUTHOR: Richardson M P; Braybrook C; Tham M; Moore G E; Stanier P

CORPORATE SOURCE: Molecular Biology Laboratory, Institute of Obstetrics and Gynaecology, Queen Charlotte's and Chelsea Hospital, London, UK.

SOURCE: GENE, (1998 Jan 5) 206 (1) 145-50.

Journal code: 7706761. ISSN: 0378-1119.

PUB. COUNTRY: Netherlands

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199802
ENTRY DATE: Entered STN: 19980306
Last Updated on STN: 19980306
Entered Medline: 19980226

AB A highly conserved laminin receptor processed pseudogene (LAMRL5) that has been isolated from a fetal **brain cDNA** library is described. The pseudogene is a complete copy (97.9% identical) of the **transcribed** laminin receptor (LAMR1) with all the introns precisely removed. The sequence has direct repeats of 18 bp at either end. It has an 885 nucleotide open reading frame from the start methionine codon to the stop codon that contains no deletions, additions or premature stop codons relative to the **expressed** LAMR1 gene and has the coding potential for a **protein** of 295 amino acids. Although TATA and CAAT boxes exist in the region 5' to the open reading frame and a polyadenylation signal is present in the 3' region, no evidence could be obtained either by reverse **transcriptase**-polymerase chain reaction (RT-PCR) or in the **expressed** sequence tag (**EST**) **database** that LAMRL5 is **expressed** in vivo. If not **expressed**, it is estimated that this LAMRL5 pseudogene was incorporated into the human genome approximately 3.5-5 million years ago.

L14 ANSWER 45 OF 67 MEDLINE

ACCESSION NUMBER: 1998110580 MEDLINE
DOCUMENT NUMBER: 98110580 PubMed ID: 9441748
TITLE: Analysis of a human gene homologous to rat ventral prostate.1 protein.
AUTHOR: Peacock R E; Keen T J; Inglehearn C F
CORPORATE SOURCE: Molecular Medicine Unit, St James University Hospital, Leeds, United Kingdom.
SOURCE: GENOMICS, (1997 Dec 15) 46 (3) 443-9.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF007189
ENTRY MONTH: 199803
ENTRY DATE: Entered STN: 19980319
Last Updated on STN: 19980319
Entered Medline: 19980309

AB We report on the analysis of a human gene homologous to the rat ventral **prostate.1 protein** (RVP.1), which is **transcriptionally** induced in the regressing rat **prostate** after castration. **EST database** searching and Northern blotting reveal that this is one of at least four different members of a gene family in the human genome that produce **transcripts** of 3.4, 2.4, 1.9, and 1.2 kb, **expressed** in a wide range of tissues. Three other members of this gene family have already been mapped to chromosomes 7q, 17p, and 22q and reported either as anonymous **ESTs** or as full-length clones. We have now characterized a fourth member (assigned the gene now characterized a fourth member (assigned the gene name C7orf1 by GDB) and localized it also to chromosome 7q. C7orf1 is almost identical over much of its length to the reported ORF of RVP.1 while the other family members are more divergent from RVP.1. The genomic sequence of C7orf1 is intron-less, is spanned by a CpG low-methylation island, and has two noncoding, nonpolymorphic STR regions immediately adjacent to the open reading frame, one 5' and one 3'. The presence of a NotI restriction site in the coding sequence results in a deficiency in

the IMAGE **cDNA** libraries, as a result of which the 3' end of the gene is not in the **EST databases**. The putative 220-amino-acid **protein** shows 89% identity to the amino terminus of rat RVP.1. Like rat RVP.1, it has four hydrophobic potential membrane-spanning regions, but it lacks 60 amino acid residues at its carboxyl terminus relative to rat RVP.1. Nevertheless, gene-specific primers from this **transcript** amplified a product in human **cDNAs** from several different tissues; its size corresponds to the 1.2-kb **transcript** seen on a Northern blot, and identical **ESTs** from several different tissues exist in the **databases**. It therefore seems likely that C7orf1 is the closest human homologue of rat RVP.1.

L14 ANSWER 46 OF 67 MEDLINE
 ACCESSION NUMBER: 1998035876 MEDLINE
 DOCUMENT NUMBER: 98035876 PubMed ID: 9367677
 TITLE: Identification and characterization of BRDT: A testis-specific gene related to the bromodomain genes RING3 and Drosophila fsh.
 AUTHOR: Jones M H; Numata M; Shimane M
 CORPORATE SOURCE: Chugai Research Institute for Molecular Medicine, 153-2 Nagai, Niihari, Ibaraki, 300-41, Japan.
 SOURCE: GENOMICS, (1997 Nov 1) 45 (3) 529-34.
 PUB. COUNTRY: Journal code: 8800135. ISSN: 0888-7543.
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF019085
 ENTRY MONTH: 199801
 ENTRY DATE: Entered STN: 19980129
 Last Updated on STN: 20020420
 Entered Medline: 19980113
 AB The RING3 gene encodes a 90-kDa mitogen-activated nuclear **protein**. In proliferating cells, including in leukemia, RING3 has serine-threonine kinase and autophosphorylation activities. The cloning of D26362, a gene closely related to RING3, suggests a gene family. RING3 and D26362 are also related to the Drosophila developmental gene fsh. A **database** search for further members of the RING3 family identified an **EST** derived from a **testis**-specific library. **cDNA** clones representing the full coding sequence of the gene were isolated. The gene encodes a **protein** of 947 amino acids with extensive homology to RING3, D26362, and fsh. Similar to these **proteins**, it possesses two bromodomain motifs and a PEST sequence. Northern analysis of 16 normal tissues and eight cancer cell lines shows **transcripts** of 3.5 and 4.0 kb **expressed** specifically in **testis**. The gene has been named BRDT (for bromodomain, **testis** specific). PCR analysis of a panel of monochromosomal human/rodent hybrid cell lines and the GeneBridge 4 panel of radiation hybrids localizes the gene to chromosome 1p between markers WI-7719 and WI-3099 (D1S2154).
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L14 ANSWER 47 OF 67 MEDLINE
 ACCESSION NUMBER: 1998004295 MEDLINE
 DOCUMENT NUMBER: 98004295 PubMed ID: 9346309
 TITLE: Characterisation of macrophage inflammatory protein-5/human

CC cytokine-2, a member of the macrophage-inflammatory-protein family of chemokines.

AUTHOR: Coulin F; Power C A; Alouani S; Peitsch M C; Schroeder J M;
Moshizuki M; Clark-Lewis I; Wells T N

CORPORATE SOURCE: Geneva Biomedical Research Institute, Switzerland.

SOURCE: EUROPEAN JOURNAL OF BIOCHEMISTRY, (1997 Sep 1) 248 (2) 507-15.
Journal code: 0107600. ISSN: 0014-2956.

PUB. COUNTRY: GERMANY: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-Z70293; SWISSPROT-Q16663

ENTRY MONTH: 199711

ENTRY DATE: Entered STN: 19971224
Last Updated on STN: 19971224
Entered Medline: 19971121

AB A human monocyte-activating CC chemokine has been identified based on sequences in an **expressed** sequence tag (**EST**) **cdna database**. The **protein** shows highest sequence identity to the macrophage inflammatory **protein** (MIP) group of chemokines, particularly MIP-3 (76.7%) and MIP-1alpha (75.4%), and has been named MIP-5. Model building confirms that the **protein** has a similar three dimensional structure to other chemokines, but has an additional third disulphide bond. Northern blot analysis and reverse-**transcriptase** PCR show that the **mRNA** for MIP-5 is **expressed** at a high levels in liver, intestine and in lung leukocytes. MIP-5 induces chemotaxis of human monocytes, T-lymphocytes and, to a lesser degree, eosinophils at nanomolar concentrations; it has no effect on neutrophil migration. In receptor-binding assays, MIP-5 shows

IC50 values of 12 nM for competition with 125I-MIP-1alpha for binding to CC-chemokine receptor (CCR)1, and 2.5 nM for competition with 125I-MCP-3 for binding to CCR3. It shows no ability to compete with ligand for binding to the two interleukin (IL)-8 receptors (CXC-chemokine receptors

1 and 2) or to CCR2, CCR4 or CCR5. Consistent with this binding data, MIP-5 was only able to induce calcium fluxes in CHO cells stably transfected with CCR1 or CCR3.

L14 ANSWER 48 OF 67 MEDLINE

ACCESSION NUMBER: 97446139 MEDLINE

DOCUMENT NUMBER: 97446139 PubMed ID: 9299237

TITLE: Gene structure and subcellular localization of FMR2, a member of a new family of putative transcription activators.

AUTHOR: Gecz J; Bielby S; Sutherland G R; Mulley J C

CORPORATE SOURCE: Department of Cytogenetics and Molecular Genetics, Women's and Children's Hospital, Adelaide, SA 5006, Australia..
jgecz@mad.adelaide.edu.au

SOURCE: GENOMICS, (1997 Sep 1) 44 (2) 201-13.
Journal code: 8800135. ISSN: 0888-7543.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AF012603; GENBANK-AF012604; GENBANK-AF012605;
GENBANK-AF012606; GENBANK-AF012607; GENBANK-AF012608;
GENBANK-AF012609; GENBANK-AF012610; GENBANK-AF012611;
GENBANK-AF012612; GENBANK-AF012613; GENBANK-AF012614;

GENBANK-AF012615; GENBANK-AF012616; GENBANK-AF012617;
GENBANK-AF012618; GENBANK-AF012619; GENBANK-AF012620;
GENBANK-AF012621; GENBANK-AF012622; GENBANK-AF012623;
GENBANK-AF012624; GENBANK-AF012625; GENBANK-AF012626;
GENBANK-U48436

ENTRY MONTH: 199712
ENTRY DATE: Entered STN: 19980109
Last Updated on STN: 20000303
Entered Medline: 19971208

AB FMR2 is the gene associated with FRAXE mental retardation. It is expressed as an 8.7-kb transcript in placenta and adult brain. A fetal-specific FMR2 transcript of approximately 12 kb was detected in fetal brain and at a lower level in fetal lung and kidney. FMR2 is a large gene composed of 22 exons spanning at least 500 kb on Xq28. Alternative splicing involving exons 2, 3, 5, 7, and 21 was not tissue specific as tested on mRNA from human fetal and infant brain. FMR2 is translated into a 1311-amino-acid nuclear protein with putative transcription transactivation potential. Subcellular localization studies with green fluorescent protein as a reporter show that both nuclear addresses found in the FMR2 sequence are functional and direct the FMR2 protein into the nucleus. FMR2 together with AF4 and LAF4 forms a new family of nuclear proteins with DNA-binding capacity and transcription transactivation potential. BLAST searches of the dbEST database revealed the presence of at least two other groups of nonoverlapping ESTs showing high similarity to the FMR2-related family of proteins. One of them, represented by the EST W26686, maps to chromosome 5q31. Amino acid similarity among the proteins encoded by members of the gene family is high in the NH2 terminus, low in the middle, and high again in the COOH end. Available information from members of the family shows that genomic organization is conserved. This FMR2-related gene family encodes nuclear proteins with involvement in mental retardation (FMR2), cancer (AF4), and lymphocyte differentiation (LAF4) or with unknown function (EST W26686 and/or AA025630).
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L14 ANSWER 49 OF 67 MEDLINE
ACCESSION NUMBER: 97306278 MEDLINE
DOCUMENT NUMBER: 97306278 PubMed ID: 9162095
TITLE: Cloning of a new human gene with short consensus repeats using the EST database.
AUTHOR: Nangaku M; Shankland S J; Kurokawa K; Bomsztyk K; Johnson R
J; Couser W G
CORPORATE SOURCE: Division of Nephrology, Box 356 521, University of Washington, Seattle, WA, USA.
CONTRACT NUMBER: DK02142 (NIDDK)
DK34198 (NIDDK)
DK43422 (NIDDK)
+
SOURCE: IMMUNOGENETICS, (1997) 46 (2) 99-103.
Journal code: 0420404. ISSN: 0093-7711.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199707
ENTRY DATE: Entered STN: 19970805
Last Updated on STN: 19970805
Entered Medline: 19970723

AB The complement system, which provides many of the effector functions of humoral immunity and inflammation, is tightly regulated by various complement regulatory **proteins**. The most common structural feature of these **proteins** is a motif called short consensus repeat (SCR). In order to identify a new human complement regulatory **protein**, we performed a similarity search using SCR on the **expressed** sequence tag (**EST**) **database** and found a partial sequence of a new human gene. Using a probe containing this partial sequence, we obtained a full-length **cDNA** of this gene from a human umbilical vein endothelial cell (HUVEC) library. The sequencing reaction demonstrated an open reading frame of 1383 nucleotides coding for a 461 amino acid polypeptide with a deduced relative molecular mass of 51 000. Structural analysis showed that the **protein** has three SCRs with one transmembrane domain. A characteristic feature of these SCR was that they have six conserved cysteines per repeat instead of the usual four. Therefore, we named this **cDNA** THECY (three hexa-cysteine motifs). A six cysteine motif is a characteristic feature of selectins. We used northern blot analysis to show that a 2.0 kilobase (kb) **transcript** was ubiquitously present in most organs studied, and the **mRNA** was most abundant in the **heart**. In conclusion, we discovered a member of a new class of membrane-bound SCR-containing molecules using the **EST database**. Utilization of the **EST database** may be useful in the search for other new immunological **proteins**. The function of this gene remains to be elucidated.

L14 ANSWER 50 OF 67 MEDLINE
 ACCESSION NUMBER: 97289529 MEDLINE
 DOCUMENT NUMBER: 97289529 PubMed ID: 9144434
 TITLE: **cDNA** cloning and tissue-specific expression of a novel basic helix-loop-helix/PAS protein (BMAL1) and identification of alternatively spliced variants with alternative translation initiation site usage.
 AUTHOR: Ikeda M; Nomura M
 CORPORATE SOURCE: Department of Physiology, Saitama Medical School, Moroyama, Japan.. mikeda@saitama-med.ac.jp
 SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1997 Apr 7) 233 (1) 258-64.
 Journal code: 0372516. ISSN: 0006-291X.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AB000812; GENBANK-AB000813; GENBANK-AB000814; GENBANK-AB000815; GENBANK-AB000816; GENBANK-D89722
 ENTRY MONTH: 199706
 ENTRY DATE: Entered STN: 19970612
 Last Updated on STN: 20000303
 Entered Medline: 19970605

AB Basic helix-loop-helix (bHLH)/PAS **proteins**, such as Sim, act as **transcriptional** factors, playing a critical role in the control of central nervous system (CNS) development. To isolate novel bHLH/PAS factors in the CNS an iterative search of a **database** for **expressed** sequence tags (**ESTs**) resulted in the location of several bHLH/PAS **protein**-like sequences. The rapid amplification of **cDNA** end (RACE) method was applied to isolate

full-length **cdnas** of these **ESTs**. Several 5' and 3' terminal sequences were isolated using primers derived from an **EST** from the human **brain cdna** library. The predicted novel factor polypeptide had bHLH and PAS domains that were highly homologous with those of Ah receptor nuclear translocator (Arnt) and Arnt2. Combination of the isolated **cdna** fragments revealed the existence of several alternatively spliced variants. The distribution of the novel bHLH/PAS factor message was analyzed by Northern blot hybridization. This detected only one **transcript**, which was 2.9 kb in size. Strong hybridization was found in the **brain**, skeletal muscle and **heart**. **Expression** of the novel bHLH/PAS factor, **brain** and muscle Arnt-like **protein 1** (BMAL1), was different from that of Arnt and Arnt2, suggesting that BMAL1 has a different function in the CNS and muscle than Arnt and Arnt2.

L14 ANSWER 51 OF 67 MEDLINE

ACCESSION NUMBER: 97186437 MEDLINE

DOCUMENT NUMBER: 97186437 PubMed ID: 9034012

TITLE: Novel transcribed sequences neighbouring a translocation breakpoint associated with schizophrenia.

AUTHOR: Devon R S; Evans K L; Maule J C; Christie S; Anderson S; Brown J; Shibasaki Y; Porteous D J; Brookes A J

CORPORATE SOURCE: MRC Human Genetics Unit, Western General Hospital, Edinburgh, United Kingdom.

SOURCE: AMERICAN JOURNAL OF MEDICAL GENETICS, (1997 Feb 21) 74 (1) 82-90.

Journal code: 7708900. ISSN: 0148-7299.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-UNKNOWN; SWISSPROT-UNKNOWN

ENTRY MONTH: 199704

ENTRY DATE: Entered STN: 19970507

Last Updated on STN: 19970507

Entered Medline: 19970430

AB A 1.3Mb chromosome 11-specific yeast artificial chromosome (YAC) that spans a t(1;11) translocation breakpoint associated with major psychosis has been used to enrich **cdnas** that are encoded within it and **expressed** in the human foetal **brain**. **Database** analysis of the selected fragments led to the identification of 54 clones matching alpha-tubulin, 4 fragments matching two anonymous human **expressed** sequence tags (**ESTs**) and 8 fragments giving no **database** matches. The clones matching alpha-tubulin led to the identification of a novel alpha-tubulin locus located approximately 250

kb

proximal to the translocation breakpoint. Extensive sequence and **expression** analysis of this locus suggests that this is a processed pseudogene, although a long open reading frame is maintained

and

the possibility that an abnormally acting **protein** may be **expressed** in a highly tissue or developmental specific manner cannot be discounted. The novel **cdna** fragments map up to 700 kb proximal to the translocation breakpoint and are associated with

potential

CpG islands. Reverse **transcriptase** polymerase chain reaction (RT-PCR) **expression** analysis and high resolution genomic mapping suggest that they may comprise up to three novel genes. No major disruption of the identified fragments could be detected in the genomic DNA of translocation carriers. The psychosis associated with this translocation may therefore be due to position effects on the

transcription of these genes or an involvement of translocated chromosome 1 sequences.

L14 ANSWER 52 OF 67 MEDLINE
ACCESSION NUMBER: 96254978 MEDLINE
DOCUMENT NUMBER: 96254978 PubMed ID: 8845841
TITLE: Cloning and characterization of the human homologue of a dystrophin related phosphoprotein found at the Torpedo electric organ post-synaptic membrane.
AUTHOR: Sadoulet-Puccio H M; Khurana T S; Cohen J B; Kunkel L M
CORPORATE SOURCE: Department of Genetics, Harvard Medical School, Boston, MA 02115, USA.
CONTRACT NUMBER: 5 R01 NS 23740-10 (NINDS)
NS29343 (NINDS)
SOURCE: HUMAN MOLECULAR GENETICS, (1996 Apr) 5 (4) 489-96.
Journal code: 9208958. ISSN: 0964-6906.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U26742; GENBANK-U26743; GENBANK-U26744;
GENBANK-U46744; GENBANK-U46745; GENBANK-U46746
ENTRY MONTH: 199610
ENTRY DATE: Entered STN: 19961106
Last Updated on STN: 19980206
Entered Medline: 19961024

AB Dystrophin is the **protein** product which is absent in Duchenne muscular dystrophy (DMD). In mammalian skeletal muscle, dystrophin is found in association with several integral and peripheral membrane **proteins**, forming a complex known as the dystrophin glycoprotein complex (DGC). In an **expressed** sequence tag (**EST**) **database** search to identify new dystrophin related genes, we isolated EST00891 which showed 57% homology to the cysteine-rich domain

of

dystrophin and localized to 18q12.1-12.2. This **EST** is also highly homologous (90%) to the Torpedo californica post-synaptic 87 kDa phosphoprotein. Screening human adult **brain** and skeletal muscle **cDNA** libraries with this **EST** resulted in cloning multiple **cDNAs** which encode several splice forms all homologous to the C-terminal domain of dystrophin. The largest open reading frame isolated shows 94% homology (86% identity) to the Torpedo 87 kDa **protein** and 50% homology to the cysteine-rich and carboxy-terminal domains of dystrophin. The other **cDNAs** isolated encode smaller splice forms of this gene which we have named dystrobrevin. The tissue distribution of dystrobrevin **mRNA** shows five distinct **transcripts** which are preferentially **expressed** between different tissues. In addition, antibodies against either the Torpedo 87 kDa **protein** or human dystrobrevin demonstrate that at least three of the splice forms are translated as **proteins** in human **brain** tissue extracts.

L14 ANSWER 53 OF 67 MEDLINE
ACCESSION NUMBER: 94004965 MEDLINE
DOCUMENT NUMBER: 94004965 PubMed ID: 8401585
TITLE: Rapid cDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library.
AUTHOR: Adams M D; Soares M B; Kerlavage A R; Fields C; Venter J C
CORPORATE SOURCE: Receptor Biochemistry and Molecular Biology Section, NINDS/NIH, Bethesda, Maryland 20892.
SOURCE: NATURE GENETICS, (1993 Aug) 4 (4) 373-80.
Journal code: 9216904. ISSN: 1061-4036.

PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-T07956; GENBANK-T07957; GENBANK-T07958;
 GENBANK-T07959; GENBANK-T07960; GENBANK-T07961;
 GENBANK-T07962; GENBANK-T07963; GENBANK-T07964;
 GENBANK-T07965; GENBANK-T07966; GENBANK-T07967;
 GENBANK-T07968; GENBANK-T07969; GENBANK-T07970;
 GENBANK-T07971; GENBANK-T07972; GENBANK-T07973;
 GENBANK-T07974; GENBANK-T07975; GENBANK-T07976;
 GENBANK-T07977; GENBANK-T07978; GENBANK-T07979;
 GENBANK-T07980; GENBANK-T07981; GENBANK-T07982;
 GENBANK-T07983; GENBANK-T07984; GENBANK-T07985; +
 ENTRY MONTH: 199311
 ENTRY DATE: Entered STN: 19940117
 Last Updated on STN: 19950307
 Entered Medline: 19931105

AB A human infant **brain cDNA** library, made specifically for production of **expressed** sequence tags (**ESTs**) was evaluated by partial sequencing of over 1,600 clones. Advantages of this library, constructed for **EST** sequencing, include the use of directional cloning, size selection, very low numbers of mitochondrial and ribosomal **transcripts**, short polyA tails, few non-recombinants and a broad representation of **transcripts**. 37% of the clones were identified, based on matches to over 320 different genes in the public **databases**. Of these, two **proteins** similar to the Alzheimer's disease amyloid precursor **protein** were identified.

L14 ANSWER 54 OF 67 MEDLINE
 ACCESSION NUMBER: 93364420 MEDLINE
 DOCUMENT NUMBER: 93364420 PubMed ID: 8358434
 TITLE: 3,400 new expressed sequence tags identify diversity of transcripts in human brain.
 COMMENT: Comment in: Nat Genet. 1994 Dec;8(4):321-2
 AUTHOR: Adams M D; Kerlavage A R; Fields C; Venter J C
 CORPORATE SOURCE: Receptor Biochemistry and Molecular Biology Section, National Institute of Neurological Disorders and Stroke, National Institutes of Health, Bethesda, Maryland 20892.
 SOURCE: NATURE GENETICS, (1993 Jul) 4 (3) 256-67.
 Journal code: 9216904. ISSN: 1061-4036.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-T04839; GENBANK-T04840; GENBANK-T04841;
 GENBANK-T04842; GENBANK-T04843; GENBANK-T04844;
 GENBANK-T04845; GENBANK-T04846; GENBANK-T04847;
 GENBANK-T04848; GENBANK-T04849; GENBANK-T04850;
 GENBANK-T04851; GENBANK-T04852; GENBANK-T04853;
 GENBANK-T04854; GENBANK-T04855; GENBANK-T04856;
 GENBANK-T04857; GENBANK-T04858; GENBANK-T04859;
 GENBANK-T04860; GENBANK-T04861; GENBANK-T04862;
 GENBANK-T04863; GENBANK-T04864; GENBANK-T04865;
 GENBANK-T04866; GENBANK-T04867; GENBANK-T04868; +
 ENTRY MONTH: 199309
 ENTRY DATE: Entered STN: 19931015
 Last Updated on STN: 19970203
 Entered Medline: 19930924

AB We present the results of the partial sequencing of over 3,400 **expressed** sequence tags (**ESTs**) from human **brain** **cDNA** clones, which increases the number of distinct genes **expressed** in the **brain**, that are represented by **ESTs**, to about 6,000. By choosing clones in an unbiased manner, it is possible to construct a profile of the **transcriptional** activity of the **brain** at different stages. **Proteins** that comprise the cytoskeleton are the most abundant; however, a large variety of regulatory **proteins** are also seen. About half of the **ESTs** predicted to contain a **protein**-coding region have no matches in the public **peptide databases** and may represent new gene families.

L14 ANSWER 55 OF 67 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2002:223827 BIOSIS

DOCUMENT NUMBER: PREV200200223827

TITLE: Cloning and functional characterization of a cation-Cl cotransporter interacting protein.

AUTHOR(S): Isenring, Paul (1); Gagnon, Edith (1); Caron, Luc (1)

CORPORATE SOURCE: (1) Groupe de Nephrologie de L'Hotel-Dieu de Quebec, Departement de Medecine, Faculte de Medecine, Universite Laval, Quebec, PQ Canada

SOURCE: Journal of the American Society of Nephrology, (September, 2000) Vol. 11, No. Program and Abstract Issue, pp.

30A-31A.

<http://www.jasn.org/>. print.

Meeting Info.: 33rd Annual Meeting of the American Society of Nephrology and the 2000 Renal Week Toronto, Ontario, Canada October 10-16, 2000

ISSN: 1046-6673.

DOCUMENT TYPE: Conference

LANGUAGE: English

AB The cation-Cl cotransporters (CCC) mediate the coupled movement of Na and/or K to that of Cl across the plasmalemma of animal cells. In polarized tissues, cation-Cl cotransport is involved in net transepithelial water and salt movement, and in non-polarized tissues, cation-Cl cotransport modulates the water and the electrolyte content of cells. To date, the CCC family comprises two branches of homologous membrane **proteins**. One branch includes the Na-K-Cl cotransporters (NKCC1 and 2) and the Na-Cl cotransporter (NCC1), and the other branch, the K-Cl cotransporters (KCC1, 2, 3, and 4). Here, we have isolated the first member of a third CCC family branch. This member was first identified in human and mouse **expressed** sequence tag (**EST**) **databases** as a 500-bp sequence homologous to a region in the carboxy-terminus of the CCCs. We isolated corresponding **cDNAs** from a human **heart cDNA** library, and the full-length clone, termed WO3.3, was found to encode a 914-residue polypeptide having a calculated molecular mass of 96.2 kDa. Overall,

WO3.3 shares apprx25% identify in amino acid sequence with each of the known CCCs. Sequence analyses predict a 12-transmembrane domain (tm) region,

two

N-linked glycosylation sites between tm5 and tm6, and a large intracellular carboxy-terminus containing **protein** kinase C phosphorylation sites. Northern blot analysis uncovers a apprx3.7-kb **transcript** present in muscle, placenta, **brain**, and **kidney**. With regard to function, WO3.3 **expressed** either in HEK-293 cells or *Xenopus laevis* oocytes does not increase Rb-, Na- and Cl-coupled transport during 5-min or 6-hour fluxes, respectively. In the oocyte, however, WO3.3 specifically inhibits human NKCC1-mediated 86Rb flux. In addition, coimmunoprecipitation studies using lysates from

WO3.3-transfected HEK-293 cells suggest a direct interaction of WO3.3 with endogenous NKCC. Thus, we have cloned and characterized the first putative

heterologous CCC interacting **protein** (CIP) known at present.

CIP1 may be part of a novel family of **proteins** that modifies the activity or kinetics of CCCs through heterodimer formation.

L14 ANSWER 56 OF 67 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2002:199005 BIOSIS

DOCUMENT NUMBER: PREV200200199005

TITLE: The transcriptome of bone marrow cells in chronic leukemias.

AUTHOR(S): Silva, Wilson A., Jr. (1); Alberto, Fernando L.; Uliana, Ronie M. (1); Simpson, Andrew J.; Costa, Fernando F.; Zago,

MARCO A. (1)
CORPORATE SOURCE: (1) Center for Cell Therapy, Regional Blood Center, Ribeirao Preto Brazil

SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 1, pp. 550a-551a. <http://www.bloodjournal.org/>. print.
Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 1 Orlando, Florida, USA December

07-11,

2001

ISSN: 0006-4971.

DOCUMENT TYPE: Conference

LANGUAGE: English

AB The complete collection of **transcripts** generated from the human genome cannot be predicted from the genome sequence, but should be directly determined for each tissue, due to variations of gene **expression** in different tissues and disease states, and because genes can encode multiple **transcripts** derived from alternate splicing and polyadenylation sites. As part of larger project that produced over 1.2 million **expressed** sequence tags (**EST**) from different cancer tissues, we constructed a set of **cdnas** obtained from **bone** marrow cells of patients with CML and CLL, that represent partial **expressed** gene sequences that are biased toward the central coding regions of the resulting **transcripts** (Dias-Neto E et al, Proc Nat Acad Sci USA 97:3491, 2000). The 51,102 **ESTs** were assembled into 5,002 contigs containing 2 to 1,008 **ESTs** (leaving 24,679 isolated sequences), of which 1,160 were classified on the basis of the annotation of the matched sequences into 8 functional categories (cell cycle 5.0%, cell motility and structure 9.3%, signaling and communication 31.0%, DNA metabolism 3.8%, RNA metabolism 10.3%, defense and homeostasis 7.9%, metabolism 24.7%, **protein** metabolism 7.9%). Of the remaining 3,842 contigs, 2,990 matched human **ESTs** (dbEST), putative **proteins** with unknown functions, DNA clones orthologs and paralogs, whereas 852 were classified as no hits.

The abundance of **ESTs** that matched the contigs formed by the larger number of **EST** in **bone** marrow cells was compared with other normal and neoplastic tissues from **breast**, **prostate**, colon, and **brain**. Of the 10 larger contigs, 5 genes were commonly **expressed** in most of the other tissues, one was exclusively found in **bone** marrow (beta-globin), and 4 were classified as no hits. Among the 50 larger contigs, the following genes were found exclusively or predominantly in **bone** marrow: lactoferrin, myeloperoxidase, defensin, epithelin, autocrine motility factor receptor, bactericidal permeability increasing **protein**, beta-globin and Xg antigen. Among 852 contigs that did not match annotated

regions of the genome (no hits), the predicted **protein** sequence of 77 contigs matched known **protein** domains when evaluated by pfam (**protein** family **database** of alignment and HMMs), representing candidate unannotated genes. To search for single nucleotide polymorphisms (SNP) in the coding region of genes, the **EST** were anchored on approximately 13,000 genes for which the complete coding sequences (CDS) are known. After exclusion of paralogs, the clusters were analyzed by PolyBayes, an algorithm that identifies SMPs by multiple alignments followed by Bayesian inference to calculate the probability associated with each candidate site (Marth GT et al, Nat Genet 23:452, 1999). A total of 278 candidate SNPs were detected in the coding region 163 genes (average 1.7 SNP/gene), of which 176 are expected to change the amino acid sequence (non synonymous). The wealth of information provided by this approach demonstrates its usefulness for the analysis of gene **expression** in specific hematopoietic tissues and diseases.

L14 ANSWER 57 OF 67 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2002:151895 BIOSIS

DOCUMENT NUMBER: PREV200200151895

TITLE: The transcriptome of bone marrow cells in chronic leukemia.

AUTHOR(S): Silva-Junior, Wilson A. (1); Alberto, Fernando L.; Uliana, Ronie M. (1); Simpson, Andrew J.; Costa, Fernando F.;

Zago,

Marco A.

CORPORATE SOURCE: (1) Center for Cell Therapy, Regional Blood Center, Ribeirao Preto Brazil

SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 2, pp. 131b. <http://www.bloodjournal.org/>. print.

Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 2 Orlando, Florida, USA December

07-11,

2001

ISSN: 0006-4971.

DOCUMENT TYPE: Conference

LANGUAGE: English

AB The complete collection of **transcripts** generated from the human genome cannot be predicted from the genome sequence, but should be directly determined for each tissue, due to variations of gene **expression** in different tissues and disease states, and because genes can encode multiple **transcripts** derived from alternate splicing and polyadenylation sites. As part of larger project that produced over 1.2 million **expressed** sequence tags (**EST**) from different cancer tissues, we constructed a set of **cdNAs** obtained from **bone** marrow cells of patients with CML and CLL, that represent partial **expressed** gene sequences that are biased toward the central coding regions of the resulting **transcripts** (Dias-Neto E et al, Proc Nat Acad Sci USA 97:3491, 2000), The 51,102 **ESTs** were assembled into 5,002 contigs containing 2 to 1,008 **ESTs** (leaving 24,679 isolated sequences), of which 1,160 were classified on the basis of the annotation of the matched sequences into 8 functional categories (cell cycle 5.0%, cell motility and structure 9.3%, signaling and communication 31.0%, DNA metabolism 3.8%, RNA metabolism 10.3%, defense and homeostasis 7.9%, metabolism 24.7%, **protein** metabolism 7.9%). Of the remaining 3,842 contigs, 2,990 matched human **ESTs** (dbEST), putative **proteins** with unknown functions, DNA clones, orthologs and paralogs, whereas 852 were classified as no hits. The abundance of **ESTs** that matched the contigs formed by the larger number of **EST** in **bone** marrow cells was compared with other normal and neoplastic tissues from **breast**, **prostate**, colon, and **brain**. Of the 10 larger contigs, 5

genes were commonly **expressed** in most of the other tissues, one was exclusively found in **bone** marrow (beta-globin), and 4 were classified as no hits. Among the 50 larger contigs, the following genes were found exclusively or predominantly in **bone** marrow: lactoferrin, myeloperoxidase, defensin, epithelin, autocrine motility factor receptor, bactericidal permeability increasing **protein**, beta-globin and Xg antigen. Among 852 contigs that did not match annotated regions of the genome (no hits), the predicted **protein** sequence of 77 contigs matched known **protein** domains when evaluated by pfam (**protein** family **database** of alignment and HMMs), representing candidate unannotated genes. To search for single nucleotide polymorphisms (SNP) in the coding region of genes, the **EST** were anchored on approximately 13,000 genes for which the complete coding sequences (CDS) are known. After exclusion of paralogs, the clusters were analyzed by PolyBayes, an algorithm that identifies SNPs by multiple alignments followed by Bayesian inference to calculate the probability associated with each candidate site (Marth GT et al, Nat Genet 23:452, 1999). A total of 278 candidate SNPs were detected in the coding region 163 genes (average 1.7 SNP/gene), of which 176 are expected to change the amino acid sequence (non synonymous). The wealth of information provided by this approach demonstrates its usefulness for the analysis of gene **expression** in specific hematopoietic tissues and diseases.

L14 ANSWER 58 OF 67 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2002:129475 BIOSIS

DOCUMENT NUMBER: PREV200200129475

TITLE: Identification of a new human gene that codes for a potential cytoskeletal protein belonging to a new

sudfamily

of Rho-GAP proteins.

AUTHOR(S): Basseres, Daniela S. (1); Tizzei, Edna R. V. (1); Costa, Fernando F. (1); Saad, Sara T. O. (1)

CORPORATE SOURCE: (1) Hematology and Hemotherapy Center, State University of Campinas, Campinas, SP Brazil

SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 1, pp. 11a-12a. <http://www.bloodjournal.org/>. print.

Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 1 Orlando, Florida, USA December

07-11,

2001

ISSN: 0006-4971.

DOCUMENT TYPE: Conference

LANGUAGE: English

AB Until recently, cytoskeletal **proteins** were thought to provide solely a mechanical support to the cell plasma membrane. Recent studies have revealed, however, that cytoskeletal **proteins** are involved in the regulation of major cell functions, such as cell signalling, **protein** trafficking, formation of specialized membrane domains, activity modulation of ion channels, membrane pumps and receptors,

control

of cell proliferation and **transcription** activity, among others. Therefore, identification of new human cytoskeletal **proteins** is crucial for improved understanding of cell function, since they are major players in signal transduction pathways. Searching the ORESTES **database**, we found the **expressed** sequence tag (**EST**) PM3-LT0032-231299-001-h11 that demonstrated similarity to the pleckstrin homology (PH) domain of the cytoskeletal **protein** beta-spectrin. The PH domain is thought to be involved in the recruitment of cytoskeletal **proteins** to the submembrane region of the cell. This **EST** was also highly similar to KIAA1424 (GenBank AB037845),

a 4655pb partial **cdna** found in human **brain**. Northern analysis of this gene revealed a **mRNA** band of approximately 7.5Kb **expressed** in many tissues, including peripheral blood leukocytes. A more abundant **expression** was observed in **brain** and muscle. RT-PCR analysis confirmed that this gene is **expressed** in hematopoietic stem cells before and after induction of erythroid differentiation with erythropoietin, with a lower **expression** in the later steps of differentiation. It is also **expressed** in **bone** marrow, tonsils and in the leukocytes of leukemia patients. In an attempt to obtain the full-length sequence of this partial **cdna**, we employed similarity searches against the human genome **database** at NCBI and used the genomic sequences obtained to search for new **ESTs** in the 5' region, which could belong to the same **transcript**. PCR and sequencing of human **brain cdna** were used to validate the inclusion of new sequences into the **transcript**. We also performed rapid amplification of **cdna** ends (RACE) in order to obtain the 5'end sequence. The **cdna** sequence is 7134pb long and potentially codes for a 1957 aminoacid **protein** containing a PH, a Rho-GAP and a PDZ domain. Rho-GAP domains activate the GTPase activity of small GTPases of the Rho family, stimulating the formation of the inactive GDP-bound form of these GTPases. PDZ domains are thought to mediate **protein-protein** interactions. Clearly, this **protein** is not a new member of the beta-spectrin family, but could represent a new class of

cytoskeletal **proteins** involved in GTPase signalling. This **protein** could also bind GTP/ATP itself through a P-loop present inside the PDZ domain. Computer generated genomic analysis of this new gene suggests that it lies on chromosome 10 and that it is composed of 25 exons. Rho-GAP **proteins** downregulate small GTPases of the Rho family, which function as molecular switches that regulate diverse cellular processes such as actin cytoskeleton organization and cell proliferation. An abnormal **expression** of **proteins** in the Rho-GTPase cascade could lead to neoplastic transformation, particularly causing tumor invasion and metastasis. The fact that this new

Rho-GAP **protein** is widely **expressed** reflects the potential importance of its function. Immunolocalization studies are currently being performed in order to better understand the role of this **protein**. Finally, we have identified a new widely **expressed** gene coding for a potential cytoskeletal **protein** involved in a major signal transduction pathway.

L14 ANSWER 59 OF 67 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 2001:492683 BIOSIS
 DOCUMENT NUMBER: PREV200100492683
 TITLE: Cloning of a novel mouse Gabarapl2 cDNA and its characterization.
 AUTHOR(S): Chen, Zheng (1); Xin, Yu-Rong; Jiang, Ying; Jiang, Ju-Xiang
 CORPORATE SOURCE: (1) School of Life Science, Suzhou University, Suzhou, 215006: zhengchen_99@yahoo.com, xinyu@umdnj.edu China
 SOURCE: Acta Pharmacologica Sinica, (August, 2001) Vol. 22, No. 8, pp. 751-755. print.
 ISSN: 0253-9756.
 DOCUMENT TYPE: Article
 LANGUAGE: English
 SUMMARY LANGUAGE: Chinese; English
 AB AIM: To clone a novel mouse GABAA-receptor-associated **protein** like 2 (Gabarapl2) gene, and to analysis its primary function. METHODS: With the aid of computer, the human GABARAPL2 **cdna** was used as

information probe to search mouse **EST database** of GenBank for mouse homolog. A series of overlapping **EST** were found and assembled into an **EST** contig using Genetics Computer Group (GCG) **ASSEMBLY** program. The existence of the gene was then identified by experiment. Northern blotting was performed to hybridize (alpha-32P) dATP labeled probe with **mRNA** of 11 different mouse tissues that had been transferred to the nylon membrane. **RESULTS:** The novel gene was deposited in GenBank under Accession No AF190644. Its **cDNA** contained an intact open reading frame and a canonical polyadenylation signal AATAAA followed by polyA. The deduced **protein** was completely identical to that of human GABARAPL2, and was termed Gabarapl2 by Mouse Gene Nomenclature Committee. The putative **protein** of Gabarapl2 has a calculated molecular weight of 13 700 and an isoelectric point of 8.56. It was also predicted to contain two **protein kinase C** phosphorylation sites and one tyrosine kinase phosphorylation site. Northern hybridization showed that Gabarapl2 was **expressed** as a single 1.35 kb **transcript**, with high levels in **brain**, thymus, **lung**, **heart**, **kidney**, and liver, and low in pancreas, **testis**, small intestine, colon, and stomach. **CONCLUSION:** A novel mouse Gabarapl2 gene was cloned and identified.

L14 ANSWER 60 OF 67 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:462511 BIOSIS

DOCUMENT NUMBER: PREV200100462511

TITLE: Molecular cloning and expression of cDNAs encoding testis-specific and non-specific ATPase inhibitor-like proteins in Bombyx mori.

AUTHOR(S): Ogura, Ichiro; Kusakabe, Takahiro (1); Kawaguchi, Yutaka; Maeda, Takuji; Koga, Katsumi

CORPORATE SOURCE: (1) Laboratory of Silkworm Science, Kyushu University Graduate School of Bioresource and Bioenvironmental Sciences, Hakozaki 6-10-1, Fukuoka, 812-8581: kusakabe@agr.kyushu-u.ac.jp Japan

SOURCE: Journal of Insect Biotechnology and Sericology, (June, 2001) Vol. 70, No. 2, pp. 121-128. print.

DOCUMENT TYPE: Article

LANGUAGE: English

SUMMARY LANGUAGE: English

AB A **cDNA** clone encoding an ATPase inhibitor-like **protein** was found in a Bombyx mori **EST** (**expressed** sequence tag) **database** and designated as BmAl-a. Also a novel **cDNA** clone encoding a different ATPase inhibitor-like **protein** was isolated from a **testis** library of B. mori after **mRNA** subtraction, and named BmAl-b. Both BmAl-a and BmAl-b **cDNA** clones were determined for their nucleotide sequences; the deduced amino acid sequences showed that the relevant **proteins** were composed of 127 and 107 amino acid residues, respectively. The

BmAl-a

and BmAl-b **proteins** have the highest homologies of 41% and 37%, respectively, with the Caenorhabditis elegans ATPase inhibitor-like **protein** Celf1 among the animal homologs so far reported.

Expression analysis by reverse **transcription** polymerase chain reaction demonstrated that the BmAl-a **mRNA** was **transcribed** in all tissues examined, while the BmAl-b **mRNA** was **expressed** exclusively in the **testis**. A

computational analysis of amino acid residues by a method available from

a

web-server, suggested that BmAl-a is located in the mitochondria, whereas BmAl-b is allocated in organelles other than the mitochondria.

L14 ANSWER 61 OF 67 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:311511 BIOSIS

DOCUMENT NUMBER: PREV200100311511

TITLE: Two unique genes cloned from differentially expressed ESTs after induction of K562 cells with sodium butyrate.

AUTHOR(S): Mitchell, T. (1); Plonczynski, M.; Hardy, C. L.; Safaya, S.; Steinberg, M. H.

CORPORATE SOURCE: (1) Pediatric Hematology/Oncology, University of Mississippi Medical Center, Jackson, MS USA

SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 1, pp. 235a. print.

Meeting Info.: 42nd Annual Meeting of the American Society of Hematology San Francisco, California, USA December 01-05, 2000 American Society of Hematology

. ISSN: 0006-4971.

DOCUMENT TYPE: Conference

LANGUAGE: English

SUMMARY LANGUAGE: English

AB We studied the temporal changes in gene **expression** in K562 cells at intervals from 2-to 48-h following induction of differentiation with sodium butyrate, using differential display-PCR and gene **expression** arrays. Globin synthesis was verified by the activity of a transduced A-globin gene promoter, and an average 62-fold increase

in -globin gene **expression** was observed during induction. This high through-put gene screening approach allowed the preparation of a partial profile of over 100 genes induced by butyrate. From this profile two novel

genes, named D12 and P30, which resulted from two unique **ESTs** were "cloned" from available **databases**. Differential **expression** of these two gene fragments was confirmed by Northern blot analysis and semi-quantitative PCR. D12 was characterized by **mRNA** of approximately 1.8 kb, and P30 was characterized by **mRNAs** of approximately 2.6 and 4.0 kb resulting from either alternative **mRNA** splicing, alternative **transcription** start sites or other **mRNA** processing. Some of the other properties of these genes were included. The TRP (tertratricopeptide) genes are active in processes such as **transcription** and mitosis. The **expression** of these two genes is unrelated to known genes and their **expression** is not restricted to erythroid cells. D12 is **expressed** primarily in **brain** and P30 is **expressed** in **heart**, skeletal muscle, **kidney** and placenta. Although the function of these novel genes in erythroid maturation is unclear, a variety of regulatory **proteins** is required for **transcription** of -globin and fetal hemoglobin in K562 cells. Their identification under these defined conditions may serve to relate previously undescribed pathways to the **transcriptional** cascades that are active in erythroid differentiation.

L14 ANSWER 62 OF 67 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:307604 BIOSIS

DOCUMENT NUMBER: PREV200100307604

TITLE: Identification of genes responsible for bone differentiation from human bone marrow derived multipotent adult stem cells (MASC).

AUTHOR(S): Qi, Huilin (1); Aguiar, Dean (1); Verfaillie, Catherine M. (1)

CORPORATE SOURCE: (1) Stem Cell Institute, Univ. of Minnesota, Minneapolis, MN USA

SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 1, pp. 70a-71a. print.

Meeting Info.: 42nd Annual Meeting of the American Society
of Hematology San Francisco, California, USA December
01-05, 2000 American Society of Hematology
..ISSN: 0006-4971.

DOCUMENT TYPE: Conference

LANGUAGE: English

SUMMARY LANGUAGE: English

AB Human **bone** marrow derived MASC are rare cells that can
differentiate into osteoblasts, chondrocytes, adipocytes, skeletal, smooth
and cardiac myocytes, endothelial cells, neurons and glial cells. In
order

to identify genes involved in commitment of MASC we examined
differentially **expressed** genes in MASC and MASC induced to
differentiate to **bone** for two days. RNA from MASC and MASC
induced with beta-glycerophosphate, ascorbic acid and dexamethasone for 2
days were hybridized with microarrays from Invitrogen (apprxeq4000
genes).

We found that 513/4000 genes were up regulated and 843/4000 down
regulated

during early **bone** differentiation. These included: a gtoreq 2
fold increase in **expression** in day 2 **bone** of 13/172
transcription factors (e.g. AP-4), 19/225 cytokines and cytokine
receptors (e.g. PDGFRB, BMP2), 3/53 cell cycle regulators (e.g. p27),

5/71

matrix **proteins** (e.g. CRTL1, ECM1). In addition, 20/172
transcription factors (e.g. POU2F2), 25/225 cytokines and
receptors (e.g. IL7R), 25/53 cell cycle regulators (e.g. CDC2), 12/71
matrix **proteins** (e.g. ITGB1) were down regulated gtoreq 2 fold
in day 2 **bone**. Genes known to play an important role in
bone differentiation such as **bone** morphogenetic
protein 2 (BMP2) increased about 3.5 fold, and **bone**
proteoglycan II precursor (PGS2) increased about 2.8 fold. We also used
subtractive hybridization as a second approach to detect differentially
expressed known as well as novel genes. Using the Clontech
PCR-Select subtraction method we have detected > 150 genes
expressed in day 2 **bone** but not MASC and > 60 genes in
MASC but not day 2 **bone**. We have sequenced and analyzed 86
individual clones present in day 2 **bone** but not MASC. Among them
we have identified 65 with significant homologies to known
proteins like human transmembrane glycoprotein (GPNMB), human HFB
30 (encoding a **protein** with ring finger motif) and human pigment
epithelium-differentiation factor (PEDF). We have also identified 21
clones with homology to **EST** sequences or with no significant
homologies to **expressed** genes present in any **database**.
Using RT-PCR and quantitative PCR we have further confirmed that five of
these novel genes are up regulated in day 2 **bone** differentiated
from MASC from different **bone** marrow donors. Studies are ongoing
to further analyze the **cDNA** array data; and to further
characterize the potential role in **bone** differentiation/loss of
multipotentiality of known and novel genes identified using these two
methods.

L14 ANSWER 63 OF 67 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:88451 BIOSIS

DOCUMENT NUMBER: PREV200100088451

TITLE: Cloning and functional characterization of a novel
beta-adrenergic-like receptor from Drosophila

melanogaster.

AUTHOR(S): Yu, E. J.; Kennedy, K.; Chatwin, H. M.; Reale, V.; Evans,
P. D.

SOURCE: Society for Neuroscience Abstracts, (2000) Vol. 26, No.

1-2, pp. Abstract No.-343.7. print.
Meeting Info.: 30th Annual Meeting of the Society of
Neuroscience New Orleans, LA, USA November 04-09, 2000
Society for Neuroscience
. ISSN: 0190-5295.

DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

AB The functional role of the small amounts of the catecholamine, norepinephrine (NE), present in the insect nervous system has been an enigma for many years and has been overshadowed by the successes achieved in studies on the functional roles of octopamine and dopamine receptors in insect nervous systems (see Evans, 1980, Adv. Insect Physiol., 15:317-473; Roeder, 1994, Comp.Biochem.Physiol., 107C:1-12).

Here

we report on the cloning and functional characterization of a novel G-protein coupled receptor from *Drosophila melanogaster* that has structural homology with vertebrate beta-adrenergic receptors. We originally identified part of the sequence of this receptor from a *Drosophila* EST database. We then obtained the full coding sequence of the receptor using PCR on *Drosophila* head mRNA. The open reading frame encodes a receptor of 322 amino acids with a predicted molecular weight of 36.5kDa. The protein has seven transmembrane domains as revealed by hydropathy plot and many other conserved features of GPCRs. Sequence comparisons reveal that it has the highest sequence homology with vertebrate beta-adrenergic receptors. Northern blot analysis of poly(A)+RNA from adult body parts indicates

that

the receptor is expressed as a single transcript of 3.7kb in heads but not bodies, consistent with a functional role in the nervous system. The receptor shows high expression in poly(A)+RNA from embryos and adults but not from larvae. When expressed in *Xenopus* oocytes, either alone or along with the promiscuous G-protein, G α -16, we could find no evidence for coupling of the receptor to either calcium or cyclic AMP based second messenger pathways. However, when stably expressed in Chinese Hamster Ovary cells, a NE induced increase in cyclic AMP levels could be detected in some cell lines.

L14 ANSWER 64 OF 67 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2000:96075 BIOSIS
DOCUMENT NUMBER: PREV200000096075
TITLE: Caveolin-1 isoforms are encoded by distinct mRNAs: Identification of mouse caveolin-1 mRNA variants caused by alternative transcription initiation and splicing.
AUTHOR(S): Kogo, Hiroshi (1); Fujimoto, Toyoshi
CORPORATE SOURCE: (1) Department of Anatomy and Molecular Cell Biology, Nagoya University School of Medicine, Showa-ku, Nagoya, 466-8550 Japan
SOURCE: FEBS Letters, (Jan. 14, 1999) Vol. 464, No. 2-3, pp. 119-123.
ISSN: 0014-5793.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
AB By searching the EST database with the known cDNA sequence encoding alpha-caveolin-1 (full-length: FL), we found a variant having a hitherto unknown sequence in place of the first exon (5'-end variant: 5'V). The expression level of 5'V mRNA was equivalent to that of FL mRNA. The entire sequences of FL and 5'V mRNA were determined by 3'- and 5'-RACE

analysis; their sizes were 2484 bp and 2533 bp, respectively, and the sequences were identical except for the region of the first exon. By Northern blotting, FL and 5'V **mRNAs** showed the same tissue distribution, and were intensely **expressed** in the **lung**, **heart**, and skeletal muscle. Analyzing the **protein** production from these **mRNAs** using green fluorescent **protein** as a tag, we found FL **mRNA** to produce the alpha-isoform predominantly, but to form little beta-isoform. The production of the beta-isoform from 5'V **mRNA** was also demonstrated. By sequence analysis of the first intron of the caveolin-1 gene, a TATA box was found at 28 bp upstream of the **transcription** initiation site for 5'V **mRNA**. This is the first demonstration of caveolin-1 **mRNA** variants generated by alternative **transcription** initiation, and it indicates that the two isoforms of caveolin-1 are produced from two distinct **mRNAs**.

L14 ANSWER 65 OF 67 CANCERLIT

ACCESSION NUMBER: 96649792 CANCERLIT

DOCUMENT NUMBER: 96649792

TITLE: Alterations in human HT29 colon cell gene expression following glutathione S-transferase inhibitor treatment (Meeting abstract).

AUTHOR: Ciaccio P J; Barone L R; Tew K D

CORPORATE SOURCE: Dept. of Pharmacology and Medical Oncology, Fox Chase Cancer Center, Philadelphia, PA 19111.

SOURCE: Proc Annu Meet Am Assoc Cancer Res, (1996). Vol. 37, pp. A2090.

ISSN: 0197-016X.

DOCUMENT TYPE: (MEETING ABSTRACTS)

FILE SEGMENT: ICDB

LANGUAGE: English

ENTRY MONTH: 199608

AB Glutathione S-transferase (GST) inhibitors can modulate cellular resistance to anticancer drugs. The GST inhibitors ethacrynic acid (EA) and gamma-glutamyl-S(benzyl)cysteinyl-R(-)-phenyl glycine diethyl ester (T.199) cause selective quantitative and qualitative alterations in the **expression** of a number of detoxification gene products in human HT29 colon cells, including dihydrodiol dehydrogenase(s), gamma-glutamylcysteine synthetase, GSTpi and MRP. We employed differential

display analysis with RNA samples from drug treated and EA resistant HT29 cells to identify novel differentially **expressed** genes that may also be critical in the early response to chemical stress. Northern blot analysis was used to confirm positive findings. Three genes were induced by EA (50 uM), two by 18 hr. Their functions are unknown but match sequences in the **EST database** (a 286 bp fragment, structurally similar (96%) to a human fetal **lung cDNA** and a 507 bp fragment, structurally similar (95%) to an infant-**brain cDNA**). A third gene, a 356 bp fragment (GA5), was 99% identical to the human heat shock, transformation sensitive **protein** IEF SSP 3521 (accession number M86752). IEF SSP 3521 contains a TPR motif and is structurally similar to the yeast STI1 **protein** which is heat-shock sensitive and transactivates members of the stress seventy-related subfamily. It has been linked with mitotic control and **transcriptional** regulation in yeast. GA5 was induced 1.5-fold by 1 hr and remained induced 1.6-fold at 24 hr under acute exposure conditions. Compared to untreated wild-type HT29 cells it was overexpressed 3-fold in a chronically exposed EA resistant cell line. Thus, following drug treatment, GA5 may be causally involved in both

early

and late gene **expression** changes.

L14 ANSWER 66 OF 67 LIFESCI COPYRIGHT 2002 CSA

ACCESSION NUMBER: 2000:47805 LIFESCI

TITLE: Molecular characterization of human and murine C11orf5, a new member of the FAUNA gene cluster

AUTHOR: Lemmens, I.H.; Farnebo, F.; Piehl, F.; Merregaert, J.; Van de Ven, W.J.M.; Larsson, C.; Kas, K.

CORPORATE SOURCE: Laboratory for Molecular Oncology, Center for Human Genetics, University of Leuven & Flanders Interuniversity Institute for Biotechnology, Center for Human Genetics, KU Leuven, Herestraat 49, B-3000 Leuven, Belgium

SOURCE: Mammalian Genome [Mamm. Genome], (20000100) vol. 11, no. 1,

pp. 78-80.

ISSN: 0938-8990.

DOCUMENT TYPE: Journal

FILE SEGMENT: G

LANGUAGE: English

SUMMARY LANGUAGE: English

AB The proximal part of the long arm of Chromosome (Chr) 11 has been extensively studied, and several disease-related loci have been assigned to this region. For some of the disease loci within 11q13 the critical genes have been identified, while others are still elusive. These latter include, for example, the loci for Bardet-Biedl syndrome-1, insulin-dependent diabetes mellitus 4, paraganglioma 2, spinocerebellar ataxia type 5, the vitreoretinopathy neovascular inflammatory disease, osteopetrosis, and Meckel syndrome. During the process of positional cloning of the gene for multiple endocrine neoplasia type 1 (MEN1), **transcription** maps, and contigs were constructed and partially sequenced. In one of these mapping studies, the cosmid clone 15.1, which contains the FAU gene, was mapped to Chr 11q13 between ZFPL1 and

D11S2196E

(Kas et al. 1992; The European consortium on MEN1 1997). This FAU-containing cosmid has also been shown to cross the t(11;17)(q13;q21) breakpoint in a B-cell non-Hodgkin's lymphoma (Wlodarska et al. 1993). In the search for candidate disease genes in this cosmid, a cluster of seven genes was identified and was named FAUNA (FAU neighboring area). From telomere to centromere, the order of genes within this 40-kb cluster are C11orf6 (NON)-C11orf4 (NOF)-FAU-C11orf5 (FON)-TM7SF2 (ANG1)-C11orf2 (ANG2)-C11orf3 (ANG3) (Kas et al. 1996; Lemmens et al. 1998). Three of

the

genes in the FAUNA cluster have been characterized previously. FAU is the cellular homolog of the fox sequence in the Finkel-Biskis-Reilly Murine Sarcoma Virus (FBR-MuSV) and encodes a fusion **protein** between the ribosomal **protein** S30 and a Ubiquitin-like **protein** (Kas et al. 1992). Its neighbor C11orf6 (NOF) is ubiquitously **expressed** and encodes a **protein** of 162 amino acids showing no homology with any known sequence in the public **databases** (Kas et al. 1996). The TM7SF2 gene is **expressed** at high levels in **heart**, liver, and **prostate**, and the carboxy-terminal half of the putative **protein** contains seven transmembrane domains showing similarity to those of the lamin B receptor and the C14/C24 sterol reductase (Lemmens et al. 1998). In the present study we have characterized the C11orf5 (FON) gene and its **expression** in human and mouse. Genomic sequence sampling of the cosmid 15.1 identified most of the genes in the FAUNA cluster, including C11orf5 (Lemmens et al. 1998). The 4-kb HindIII fragment of this cosmid was subcloned and sequenced, and by sequence homology searches three

human

and three mouse **ESTs** were identified. The corresponding human (140277, 142896, and 154581) and mouse (553602, 445457 and 373913)

cDNA clones were obtained from the Image consortium and sequenced entirely on both strands. Genomic sequences were obtained by sequencing with specific oligonucleotide primers on cosmid 15.1 or its 4-kb HindIII fragment.

L14 ANSWER 67 OF 67 BIOTECHDS COPYRIGHT 2002 THOMSON DERWENT AND ISI

ACCESSION NUMBER: 1998-06888 BIOTECHDS

TITLE: Method for detecting a target PS112 polynucleotide;
mRNA sequence for prostate cancer diagnosis, prevention,
therapy or gene therapy

AUTHOR: Cohen M; Friedman P N; Gordon J; Hodges S C; Klass M R;
Kratovich J D; Roberts-Rapp L; Russell J C; Stroupe S D

PATENT ASSIGNEE: Abbott-Lab.

LOCATION: Abbott Park, IL, USA.

PATENT INFO: WO 9815657 16 Apr 1998

APPLICATION INFO: WO 1997-US18290 8 Oct 1997

PRIORITY INFO: US 1996-727688 8 Oct 1996

DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: WPI: 1998-240838 [21]

AN 1998-06888 BIOTECHDS

AB A new method for detecting the presence of a target PS112 polynucleotide (specifically mRNA) involves contacting a test sample with at least one PS112-specific polynucleotide (RNA sequence specified), for hybridization to occur. Also claimed is a recombinant expression system, consisting of a nucleic acid sequence that includes an open reading frame derived from PS112 operably linked to a control sequence compatible with a desired host, and a cell transfected with the expression system, for production of recombinant PS112 protein. The method can be used for diagnosis of prostate cancer. Antibodies against the proteins may be used as markers, or to treat prostate cancer. In an example, partial sequences of cDNA clone inserts (expression sequence tags, ESTs) were derived from cDNA libraries made from prostate tumor tissues, prostate non-tumor tissues and other tissues, and entered into a database as gene transcript images. The transcript images were then evaluated to identify EST clusters that were represented primarily by prostate tissue libraries. (107pp)

=> log h

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
291.76	291.97

FULL ESTIMATED COST

SESSION WILL BE HELD FOR 60 MINUTES

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PASSWORD:

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FULL ESTIMATED COST	291.76	291.97

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FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
19:04:09
ON 08 JUL 2002

L1 13496 S EST
L2 34 S L1(S) (NO#(W) CORRELAT?)
L3 21 DUP REM L2 (13 DUPLICATES REMOVED)
L4 3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5 1972 S L4(S) (PROTEIN OR PEPTIDE)
L6 1748 S L5(S) (EXPRESS?)
L7 775 S L6(S) DATABASE#
L8 355 DUP REM L7 (420 DUPLICATES REMOVED)
L9 96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
L10 47 S L8(S) GENBANK
L11 87 S L8(S) (HEART OR BONE OR BRAIN)
L12 137 S L11 OR L9
L13 1 S L12 AND (NO#(W) EXPRESS?)
L14 67 S L12(S) (TRANSCRI?)

=> s l8(s) northern

L15 86 L8(S) NORTHERN

=> s l1(s) (no#(2w) correlat?)

L16 50 L1(S) (NO#(2W) CORRELAT?)

=> s l16 not l2

L17 16 L16 NOT L2

=> dup rem l17

PROCESSING COMPLETED FOR L17

L18 12 DUP REM L17 (4 DUPLICATES REMOVED)

=> d ibib abs tot

L18 ANSWER 1 OF 12	MEDLINE	DUPLICATE 1
ACCESSION NUMBER:	1998367760	MEDLINE
DOCUMENT NUMBER:	98367760	PubMed ID: 9702383
TITLE:	Left ventricular function and exercise tolerance in patients with type II diabetes mellitus.	
AUTHOR:	Irace L; Iarussi D; Guadagno I; De Rimini M L; Lucca P; Spadaro P; Romano A; Mansi L; Iacono A	
CORPORATE SOURCE:	Cardiology Medicine Institute, Medical School, II University of Naples, Italy.	
SOURCE:	CLINICAL CARDIOLOGY, (1998 Aug) 21 (8) 567-71.	
	Journal code: 7903272. ISSN: 0160-9289.	
PUB. COUNTRY:	United States	

Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199810
ENTRY DATE: Entered STN: 19981029
Last Updated on STN: 19981029
Entered Medline: 19981019

AB BACKGROUND: Left ventricular (LV) preload changes may alter exercise tolerance (ET), probably lessening activation of the Maestrini-Starling mechanism. Reduced LV filling (pre-load) during the diastolic phase, usually impaired in diabetic patients, could affect ventricular function. HYPOTHESIS: To evaluate the relationship between some echocardiographic

LV function indices and ET, 24 patients (age 43-75 years, mean 54 +/- 13 years, Group A) with type II diabetes mellitus (DM), not suffering from other pathologies, and for whom the ergometric stress test (EST) resulted in an early interruption because of muscular fatigue and/or dyspnea, and 14 patients (age 38-70 years, mean 53 +/- 12 years, Group B) with type II DM and maximal ergometric stress test, used as control

group, were studied. METHODS: The EST was performed by increasing the load by 25 W every 2 min; its duration was used as an ET index and correlated with clinical parameters of LV function obtained with M-mode, two-dimensional, and Doppler echocardiography. RESULTS: No patients in either Group A or Group B showed a high systolic blood pressure value at rest and/or an LV hypertrophy and/or an alteration of systolic functional indices. In neither group was there significant correlation between ET

and duration of DM, basal heart rate, basal and max systolic blood pressure, and EF values. Linear regression analysis showed a significant

correlation between Doppler parameters of the diastolic function and ET index in

Group A, while there was **no significant correlation** in Group B. CONCLUSION: From these data we can deduce that in absence of left systolic ventricular dysfunction the impairment of LV relaxation in DM

can influence exercise tolerance, probably by limiting activation of the contractile reserve.

L18 ANSWER 2 OF 12 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 1998226408 MEDLINE
DOCUMENT NUMBER: 98226408 PubMed ID: 9566756
TITLE: Identification and characterization of cytosolic sulfotransferases in normal human endometrium.
AUTHOR: Falany J L; Azziz R; Falany C N
CORPORATE SOURCE: Department of Pharmacology and Toxicology, University of Alabama, Birmingham 35294, USA..

Charles.Falany@CCC.UAB.EDU
CONTRACT NUMBER: GM38953 (NIGMS)
SOURCE: CHEMICO-BIOLOGICAL INTERACTIONS, (1998 Feb 20) 109 (1-3) 329-39.

Journal code: 0227276. ISSN: 0009-2797.

PUB. COUNTRY: Ireland
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199805
ENTRY DATE: Entered STN: 19980520
Last Updated on STN: 19980520
Entered Medline: 19980508

AB Understanding the factors which alter estrogen metabolism and activity in endometrial tissue is important because unopposed estrogen stimulation is an important risk factor in the development of endometrial carcinoma. The cyclic progression of the endometrium through proliferative and secretory phases is normally under the control of the ovarian hormones beta-estradiol (E2) and progesterone. One mechanism by which progesterone inhibits the activity of E2 in secretory endometrium is by elevating the degree of E2 sulfation, thereby reducing its ability to bind to the estrogen receptor and elicit a cellular response. Our laboratories have investigated the cytosolic sulfotransferases (STs) found in biopsies of both proliferative and secretory endometrium obtained from five normal pre-menopausal women who were not taking any drugs or steroids. Two of

the human cytosolic STs were detected in human endometrial tissues. The phenol-sulfating form of phenol ST (P-PST) was found at varying levels in cytosol from both proliferative and secretory endometrium in all of the women studied but with **no** consistent **correlation** to the phase of the menstrual cycle. In contrast, estrogen ST (**EST**) was not detected in the proliferative endometrial cytosol of any of the women studied but was consistently found in all of the secretory endometrial cytosols. The presence and levels of these STs was confirmed by ST activity studies, immunoblot analysis and Northern blot analysis. These results indicate that the expression of **EST** in human endometrial tissues varies with the phase of the menstrual cycle and is most likely regulated by progesterone secreted from the ovaries.

L18 ANSWER 3 OF 12 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 97224500 MEDLINE
DOCUMENT NUMBER: 97224500 PubMed ID: 9070934
TITLE: Chromosomal assignment of 311 sequences transcribed in human adult testis.
AUTHOR: Jones M H; Zhang Y; Tirosvoutis K N; Davey P M; Webster A R; Walsh D; Spurr N K; Affara N A
CORPORATE SOURCE: Department of Pathology, University of Cambridge, England, United Kingdom.
SOURCE: GENOMICS, (1997 Feb 15) 40 (1) 155-67.
JOURNAL CODE: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
JOURNAL; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AJ223808; GENBANK-AJ223809; GENBANK-AJ223810;
GENBANK-AJ223811; GENBANK-AJ224923; GENBANK-AJ224924;
GENBANK-AJ224925
ENTRY MONTH: 199706
ENTRY DATE: Entered STN: 19970709
Last Updated on STN: 20000303
Entered Medline: 19970623

AB A total of 311 expressed sequence tags (**ESTs**) derived from human adult testis have been assigned to human chromosomes by Southern analysis of a monochromosome somatic cell hybrid panel. Over 70% of the **ESTs** show conservation to hamster and mouse DNA, and the overall distribution of transcripts correlates well with physical chromosome size and to a greater extent with male meiotic chromosome length. The notable exception is the X chromosome, for which the number of testis-derived **ESTs** is greatly underrepresented. This finding may reflect inactivation of the X chromosome during the meiotic phase of spermatogenesis and a consequent selection against large numbers of X-linked germ cell transcripts. Further analysis of the distribution of testis **ESTs** showed that the **EST** density remains significantly correlated with the recombination density of each autosome.

Analysis of a comparable number (320) of brain **EST** autosome assignments showed **no** similar **correlation**. These data suggest a specific association between transcription in testis tissue and male meiotic recombination.

L18 ANSWER 4 OF 12 CANCERLIT

ACCESSION NUMBER: 96712308 CANCERLIT

DOCUMENT NUMBER: 96712308

TITLE: Retrospective estimation of carboplatin exposure by Calvert's and Chatelut's formulae and correlation with pharmacodynamic effects in metastatic non-small cell lung cancer (NSCLC) (Meeting abstract).

AUTHOR: Belani C P; Kim K; Bonomi P; Johnson D

CORPORATE SOURCE: Eastern Cooperative Oncology Group (ECOG) Boston, MA.

SOURCE: Proc Annu Meet Am Soc Clin Oncol, (1996). Vol. 15, pp. A1119.

ISSN: 0732-183X.

DOCUMENT TYPE: (MEETING ABSTRACTS)

(CLINICAL TRIAL)

(RANDOMIZED CONTROLLED TRIAL)

FILE SEGMENT: ICDB

LANGUAGE: English

ENTRY MONTH: 199611

AB Carboplatin exposure has been recognized to correlate with therapeutic outcome. The formulae developed by Calvert and Chatelut are used to individualize dosage of carboplatin based on exposure. In **EST** 1583, a randomized ECOG study for patients with metastatic NSCLC, 84 eligible patients received carboplatin on one of the arms at a fixed dose of 320 or 400 mg/m² with a median total dose of 706 mg (range 432-900). The objective response rate was 9% with a median survival of 31.7 wk. The carboplatin exposure in terms of area under the concentration time curve (AUC) was calculated using both the Calvert's and Chatelut's formulae. Carboplatin exposure and response-relationship could not be established because of the low response rate. Data are presented in a table. The estimated AUCs based on Calvert's Formula (median 6.95 mg/ml/min) were higher as compared to those calculated by Chatelut's formula (median 5.90 mg/ml/min). There was **no** significant **correlation** between the degree of carboplatin exposure (AUC) as estimated by either

of the formulae and overall survival, however Chatelut's formula appeared to have a better capability in predicting prolongation of survival as compared to that observed by using Calvert's formula. A trend toward improved survival was observed with carboplatin AUCs greater than 5.90 mg/ml/min estimated with the Chalelut formula, but was not as obvious

when Calvert's formulae was applied. The detailed analysis and Kaplan Meier plots will be presented. This relationship of carboplatin exposure and survival in patients with metastatic NSCLC should be applied and

validated in a larger sample size before any definitive conclusions can be made.

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L18 ANSWER 5 OF 12 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1994:59724 BIOSIS

DOCUMENT NUMBER: PREV199497072724

TITLE: Expression of insulin receptor spliced variants and their functional correlates in muscle from patients with non-insulin-dependent diabetes mellitus.

AUTHOR(S): Hansen, Torben (1); Bjorbaek, C.; Vestergaard, H.; Gronskov, K.; Bak, J. F.; Pedersen, O.

CORPORATE SOURCE: (1) Steno Diabetes Cent., Niels Steensen Vej 2, DK-2820
Gentofte Denmark
SOURCE: Journal of Clinical Endocrinology & Metabolism, (1993)
Vol. 77, No. 6, pp. 1500-1505.
ISSN: 0021-972X.

DOCUMENT TYPE: Article
LANGUAGE: English

AB Due to alternative splicing of exon 11 of the receptor gene, the human insulin receptor exists in two forms, that have distinct tissue-specific expression and are functionally different. Needle biopsies obtained from vastus lateralis muscle from 20 patients with noninsulin-dependent diabetes mellitus (NIDDM) and 20 normal control subjects were analyzed for the relative expression of insulin receptor mRNA variants in a novel assay using fluorescence-labeled primers and subsequent analysis on an automated DNA sequencer. In subgroups of patients and control subjects, insulin binding and tyrosine kinase activity were examined in wheat germ agglutinin-purified insulin receptors isolated from muscle biopsies. Moreover, insulin-stimulated glucose disposal was studied by means of the euglycemic hyperinsulinemic clamp technique. No difference in the relative expression of spliced variants of the insulin receptor mRNA was observed (control subjects, 71.4 \pm 1.3% insulin receptor mRNA with exon 11; NIDDM patients, 71.5 \pm 1.3% insulin receptor mRNA with exon 11). No significant interrelationships were demonstrated among the relative expression of insulin receptor mRNA variants, insulin binding, and tyrosine kinase activity toward the exogenous substrate poly(Glu-Tyr(4:1)). Furthermore, no significant relationship was demonstrated between the glucose disposal rate and the relative expression of insulin receptor splice variants. In conclusion, in skeletal muscle from both normal control subjects and NIDDM patients, the proportion of insulin receptor mRNA with exon 11 is about 70%. In addition, **no significant correlations** **est** among insulin binding, insulin receptor tyrosine kinase activity, glucose disposal rate, and expression of alternative spliced insulin receptors in human skeletal muscle.

L18 ANSWER 6 OF 12 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1989:181652 BIOSIS
DOCUMENT NUMBER: BA87:92918
TITLE: TRANSMISSION GENETICS OF ISOZYME LOCI IN RAPHANUS-SATIVUS
BRASSICACEAE STRESS-DEPENDENT NON-MENDELIAN SEGREGATION.
AUTHOR(S): ELLSTRAND N; DEVLIN B
CORPORATE SOURCE: DEP. BOT. PLANT SCI., UNIV. CALIF., RIVERSIDE, CALIF.
92521-0124.
SOURCE: AM J BOT, (1989) 76 (1), 40-46.
CODEN: AJBOAA. ISSN: 0002-9122.
FILE SEGMENT: BA; OLD
LANGUAGE: English

AB Deviations from Mendelian ratios are frequently treated as an intrinsic property of individuals, independent of the environment. We tested whether the environment of the parents could alter patterns of inheritance in the wild radish, *Raphanus sativus*. We demonstrated the genetic basis of 12 isozyme loci by controlled pollinations of unstressed plants. The frequency of deviant segregation detected was not different than that expected by chance. Controlled pollinations among stressed plants showed over 3 times as much deviant segregation as the unstressed controls.

No genetic **correlations** of segregation bias were detected. Linkage was assessed for 64 of the 66 pairs of loci. Two linkage groups were detected, one involving four loci (PGM2-ACO-ACP-LAP), the other involving a single pair (**EST-PRX**). The second linkage group is apparently associated with a locus or tightly linked loci which may segregate for "balanced" lethals on the same chromosome. Deviant segregation did not appear to act primarily by selection on a particular gamete. Postzygotic selection was the probable source of at least some of the aberrant segregation. Because no particular allele was favored in such situations, selection is apparently operating on alleles at linked loci rather than on the allozyme loci per se. Data from other studies on wild radish support the suggestion that postzygotic selection might be an important influence on progeny segregation ratios. Because wild radishes often encounter a variety of stresses in the field, in this species, aberrant segregation may be common under natural conditions.

L18 ANSWER 7 OF 12 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 1987:186003 BIOSIS
 DOCUMENT NUMBER: BA83:94127
 TITLE: TAXONOMY AND CYTOLOGY OF THE GENUS ALBUCA HYACINTHACEAE IN EAST AFRICA.
 AUTHOR(S): KNUDTZON S H; STEDJE B
 CORPORATE SOURCE: DEP. BOT., UNIV. OSLO, P.O. BOX 1045, BLINDERN, N-0316 OSLO
 SOURCE: 3, NORW.
 NORD J BOT, (1986 (RECD 1987)) 6 (6), 773-786.
 CODEN: NJBODK. ISSN: 0107-055X.
 FILE SEGMENT: BA; OLD
 LANGUAGE: English
 AB The following taxa are represented in **Est** Africa (Kenya, Tanzania, Uganda): *Albucca kirkii* (Bak.) Brenan (2n = 18), *A. abyssinica* Murr. (2n = 18, 36), *A. tenuis* Knudtzon sp. nov. (2n = 18). The general haploid karyotype is 3L + 6S. The two first species are fairly heterogenous, with characteristic facies in local populations, but with little or **no** constant **correlation** of characters over wide areas. Intraspecific incompatibility is observed, but only slightly combined with differences in morphology or level of ploidy.

L18 ANSWER 8 OF 12 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC. DUPLICATE
 4
 ACCESSION NUMBER: 1987:125606 BIOSIS
 DOCUMENT NUMBER: BA83:64667
 TITLE: ALLELE FREQUENCY VARIATION AT THE EST-2 LOCUS IN ARCTIC CHARR IS IT CLINICAL.
 AUTHOR(S): HINDAR K
 CORPORATE SOURCE: DEP. OF BIOL., DIV. OF ZOOL., UNIV. OF OSLO, P.O. BOX 1050 BLINDERN, N-0316 OSLO 3, NORWAY.
 SOURCE: HEREDITAS, (1986) 105 (1), 23-28.
 CODEN: HEREAY. ISSN: 0018-0661.
 FILE SEGMENT: BA; OLD
 LANGUAGE: English
 AB The geographical distribution of allele frequencies at the **EST-2** locus in Arctic charr (*Salvelinus alpinus* (L.)) was studied by examining literature data for 209 Arctic charr populations from most of the species range. A **non-significant** positive **correlation** was demonstrated between the frequency of the **EST-2** (100) allele and latitude. This result is contrary to the suggestion by NYMAN and SHAW (1971; Comp. Biochem. Physiol. 40B:563-566) that these variables are

negatively correlated as a result of selection against the **EST**-2(100) allele at low temperatures. Three observations suggest that genetic drift may often override possibly existing temperature-dependent selection in determining esterase allele frequencies in the Arctic charr. Firstly, esterase allele frequencies show considerable variation within restricted geographical areas. Secondly, fixation for either of the esterase alleles is common in small populations. Thirdly, the proportion of populations fixed for one allele varies with the regional average frequency of that allele. On this background, selection appears to be of less importance in determining esterase allele frequencies in the Arctic charr than has hitherto been suggested.

L18 ANSWER 9 OF 12 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 1982:251879 BIOSIS
 DOCUMENT NUMBER: BA74:24359
 TITLE: LATITUDINAL RELATIONSHIP OF ESTERASE 6 AND PHOSPHO GLUCO
 MUTASE GENE FREQUENCIES IN DROSOPHILA-MELANOGASTER.
 AUTHOR(S): OAKESHOTT J G; CHAMBERS G K; GIBSON J B; WILLCOCKS D A
 CORPORATE SOURCE: DEP. POPULATION BIOL. RES. SCH. BIOL. SCI., AUST. NATL.
 UNIV., P.O. BOX 475, CANBERRA CITY A.C.T. 2601, AUST.
 SOURCE: HEREDITY, (1981 (RECD 1982)) 47 (3), 385-396.
 CODEN: HDTYAT. ISSN: 0018-067X.

FILE SEGMENT: BA; OLD
 LANGUAGE: English

AB Geographic variation in esterase-6 (**Est**-6) and
 phosphoglucomutase (Pgm) gene frequencies in Australasian populations of
 D. melanogaster are compared with analogous data collated from 16

previous
 reports for North America and Europe/Asia. A large-scale latitudinal
 cline

is found on all 3 zoogeographic zones for **Est**-6 and overall,
Est-61.00 frequency increases from about 20% around 20.degree.
 latitude to about 80% approaching 50.degree. latitude. In contrast, there
 is no consistent evidence for a latitudinal cline in Pgm gene frequencies
 in any of the 3 zones, with Pgm1.00 frequency generally about 85% and
 Pgm1.20 and Pgm0.70 frequencies each between 5% and 10%. The consistent
Est-6 clines are attributed to latitudinal selection gradients but
 no consistent correlations are found between **Est**
 -6 gene frequencies and maximum or minimum temperature or rainfall which
 might be associated with these gradients. The directions of the
Est-6 clines in fact run counter to expectations based on the in
 vitro thermostabilities of the respective allozymes.

L18 ANSWER 10 OF 12 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 1979:200420 BIOSIS
 DOCUMENT NUMBER: BA68:2924
 TITLE: EVALUATION OF COMMON BEAN CULTIVAR RELATIONSHIPS BY MEANS
 OF ISOZYME ELECTROPHORETIC PATTERNS.
 AUTHOR(S): BASSIRI A; ADAMS M W
 CORPORATE SOURCE: DEP. AGRON., COLL. AGRIC., PAHLAVI UNIV., SHIRAZ, IRAN.
 SOURCE: EUPHYTICA, (1978 (RECD 1979)) 27 (3), 707-720.
 CODEN: EUPHAA. ISSN: 0014-2336.

FILE SEGMENT: BA; OLD
 LANGUAGE: English

AB Electrophoretic isozyme technique was applied on primary leaf, stem and
 root tissues from seedlings of 34 USA major common bean (Phaseolus
 vulgaris L.) cultivars belonging to 19 commercial classes (Great

Northern,
 Kidney, Navy, Pinto, Red Mexican, Tropical Black, California Small White,
 Idaho Flat Small White, Pink and Cranberry). Among the isozyme systems
 studied, peroxidase (PER) and esterase (**EST**) were suitable for

cultivar identification within most commercial and for estimating the genetic relationships among the cultivars of the same class or among the classes. Acid phosphatase (PHOS), due to high proportions of monomorphic bands, could not be considered a good system for such purposes. Within each isozyme system, no pattern was exclusive to any particular commercial class. Based on the number of polymorphic bands in common between each cultivar pair, a banding-similarity index was calculated. The indices were highly significantly correlated with genetic distances obtained by Principal Component Analysis (PCA). In those comparisons where a pedigree relationship could be calculated, a **non-significant correlation** with similarity indices was obtained. Certain cultivar pair relationships, a minority of the whole were incorrectly predicted by the isozyme technique. Caution is indicated when this technique is the only basis of assigning relationship. In a few cases, the similarity indices pointed either to close genetic relationships or the lack of such relationships, whereas the reverse is known from pedigree or PCA distance estimates. The reason for such discrepancies is discussed. Some isozymes were unique to a certain tissue, while others were present in more than one. Upon the compilation of bands from all the cultivars, for the leaf, stem, and root tissues, respectively, and 0, 10 and 8 PHOS, and 7, 6 and 7 PER bands were obtained.

L18 ANSWER 11 OF 12 CANCERLIT
ACCESSION NUMBER: 78800992 CANCERLIT
DOCUMENT NUMBER: 78800992
TITLE: CHEMOTHERAPY OF NON-HODGKIN'S LYMPHOMAS: EASTERN COOPERATIVE ONCOLOGY GROUP EXPERIENCE.
AUTHOR: Bennett J M; Lenhard R E; Ezdinli E; Johnson G J; Carbone P
P; Pocock S J
CORPORATE SOURCE: Univ. Rochester Cancer Center, Rochester, NY 14642.
SOURCE: Cancer Treat Rep, (1977). Vol. 61, No. 6, pp. 1079-1083.
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
FILE SEGMENT: CATH
LANGUAGE: English
ENTRY MONTH: 197802

AB Nine Phase II and III combination chemotherapy trials conducted by the Eastern Cooperative Oncology Group (ECOG) in patients with malignant non-Hodgkin's lymphomas are reviewed. Early trials comparing treatment with cyclophosphamide alone with combinations of cyclophosphamide, vincristine, and prednisone (CVP) revealed a correlation between increased number of complete remissions (CR) and addition of prednisone to the schedule. In other studies, length of survival correlated with nodal pattern and cell type and with achievement of CR. In two Phase III trials carmustine (BCNU) was found to be active against non-Hodgkin's lymphomas. BCNU or cyclophosphamide combinations with prednisone achieved CRs comparable with those obtained with a cyclophosphamide plus vincristine program, but neither was as effective as the CVP program. Study **EST 3472 indicated no positive correlation** between CR rate and toxicity level. In this program estimated mean survival following CVP treatment is significantly longer than with cyclophosphamide plus prednisone, or BCNU plus CVP. Percentage of treatment failures in unfavorable histologic categories is higher than in favorable categories. In Phase II trials with advanced lymphoma patients whose disease was resistant to or progressive after standard chemotherapeutic approaches, low-dose bleomycin and hexamethylmelamine

was

superior to high-dose bleomycin. (5 Refs)

L18 ANSWER 12 OF 12 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 1994:272248 BIOSIS

DOCUMENT NUMBER: PREV199497285248

TITLE: Characterization and discrimination of three Rhopalosiphum species (Homoptera: Aphididae) based on isozymes.

AUTHOR(S): Lazzari, Sonia M. N.

CORPORATE SOURCE: Dep. Zool., Univ. Federal do Parana, C.P. 19020, 81531-970 Curitiba, Parana Brazil

SOURCE: Revista Brasileira de Zoologia, Vol. 9, No. 1-2, pp. 139-151.

ISSN: 0101-8175.

DOCUMENT TYPE: Article

LANGUAGE: English

AB Seventeen clones of Rhopalosiphum padi (Linnaeus, 1758), 14 of R. maidis (Fitch, 1856), and two of R. insertum (Walker, 1849), representing a wide range of host plants and geographic distribution, were examined electrophoretically to determine intra and interspecific variation. Twenty-one enzyme systems were tested using starch-gel techniques. The electrophoretic variation within species was low, as expected for parthenogenetic organisms. Frequency of heterozygotes was also relatively low for most populations. The percentage of polymorphic loci ranged from 0% to 27.3% in R. padi, but it was lower (0% to 18.2%) in the completely anholocyclic R. maidis. **No consistent correlation** between band patterns and host plant or geographic origin could be established for R. padi and R. maidis. The distinction between R. padi

and

R. insertum was made by **Est-1**, Lap-2, Pgm, Got-1, and alpha-gpdh. The enzymes **Est-2**, G-3pdh, Sdh, and Got-2 were useful to separate R. maidis from R. padi, while **Est-1**, Lap-2, Got-1, and alpha-gpdh, in addition to the first three mentioned above, separated R. maidis from R. insertum. However, many other loci shared

only

one electrophoretic band and had another that was useful to partially distinguish the species. The utilization of starch-gel electrophoresis as a taxonomic tool in distinguishing populations and species of aphids and its combination with other taxonomic methods are briefly discussed.

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT 19:04:09

ON 08 JUL 2002

L1 13496 S EST
L2 34 S L1(S) (NO#(W) CORRELAT?)
L3 21 DUP REM L2 (13 DUPLICATES REMOVED)
L4 3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5 1972 S L4(S) (PROTEIN OR PEPTIDE)
L6 1748 S L5(S) (EXPRESS?)
L7 775 S L6(S) DATABASE#
L8 355 DUP REM L7 (420 DUPLICATES REMOVED)
L9 96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN)
L10 47 S L8(S) GENBANK
L11 87 S L8(S) (HEART OR BONE OR BRAIN)
L12 137 S L11 OR L9
L13 1 S L12 AND (NO#(W) EXPRESS?)
L14 67 S L12(S) (TRANSCRIPT?)

L15 86 S L8(S)NORTHERN
 L16 50 S L1(S) (NO#(2W)CORRELAT?)
 L17 16 S L16 NOT L2
 L18 12 DUP REM L17 (4 DUPLICATES REMOVED)

=> s l1(s) (no#(3w)correlat?)
 L19 54 L1(S) (NO#(3W) CORRELAT?)

=> s l19 not l1
 L20 0 L19 NOT L1

=> s l19 not l2
 L21 20 L19 NOT L2

=> s l21 not l16
 L22 4 L21 NOT L16

=> d ibib abs tot

L22 ANSWER 1 OF 4 MEDLINE
 ACCESSION NUMBER: 92406553 MEDLINE
 DOCUMENT NUMBER: 92406553 PubMed ID: 1526853
 TITLE: A study of interlocus allozyme heterozygosity
 correlations: implications for neutral theory.
 AUTHOR: Woodwark M; Skibinski D O; Ward R D
 CORPORATE SOURCE: School of Biological Sciences, University College of
 Swansea, U.K.
 SOURCE: HEREDITY, (1992 Aug) 69 (Pt 2) 190-8.
 Journal code: 0373007. ISSN: 0018-067X.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199210
 ENTRY DATE: Entered STN: 19921106
 Last Updated on STN: 19921106
 Entered Medline: 19921020

AB Using a database of allozyme studies, correlations in heterozygosity between selected enzyme loci (MDH, alpha GPDH, IDH, 6PGDH, LDH, SOD, AAT, PGM, **EST**, PGI) were calculated across vertebrate species. Large and positive correlations were observed with untransformed heterozygosity values. However, after transformation to correct for mean species heterozygosity, correlations were substantially reduced and median values were closer to zero. Some enzymes were more often involved in significant correlations than others, and correlations calculated across species within vertebrate classes were significant for different enzyme pairs in different classes. There was **no** evidence that significant **correlations** occurred primarily between functionally related enzymes. It is suggested that the observed correlations are best explained by variation between enzyme loci in functional constraint and effective neutral mutation rate.

L22 ANSWER 2 OF 4 MEDLINE
 ACCESSION NUMBER: 79208422 MEDLINE
 DOCUMENT NUMBER: 79208422 PubMed ID: 36863
 TITLE: Lateral cerebral ventricular enlargement in chronic schizophrenia.
 AUTHOR: Weinberger D R; Torrey E F; Neophytides A N; Wyatt R J
 SOURCE: ARCHIVES OF GENERAL PSYCHIATRY, (1979 Jul) 36 (7) 735-9.

JOURNAL code: 0372435. ISSN: 0003-990X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 197908
ENTRY DATE: Entered STN: 19900315
Last Updated on STN: 19950206
Entered Medline: 19790829

AB To investigate if cerebral ventricular enlargement is associated with chronic schizophrenia, computerized tomography scans from 73 psychiatric patients were compared with 56 asymptomatic volunteers all less than 50 years old. Ventricular size was significantly greater in the subgroup of 58 chronic schizophrenic patients than in the controls. Of the chronic schizophrenic patients, 40% were outside the control range; 53% exceeded

2

SDs of the control mean. Neither duration of illness **nor** length of hospitalization **correlated** with ventricular size. The 44 chronic schizophrenic patients who had never been treated with electroshock therapy (**EST**) had larger ventricles than controls. A group of seven nonchronic schizophrenic patients also had enlarged ventricles; the eight patients who were either schizoaffective or nonschizophrenic did not differ from controls. This study shows that lateral cerebral ventricular enlargement is associated with chronic schizophrenia; it suggests that this is not a result of treatment.

L22 ANSWER 3 OF 4 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1992:454402 BIOSIS
DOCUMENT NUMBER: BA94:95802
TITLE: A STUDY OF INTERLOCUS ALLOZYME HETEROZYGOSITY CORRELATIONS IMPLICATIONS FOR NEUTRAL THEORY.
AUTHOR(S): WOODWARD M; SKIBINSKI D O F; WARD R D
CORPORATE SOURCE: SCH. BIOLOGICAL SCI., UNIV. COLL. SWANSEA, SINGLETON PARK, SWANSEA SA2 8PP, UK.
SOURCE: HEREDITY, (1992) 69 (2), 190-198.
CODEN: HDTYAT. ISSN: 0018-067X.
FILE SEGMENT: BA; OLD
LANGUAGE: English

AB Using a database of allozyme studies, correlations in heterozygosity between selected enzyme loci (MDH, .alpha.GPDH, IDH, 6PGDH, LDH, SOD, AAT, PGM, **EST**, PGI) were calculated across vertebrate species. Large and positive correlations were observed with untransformed heterozygosity values. However, after transformation to correct for mean species heterozygosity, correlations were substantially reduced and median values were closer to zero. Some enzymes were more often involved in significant correlations than others, and correlations across species within vertebrate classes were significant for different enzyme pairs in different classes. There was **no** evidence that significant **correlations** occurred primarily between functionally related enzymes. It is suggested that the observed correlations are best explained by variation between enzyme loci in functional constraint and effective neutral mutation rate.

L22 ANSWER 4 OF 4 LIFESCI COPYRIGHT 2002 CSA
ACCESSION NUMBER: 94:27607 LIFESCI
TITLE: A study of interlocus allozyme heterozygosity correlations:
Implications for neutral theory
AUTHOR: Woodward, M.; Skibinski, D.O.F.; Ward, R.D.

CORPORATE SOURCE: Sch. Biol. Sci., Univ. Coll. Swansea, Singleton Park,
 Swansea SA2 8PP, UK
 SOURCE: HEREDITY, (1992) vol. 69, no. 2, pp. 190-198.
 DOCUMENT TYPE: Journal
 FILE SEGMENT: G
 LANGUAGE: English
 SUMMARY LANGUAGE: English

AB Using a database of allozyme studies, correlations in heterozygosity between selected enzyme loci (MDH, aGPDH, IDH, 6PGDH, LDH, SOD, AAT, PGM, **EST**, PGI) were calculated across vertebrate species. Large and positive correlations were observed with untransformed heterozygosity values. However, after transformation to correct for mean species heterozygosity, correlations were substantially reduced and median values were closer to zero. Some enzymes were more often involved in significant correlations than others, and correlations calculated across species within vertebrate classes were significant for different enzyme pairs in different classes. There was **no** evidence that significant **correlations** occurred primarily between functionally related enzymes.

=> file medline biosis

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
316.50	316.71

FULL ESTIMATED COST

FILE 'MEDLINE' ENTERED AT 20:42:05 ON 08 JUL 2002

FILE 'BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002
 COPYRIGHT (C) 2002 BIOLOGICAL ABSTRACTS INC.(R)

=> s EST or (sequence(w)tag#)

L23 13496 EST OR (SEQUENCE(W) TAG#)

=> s l23 and database#/ti

L24 234 L23 AND DATABASE#/TI

=> s l24 and (no(3w)correlat?)

L25 0 L24 AND (NO(3W) CORRELAT?)

=> s l24(s)database#

PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
 FIELD CODE - 'AND' OPERATOR ASSUMED 'L141(S)DATABASE#'

PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
 FIELD CODE - 'AND' OPERATOR ASSUMED 'L142(S)DATABASE#'

L26 234 L24(S) DATABASE#

=> s l23(s)database#

L27 2221 L23(S) DATABASE#

=> s l27(s)(no#(3w)correlat?)

L28 4 L27(S) (NO#(3W) CORRELAT?)

=> d ibib abs tot

L28 ANSWER 1 OF 4

MEDLINE

ACCESSION NUMBER: 92406553 MEDLINE

DOCUMENT NUMBER: 92406553 PubMed ID: 1526853

TITLE: A study of interlocus allozyme heterozygosity

correlations: implications for neutral theory.

AUTHOR: Woodward M; Skibinski D O; Ward R D
CORPORATE SOURCE: School of Biological Sciences, University College of
Swansea, U.K.
SOURCE: HEREDITY, (1992 Aug) 69 (Pt 2) 190-8.
Journal code: 0373007. ISSN: 0018-067X.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199210
ENTRY DATE: Entered STN: 19921106
Last Updated on STN: 19921106
Entered Medline: 19921020

AB Using a **database** of allozyme studies, correlations in heterozygosity between selected enzyme loci (MDH, alpha GPDH, IDH, 6PGDH, LDH, SOD, AAT, PGM, **EST**, PGI) were calculated across vertebrate species. Large and positive correlations were observed with untransformed heterozygosity values. However, after transformation to correct for mean species heterozygosity, correlations were substantially reduced and median values were closer to zero. Some enzymes were more often involved in significant correlations than others, and correlations calculated across species within vertebrate classes were significant for different enzyme pairs in different classes. There was **no** evidence that significant **correlations** occurred primarily between functionally related enzymes. It is suggested that the observed correlations are best explained by variation between enzyme loci in functional constraint and effective neutral mutation rate.

L28 ANSWER 2 OF 4 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:343948 BIOSIS
DOCUMENT NUMBER: PREV200200343948
TITLE: Analysis of differential gene expression in peripheral blood eosinophils of atopic dermatitis patients.
AUTHOR(S): Ogawa, Kaoru (1); Hashida, Ryoichi (1); Itoh, Mikito (1); Miyagawa, Masami (1); Sugita, Yuji (1); Takahashi, Eiki; Tsujimoto, Gozoh; Katsunuma, Toshio; Akasawa, Akira; Matsumoto, Kenji; Saito, Hirohisa
CORPORATE SOURCE: (1) Genox Research, Inc, 907 Nogawa, Miyamae-ku, Kawasaki, Kanagawa, 216-0001 Japan
SOURCE: FASEB Journal, (March 20, 2002) Vol. 16, No. 4, pp. A674.
<http://www.fasebj.org/>. print.
Meeting Info.: Annual Meeting of the Professional Research Scientists on Experimental Biology New Orleans, Louisiana, USA April 20-24, 2002
ISSN: 0892-6638.
DOCUMENT TYPE: Conference
LANGUAGE: English

AB To identify the genes related to atopic dermatitis (AD), we compared differentially expressed genes in peripheral blood eosinophils from AD patients and healthy volunteers. RNA was prepared from peripheral blood eosinophils, and gene expression was monitored by fluorescent differential display (FDD) and real-time PCR (ABI PRISM 7700). Approximately 20 new genes and **ESTs** (expressed **sequence tags**) were expressed at higher levels in eosinophils of AD patients than in those of healthy volunteers. The functions of most of these genes are unknown. Nonetheless, we analyzed the relationship between the expression of each gene and clinical markers such as the number of eosinophils and the amount of IgE. There was **no correlation** between gene expression and clinical markers. Multivariate studies of the gene

expression data in each sample showed a very high coefficient of relation among the copy numbers of each gene. The genes under investigation were also expressed in cultured blood eosinophils after IL-4 stimulation. We were able to estimate the function of some of the sequences by scanning the human genome **database**.

L28 ANSWER 3 OF 4 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:294151 BIOSIS
DOCUMENT NUMBER: PREV200100294151
TITLE: Identification of a novel polymorphism in the human FCGR2B gene: Correlation with response to rituximab treatment in patients with follicular lymphoma.
AUTHOR(S): Fitzgibbon, Jude (1); Hill, Alexander S. (1); Arch, Rachael S. (1); Sutcliffe, Catherine (1); Summers, Karin E. (1); Lister, Andrew (1)
CORPORATE SOURCE: (1) ICRF Medical Oncology Unit, St. Bartholomew's Hospital Medical College, London UK
SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 2, pp. 179b. print.
Meeting Info.: 42nd Annual Meeting of the American Society of Hematology San Francisco, California, USA December 01-05, 2000 American Society of Hematology
. ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Rituximab (IDEC-C2B8) is a chimeric anti-CD20 monoclonal antibody used in the treatment of patients with B cell lymphoma. It is a clinically active and well tolerated therapy of patients with follicular lymphoma (FL), giving an overall response rate of approximately 50%. Using a xenograft model of B cell lymphoma Clynes and co-workers (2000) recently demonstrated that mice deficient in the immunoglobulin G low affinity inhibitory Fc receptor FcγRIIB (FCGR2B) responded better to Rituximab treatment compared to wild-type mice. The response to Rituximab treatment may therefore be influenced by polymorphisms present within this inhibitory receptor that affect expression or alter its antibody binding efficiency. To date, no common polymorphic variants have been described for FCGR2B. Sequence redundancy present in the expressed **sequence tag database** and sequence analysis identified a common G (0.65) to A (0.35) transition at nucleotide position 1180 of the FCGR2B gene. Genotype analysis of this variant was carried out in 67 FL patients treated with single agent Rituximab (29 responders v 38 non-responders). No significant difference in genotype or allele frequencies was observed between controls and FL patients. There was also **no correlation** in genotype status and response to treatment. Additional FCGR2B polymorphisms will be characterized and their effect on response to Rituximab treatment determined. These association studies may help explain the heterogeneity of response to Rituximab treatment of patients with FL.

L28 ANSWER 4 OF 4 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1992:454402 BIOSIS
DOCUMENT NUMBER: BA94:95802
TITLE: A STUDY OF INTERLOCUS ALLOZYME HETEROZYGOSITY CORRELATIONS IMPLICATIONS FOR NEUTRAL THEORY.
AUTHOR(S): WOODWARK M; SKIBINSKI D O F; WARD R D
CORPORATE SOURCE: SCH. BIOLOGICAL SCI., UNIV. COLL. SWANSEA, SINGLETON PARK, SWANSEA SA2 8PP, UK.
SOURCE: HEREDITY, (1992) 69 (2), 190-198.
CODEN: HDTYAT. ISSN: 0018-067X.

FILE SEGMENT: BA; OLD
 LANGUAGE: English
 AB Using a **database** of allozyme studies, correlations in heterozygosity between selected enzyme loci (MDH, .alpha.GPDH, IDH, 6PGDH, LDH, SOD, AAT, PGM, **EST**, PGI) were calculated across vertebrate species. Large and positive correlations were observed with untransformed heterozygosity values. However, after transformation to correct for mean species heterozygosity, correlations were substantially reduced and median values were closer to zero. Some enzymes were more often involved in significant correlations than others, and correlations across species within vertebrate classes were significant for different enzyme pairs in different classes. There was **no** evidence that significant **correlations** occurred primarily between functionally related enzymes. It is suggested that the observed correlations are best explained by variation between enzyme loci in functional constraint and effective neutral mutation rate.

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT 19:04:09
 ON 08 JUL 2002

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L1      13496 S EST
L2      34 S L1(S) (NO#(W)CORRELAT?)
L3      21 DUP REM L2 (13 DUPLICATES REMOVED)
L4      3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5      1972 S L4(S) (PROTEIN OR PEPTIDE)
L6      1748 S L5(S) (EXPRESS?)
L7      775 S L6(S)DATABASE#
L8      355 DUP REM L7 (420 DUPLICATES REMOVED)
L9      96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
L10     47 S L8(S)GENBANK
L11     87 S L8(S) (HEART OR BONE OR BRAIN)
L12     137 S L11 OR L9
L13     1 S L12 AND (NO#(W)EXPRESS?)
L14     67 S L12(S) (TRANSCRI?)
L15     86 S L8(S)NORTHERN
L16     50 S L1(S) (NO#(2W)CORRELAT?)
L17     16 S L16 NOT L2
L18     12 DUP REM L17 (4 DUPLICATES REMOVED)
L19     54 S L1(S) (NO#(3W)CORRELAT?)
L20     0 S L19 NOT L1
L21     20 S L19 NOT L2
L22     4 S L21 NOT L16
```

FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002

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L23     13496 S EST OR (SEQUENCE(W)TAG#)
L24     234 S L23 AND DATABASE#/TI
L25     0 S L24 AND (NO(3W)CORRELAT?)
L26     234 S L24(S)DATABASE#
L27     2221 S L23(S)DATABASE#
L28     4 S L27(S) (NO#(3W)CORRELAT?)
```

=> s l23(s) (bladder or prostate or kidney or heart or lung or ovary or skin)
 L29 1174 L23(S) (BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVARY

OR SKIN)

=> s 129(s)northern
L30 310 L29(S) NORTHERN

=> s 130 and database#
L31 133 L30 AND DATABASE#

=> dup rem 131
PROCESSING COMPLETED FOR L31
L32 78 DUP REM L31 (55 DUPLICATES REMOVED)

=> d ibib abs tot

L32 ANSWER 1 OF 78 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2002299254 IN-PROCESS
DOCUMENT NUMBER: 22035872 PubMed ID: 12040005
TITLE: Identification of Gasz, an Evolutionarily Conserved Gene
Expressed Exclusively in Germ Cells and Encoding a Protein
with Four Ankyrin Repeats, a Sterile-alpha Motif, and a
Basic Leucine Zipper.
AUTHOR: Yan Wei; Rajkovic Aleksandar; Viveiros Maria M; Burns
Kathleen H; Eppig John J; Matzuk Martin M
CORPORATE SOURCE: Departments of Pathology (W.Y., M.M.M.), Department of
Molecular and Cellular Biology (M.M.M.), Department of
Molecular and Human Genetics (M.M.M., K.H.B.), Department
of Obstetrics and Gynecology (A.R.), Baylor College of
Medicine, Houston, Texas 77030.
SOURCE: MOLECULAR ENDOCRINOLOGY, (2002 Jun) 16 (6) 1168-84.
Journal code: 8801431. ISSN: 0888-8809.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020602
Last Updated on STN: 20020602

AB To discover causes of infertility and potential contraceptive targets, we
used in silico subtraction and genomic **database** mining to
identify conserved genes with germ cell-specific expression. In silico
subtraction identified an expressed **sequence tag** (**EST**) present exclusively in a newborn mouse **ovary**
library. The full-length cDNA sequence corresponding to this **EST**
encodes a novel protein containing four ankyrin (ANK) repeats, a
sterile-alpha motif (SAM), and a putative basic leucine zipper (bZIP)
domain. **Northern** blot and semiquantitative RT-PCR analyses
demonstrated that the mRNA is exclusively expressed in the mouse testis
and **ovary**. The expression sites were localized by in situ
hybridization to pachytene spermatocytes in the testis and oocytes in the
ovary. Immunohistochemistry showed that the novel protein is
localized to the cytoplasm in pachytene spermatocytes and early
spermatids, oocytes at all stages of oogenesis, and in early
preimplantation embryos. Based on its germ cell-specific expression and
the presence of ANK, SAM, and basic leucine zipper domains, we have
termed

this novel protein GASZ. The mouse Gasz gene, which consists of 13 exons
and spans 60 kb, is located on chromosome 6 between the Wnt2 and cystic
fibrosis transmembrane conductance regulator (Cftr) genes. Using genomic
database mining, orthologous genes encoding GASZ were identified
in the rat, cow, baboon, chimpanzee, and human. Phylogenetic analyses
reveal that the GASZ proteins are highly conserved among these species.
Human and mouse GASZ proteins share 85.3% amino acid identity, and human

and chimpanzee GASZ proteins differ by only 3 out of 475 amino acids. In humans, the GASZ gene resides on chromosome 7 and is similarly composed of

13 exons. Because both ANK repeats and the SAM domain function as protein-protein interaction modules that mediate signal transduction cascades in some systems, GASZ may represent an important cytoplasmic signal transducer that mediates protein-protein interactions during germ cell maturation in both males and females and during preimplantation embryogenesis.

L32 ANSWER 2 OF 78 MEDLINE
ACCESSION NUMBER: 2002353498 IN-PROCESS
DOCUMENT NUMBER: 22091578 PubMed ID: 12096622
TITLE: Mapping and expression analysis of a different expression cDNA fragment from lung adenocarcinoma cell line.
AUTHOR: Fan Hong; Li Yu; Feng Hui-Chen; Lu Bing-Jie; Fu Song-Bin; Zhang Gui-Yin; Li Pu
CORPORATE SOURCE: Laboratory of Medical Genetics, Ha'erbin Medical University, Ha'erbin 150086, China.
SOURCE: I CHUAN HSUEH PAO. ACTA GENETICA SINICA, (2002 Jun) 29 (6) 476-80.
Journal code: 7900784. ISSN: 0379-4172.
PUB. COUNTRY: China
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: Chinese
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020705
Last Updated on STN: 20020705
AB **Lung** cancer is one of the most common malignant tumors in humans. Metastasis is the basic biological feature of malignant tumors, which is the main cause of death. Molecular mechanism of metastasis is still unclear, although lots of studies have been done in tumor metastasis. To study and explore the molecular basis of metastasis in **lung** cancer, and isolate tumor metastasis-related genes, two human **lung** adenocarcinoma cell lines AGZY 83-a and Anip 973 were chosen as research materials. The Anip973 was derived from AGZY83-a, but manifested much higher metastasis potential than the parent line. Using mRNA differential display technique, an unknown cDNA fragment, OPB7-1, which is over-expressive in Anip973 cell line, was obtained. It was used as a template to isolate its corresponding cDNA through dbEST searching and PCR. To search and clone **lung** adenocarcinoma metastasis-related candidate gene, and to explore the molecular basis of development of **lung** carcinoma, differential expression of OPB7-1 cDNA fragment among 9 human **lung** adenocarcinoma cell lines and 12 normal human tissues were detected using cell culture, cDNA clone, **Northern** blot analysis and bioinformation technology. Results showed that there were significant differences in OPB7-1 expression among 9 human **lung** adenocarcinoma cell lines. High expression tendency was observed in Anip973 cell line with high metastasis potential, TKB-18 cell line with high invasion potential and GLC-82 cell line with low differentiation potential. Besides, a bigger fragment can be found in Anip973 cell line on the **Northern** blot hybridization. The 3.0 kb transcriptions were found in various tissues. Over-expression in **heart** and skeletal muscle could be observed, whereas expression in spleen, liver, **kidney**, placental and **lung** could be found except colon, thyroid gland and small intestine. These manifests indicate that OPB7-1 gene has a wide-range expression in human multiple tissues. A 1.0 kb cDNA fragment was acquired by linking up **EST** fragments homologous match 5' end and PCR. BLAST analysis revealed that OPB7-1 gene has extremely low sequence identity with any known genes from GenBank and any sequences from **EST database**. The

chromosomal localization of it was determined by RH location method. The OPB7-1 fragment was localized to chromosome 1p31-34. That OPB7-1 gene has an extensive expression pattern, may be a novel tumor gene related to **lung** carcinoma. Further research needs to be done to obtain the full-length cDNA of OPB7-1 gene. It will be helpful to investigate the expression in **lung** cancer cases and other tumor tissues for further determining the function of OPB7-1 gene in development of tumor.

L32 ANSWER 3 OF 78 MEDLINE DUPLICATE 2

ACCESSION NUMBER: 2002050047 MEDLINE
DOCUMENT NUMBER: 21634684 PubMed ID: 11774267
TITLE: Identification and characterization of 9D7, a novel human protein overexpressed in renal cell carcinoma.
COMMENT: Erratum in: Int J Cancer 2002 Apr 20;98(6):956
AUTHOR: Klade Christoph S; Dohnal Alexander; Furst Walter; Sommergruber Wolfgang; Heider Karl-Heinz; Gharwan Helen; Ratschek Manfred; Adolf Gunther R
CORPORATE SOURCE: Boehringer Ingelheim Austria GmbH, Research and Development, Vienna, Austria.. cklade@intercell.co.at
SOURCE: INTERNATIONAL JOURNAL OF CANCER, (2002 Jan 10) 97 (2) 217-24.
Journal code: 0042124. ISSN: 0020-7136.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200201
ENTRY DATE: Entered STN: 20020125
Last Updated on STN: 20020502
Entered Medline: 20020117

AB With the objective of discovering novel tumor-associated antigens of the cancer/testis type, we compared the transcriptional profiles of renal cell carcinoma (RCC) and non-tumorous **kidney** and further screened for genes expressed in RCC and testis, but not other normal tissues. In a first step, a representational difference analysis library consisting of approximately 1,900 RCC cDNA clones was generated. Clones were then spotted onto filters and hybridized with cDNA probes derived from a testis-specific cDNA library, a pool of RCCs and a pool of 10 healthy normal tissues, respectively. Based on strong hybridization signals with both RCC and testis, but not normal tissue probes, 185 clones were sequenced and annotated. After **EST-database** comparison, 35 clones were selected for experimental analysis, including conventional and quantitative RT-PCR as well as **Northern** blotting. Clone 9D7 showed strong mRNA expression in RCC as well as in several other major tumor types. In normal tissues there was little or no mRNA expression with the exception of **heart**. 9D7 was cloned to full-size and found to represent a novel human gene containing 5 exons residing on chromosome 14. Alternative splicing within exon 1 generates 2 open-reading-frames consisting of 717 or 435 bp corresponding to predicted proteins of 239 or 145 amino acids. 9D7 shows high homology (227/239 amino acids or 95% identity) to a growth factor-inducible gene of *Rattus norvegicus* involved in apoptosis. In situ hybridization as well as immunohistochemical analysis using 9D7-specific antisera confirmed overexpression of 9D7 in RCCs as compared to normal **kidney** tissue.
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L32 ANSWER 4 OF 78 MEDLINE

ACCESSION NUMBER: 2002296564 IN-PROCESS
DOCUMENT NUMBER: 22032968 PubMed ID: 12036595
TITLE: Characterization and expression of the mouse tat
interactive protein 60 kD (TIP60) gene.
AUTHOR: McAllister Donna; Merlo Xanthi; Lough John
CORPORATE SOURCE: Department of Cell Biology, Neurobiology and Anatomy and
Cardiovascular Research Center, Medical College of
Wisconsin, 8701 West Watertown Plank Road, Milwaukee, WI
53226, USA.
SOURCE: GENE, (2002 May 1) 289 (1-2) 169-76.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020531
Last Updated on STN: 20020531

AB Tat interactive protein-60 (TIP60) is a novel histone acetyltransferase-
containing protein that has been implicated in the regulation of
transcription, DNA repair and apoptosis. In this report we describe the
structure and expression of the mouse TIP60 gene, as well the
localization
of TIP60 protein at the cellular level. The gene contains 14 exons within
a DNA sequence interval of 6611 bp. The assembled exons comprise a 1,539
bp DNA complementary to RNA (cDNA) having 91.7 and 78.7% homology with
respective human and chick TIP60 cDNAs. Translation predicts a
approximately 59 kD protein having 99.6 and 91.6% sequence homology with
respective human and chick proteins. Alignment with mouse expressed
sequence tag database entries indicates,
similar to human and chick TIP60, the existence of an alternative splice
created by removal of exon 5 that results in a 1383 bp cDNA with a
predicted translation product of approximately 53 kD. **Northern**
hybridization analysis reveals a peak of TIP60 expression during mouse
embryogenesis at E11; in adult tissues TIP60 is expressed in the
following
order of intensity: testis>**heart**>brain>**kidney**>liver>
lung, with little to no expression in spleen and skeletal muscle.
Cellular localization using green fluorescent protein-TIP fusion
constructs and immunohistochemistry reveal that TIP53 and TIP60 are
nuclear proteins.

L32 ANSWER 5 OF 78 MEDLINE
ACCESSION NUMBER: 2002312767 IN-PROCESS
DOCUMENT NUMBER: 22050200 PubMed ID: 12054757
TITLE: A novel gene IC53 stimulates ECV304 cell proliferation and
is upregulated in failing heart.
AUTHOR: Chen Jingzhou; Liu Baohua; Liu Yuqing; Han Yu; Yu Hui;
Zhang Yinhui; Lu Lihe; Zhen Yisong; Hui Rutai
CORPORATE SOURCE: Sino-German Laboratory for Molecular Medicine and Center
for Molecular Cardiology, Fuwai Hospital, Peking Union
Medical College and Chinese Academy of Medical Sciences,
167 Beilishilu, Beijing 100037, China.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2002
May 31) 294 (1) 161-6.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020611
Last Updated on STN: 20020611

AB C53, cloned from rat brain cDNA library, can bind to p35, the precursor of activator of Cdk5. A novel gene with 84% homolog to C53, named IC53, was cloned from our 5300 **EST database** of human aorta cDNA library (GenBank Accession No. AF110322). Computational analysis showed that IC53 cDNA is 2538 bp long, encoding 419 amino acids, mapped to chromosome 17q21.31 with 12 exons, ubiquitously expressed in 12 tested normal tissues and 8 tumor cell lines from MTN membranes and vascular endothelial cells by **Northern blot** and in situ hybridization, and upregulated in the rat models of subacute **heart failure** and chronic ischemic **heart failure** by left coronary ligation. Stable transfection of IC53 stimulates ECV304 cell proliferation by 2.1-fold compared to cells with empty vector ($P < 0.05$). The results support that IC53 is a novel gene, mainly expressed in vascular endothelial cells and mediates cell proliferation. (c) 2002 Elsevier Science (USA).

L32 ANSWER 6 OF 78 MEDLINE DUPLICATE 3
 ACCESSION NUMBER: 2002078855 MEDLINE
 DOCUMENT NUMBER: 21664104 PubMed ID: 11804785
 TITLE: Nobox is a homeobox-encoding gene preferentially expressed in primordial and growing oocytes.
 AUTHOR: Suzumori Nobuhiro; Yan Changning; Matzuk Martin M; Rajkovic Aleksandar
 CORPORATE SOURCE: Department of Pathology, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.
 CONTRACT NUMBER: HD00849 (NICHD)
 HD33438 (NICHD)
 HD37231 (NICHD)
 SOURCE: MECHANISMS OF DEVELOPMENT, (2002 Feb) 111 (1-2) 137-41. Journal code: 9101218. ISSN: 0925-4773.
 PUB. COUNTRY: Ireland
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: PDB-AY061761
 ENTRY MONTH: 200206
 ENTRY DATE: Entered STN: 20020128
 Last Updated on STN: 20020615
 Entered Medline: 20020614

AB To identify novel genes involved in early mammalian folliculogenesis, we used the Unigene collection of mouse cDNA libraries to identify unique expressed **sequence tags** in a newborn mouse **ovary** cDNA library. Nobox (newborn **ovary** homeobox-encoding gene) was one of several genes identified by in silico (electronic **database**) subtraction. We cloned the mouse Nobox cDNA and characterized its genomic organization. The gene spans 14kb and is encoded by eight exons. The Nobox gene maps to proximal chromosome 6

in the mouse, and we identified a portion of the human gene encoding a NOBOX homolog which resides at a syntenic position on chromosome 7q35. Reverse transcriptase polymerase chain reaction and **Northern blot** analyses show that Nobox is preferentially expressed in the **ovary** at high levels. In situ hybridization analysis demonstrates that Nobox mRNA is present in primordial and growing oocytes. Nobox is one of the first homeobox-encoding genes preferentially expressed during mammalian folliculogenesis.

L32 ANSWER 7 OF 78 MEDLINE
 ACCESSION NUMBER: 2002132101 MEDLINE
 DOCUMENT NUMBER: 21856794 PubMed ID: 11867260

TITLE: Digital expression profiles of the prostate
 androgen-response program.
 AUTHOR: Clegg Nigel; Eroglu Burak; Ferguson Camari; Arnold Hugh;
 Moorman Alec; Nelson Peter S
 CORPORATE SOURCE: Division of Human Biology, Fred Hutchinson Cancer Research
 Center, 1100 Fairview Avenue North, Seattle, WA 98109,
 USA.
 CONTRACT NUMBER: CA75173 (NCI)
 SOURCE: JOURNAL OF STEROID BIOCHEMISTRY AND MOLECULAR BIOLOGY,
 (2002 Jan) 80 (1) 13-23.
 Journal code: 9015483. ISSN: 0960-0760.
 PUB. COUNTRY: England: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200205
 ENTRY DATE: Entered STN: 20020228
 Last Updated on STN: 20020515
 Entered Medline: 20020514

AB The androgen receptor (AR) and cognate ligands regulate vital aspects of
prostate cellular growth and function including proliferation,
 differentiation, apoptosis, lipid metabolism, and secretory action. In
 addition, the AR pathway also influences pathological processes of the
prostate such as benign prostatic hypertrophy and **prostate**
 carcinogenesis. The pivotal role of androgens and the AR in
prostate biology prompted this study with the objective of
 identifying molecular mediators of androgen action. Our approach was
 designed to compare transcriptomes of the LNCaP **prostate** cancer
 cell line under conditions of androgen depletion and androgen stimulation
 by generating and comparing collections of expressed **sequence**
tags (ESTs). A total of 4400 **ESTs** were
 produced from LNCaP cDNA libraries and these **ESTs** assembled into
 2486 distinct transcripts. Rigorous statistical analysis of the
 expression
 profiles indicated that 17 genes exhibited a high probability ($P > 0.9$) of
 androgen-regulated expression. **Northern** analysis confirmed that
 the expression of KLK3/PSA, FKBP5, KRT18, DKFZP564K247, DDX15, and HSP90
 is regulated by androgen exposure. Of these, only KLK3/PSA is known to be
 androgen-regulated while the other genes represent new members of the
 androgen-response program in **prostate** epithelium. LNCaP gene
 expression profiles defined by two independent experiments using the
 serial analysis of gene expression (SAGE) method were compared with the
EST profiles. Distinctly different expression patterns were
 produced from each dataset. These results are indicative of the
 sensitivity of the methods to experimental conditions and demonstrate the
 power and the statistical limitations of digital expression analyses.

L32 ANSWER 8 OF 78 MEDLINE DUPLICATE 4
 ACCESSION NUMBER: 2001433969 MEDLINE
 DOCUMENT NUMBER: 21374363 PubMed ID: 11459928
 TITLE: Identification of a chloride-formate exchanger expressed
 on
 the brush border membrane of renal proximal tubule cells.
 AUTHOR: Knauf F; Yang C L; Thomson R B; Mentone S A; Giebisch G;
 Aronson P S
 CORPORATE SOURCE: Departments of Internal Medicine and Cellular and
 Molecular
 Physiology, Yale University School of Medicine, New Haven,
 CT 06520-8029, USA.
 CONTRACT NUMBER: DK-17433 (NIDDK)
 DK-33793 (NIDDK)

SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE
UNITED STATES OF AMERICA, (2001 Jul 31) 98 (16) 9425-30.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AY032863
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010903
Last Updated on STN: 20010903
Entered Medline: 20010830

AB A key function of the proximal tubule is retrieval of most of the vast quantities of NaCl and water filtered by the **kidney**. Physiological studies using brush border vesicles and perfused tubules have indicated that a major fraction of Cl(-) reabsorption across the apical membrane of proximal tubule cells occurs via Cl(-)-formate exchange. The molecular identity of the transporter responsible for renal brush border Cl(-)-formate exchange has yet to be elucidated. As a strategy to identify one or more anion exchangers responsible for mediating Cl(-) reabsorption in the proximal tubule, we screened the expressed **sequence tag database** for homologs of pendrin, a transporter previously shown to mediate Cl(-)-formate exchange. We now report the cDNA cloning of CFEX, a mouse pendrin homolog with expression in the **kidney** by **Northern** analysis. Sequence analysis indicated that CFEX very likely represents the mouse ortholog of human SLC26A6. Immunolocalization studies detected expression of CFEX, but not pendrin, on the brush border membrane of proximal tubule cells. Functional expression studies in *Xenopus* oocytes demonstrated that CFEX mediates Cl(-)-formate exchange. Taken together, these observations identify CFEX as a prime candidate to mediate Cl(-)-formate exchange in the proximal tubule and thereby to contribute importantly to renal NaCl reabsorption. Given its wide tissue distribution, CFEX also may contribute to transcellular Cl(-) transport in additional epithelia such as the pancreas and contribute to transmembrane Cl(-) transport in nonepithelial tissues such as the **heart**.

L32 ANSWER 9 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:539361 BIOSIS
DOCUMENT NUMBER: PREV200100539361
TITLE: The PKCzeta gene produces a heterogeneous population of messenger RNA in rat hippocampus.
AUTHOR(S): Crary, J. F. (1); Hernandez, I. (1); Tcherepanov, A. (1); Bergold, P. (1); Sacktor, T. C. (1)
CORPORATE SOURCE: (1) Physiology and Pharmacology, SUNY Downstate Brooklyn, Brooklyn, NY USA
SOURCE: Society for Neuroscience Abstracts, (2001) Vol. 27, No. 2, pp. 1596. print.
Meeting Info.: 31st Annual Meeting of the Society for Neuroscience San Diego, California, USA November 10-15, 2001
ISSN: 0190-5295.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English
AB PKMzeta, the catalytic fragment of PKCzeta, has been implicated in the maintenance of LTP and LTD. The rat PKCzeta gene encodes two mRNAs with distinct 5' ends. One mRNA contains an open-reading frame (ORF) for full-length PKCzeta, whereas the second contains an ORF for PKMzeta. To study the expression of the PKCzeta gene, a modified 5' RACE that

eliminates uncapped truncated mRNAs was used to amplify both PKMzeta and PKCzeta transcripts from rat hippocampus and **kidney**. 5' RACE using a specific primer for PKCzeta yielded a homogeneous population of cDNA regardless of tissue origin. In contrast, 5' RACE using a PKMzeta specific primer yielded products of at least 9 different sizes from the hippocampus but products of only one size from the **kidney**. Two PKCzeta mRNA bands at apprx2.4 kb and apprx4.5 kb that were enriched in cerebellum and **kidney** were detected by **Northern blot** of total RNA. In contrast, a apprx2.4 and a apprx4.5 kb PKMzeta mRNA were enriched in cerebellum, cortex and hippocampus. Seven human cDNAs containing sequences with high homology to rat PKMzeta mRNA were found in Genbank's **EST database**, demonstrating phylogenetic conservation. In conclusion, a heterogeneous population of PKMzeta mRNAs arise from the PKCzeta gene and may be an evolutionarily conserved mechanism of forming PKMzeta. It has been proposed that the PKMzeta mRNA comes from an internal promotor within the PKCzeta gene (Marshall et al., DNA Cell Biol. 2000 Dec; 19(12):707-19). Our results are consistent with this hypothesis since there was no identify between the extreme 5' end of the PKCzeta and PKMzeta mRNAs. A CRE found in the putative rat PKMzeta promoter is conserved in the human genome.

L32 ANSWER 10 OF 78 MEDLINE DUPLICATE 5
 ACCESSION NUMBER: 2001700837 MEDLINE
 DOCUMENT NUMBER: 21617007 PubMed ID: 11741334
 TITLE: Molecular cloning of novel mouse and human putative citrate lyase beta-subunit.
 AUTHOR: Morikawa J; Nishimura Y; Uchida A; Tanaka T
 CORPORATE SOURCE: Department of Molecular and Cellular Pharmacology, Mie University School of Medicine, 2-174 Edobashi, Tsu, Mie, 514-8507, Japan.
 SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2001 Dec 21) 289 (5) 1282-6.
 Journal code: 0372516. ISSN: 0006-291X.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF428253; GENBANK-AF428254
 ENTRY MONTH: 200202
 ENTRY DATE: Entered STN: 20011220
 Last Updated on STN: 20020220
 Entered Medline: 20020219
 AB Using a fluorescent differential display (FDD) technique, a novel cDNA was identified by screening for gene expressed differentially between the Dunn osteosarcoma cell line and the LM8 cell line, an isolated variant of the Dunn cell line that has high metastatic potential to the **lung**. Molecular cloning of the cDNA revealed the clone has similarity to a bacterial fermentation enzyme, the citrate lyase beta-subunit (CL-beta). **Northern blot** and competitive reverse transcription-PCR (RT-PCR) analysis revealed up-regulation of the gene in the LM8 cell line. An RNA Master blot indicated that the mRNA encoding CL-beta is expressed abundantly in murine **heart**, liver, and **kidney**. A human expressed **sequence tag (EST)** **database** search suggested that a similar cDNA is expressed in humans. A gene with identical sequence is located on chromosome 13 in the genome **database** (Sanger centre, UK). These data suggest that a citrate fermentation pathway may exist in eukaryotes including mammals.

L32 ANSWER 11 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:245085 BIOSIS

DOCUMENT NUMBER: PREV200100245085

TITLE: Identification and characterisation of ACEH, a human homolog of angiotensin-converting enzyme.

AUTHOR(S): Tipnis, Sarah R. (1); Hooper, Nigel M. (1); Christie, Gary;

Turner, Anthony J. (1)

CORPORATE SOURCE: (1) School of Biochemistry and Molecular Biology, University of Leeds, Leeds, West Yorkshire, LS2 9JT UK

SOURCE: FASEB Journal, (March 8, 2001) Vol. 15, No. 5, pp. A875. print.

Meeting Info.: Annual Meeting of the Federation of

American

Societies for Experimental Biology on Experimental Biology
2001 Orlando, Florida, USA March 31-April 04, 2001
ISSN: 0892-6638.

DOCUMENT TYPE: Conference

LANGUAGE: English

SUMMARY LANGUAGE: English

AB A novel human zinc metalloprotease with considerable homology to angiotensin-converting enzyme (ACE) has been identified from an **EST database**. Following isolation of a partial clone from a cDNA library, the full length cDNA was deduced in conjunction with 3' and 5' RACE. The translated protein, termed ACEH, contains a zinc binding motif (HEMGH), an N-terminal signal sequence, a C-terminal transmembrane domain and has 7 potential N-linked glycosylation sites. Unlike somatic ACE, it has only a single catalytic domain. Expression of

a C-terminally truncated ACEH cDNA, lacking the transmembrane and cytosolic domains, in mammalian cells produces a protein of molecular mass 120kDa. Upon deglycosylation this mass is reduced to 85kDa. The expressed protein is able to hydrolyse angiotensin I and II, however it has a different action to ACE. It appears to act as a carboxypeptidase A-like enzyme and removes a single residue from the C-terminal of these substrates. In contrast to ACE, ACEH does not hydrolyse bradykinin and it does not

appear

to be inhibited by typical ACE inhibitors such as captopril, lisinopril and enalaprilat. The genomic sequence of ACEH has also been identified

and

is located on the X chromosome in position p22 and has many similarities to the ACE gene. Northern blotting analyses have shown that the mRNA encoding this protein is approximately 3.4kb and is most highly expressed in **heart, kidney** and testis. The precise requirements for substrate specificity and inhibitor binding are being defined.

L32 ANSWER 12 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:492683 BIOSIS

DOCUMENT NUMBER: PREV200100492683

TITLE: Cloning of a novel mouse Gabarapl2 cDNA and its characterization.

AUTHOR(S): Chen, Zheng (1); Xin, Yu-Rong; Jiang, Ying; Jiang, Ju-Xiang

CORPORATE SOURCE: (1) School of Life Science, Suzhou University, Suzhou, 215006: zhengchen_99@yahoo.com, xinyu@umdnj.edu China

SOURCE: Acta Pharmacologica Sinica, (August, 2001) Vol. 22, No. 8, pp. 751-755. print.

ISSN: 0253-9756.

DOCUMENT TYPE: Article

LANGUAGE: English

SUMMARY LANGUAGE: Chinese; English

AB AIM: To clone a novel mouse GABAA-receptor-associated protein like 2 (Gabarapl2) gene, and to analysis its primary function. METHODS: With the aid of computer, the human GABARAPL2 cDNA was used as information probe to

search mouse **EST database** of GenBank for mouse homolog. A series of overlapping **EST** were found and assembled into an **EST** contig using Genetics Computer Group (GCG) ASSEMBLY program. The existence of the gene was then identified by experiment. **Northern** blotting was performed to hybridize (alpha-32P) dATP labeled probe with mRNA of 11 different mouse tissues that had been transferred to the nylon membrane. RESULTS: The novel gene was deposited in GenBank under Accession No AF190644. Its cDNA contained an intact open reading frame and a canonical polyadenylation signal AATAAA followed by polyA. The deduced protein was completely identical to that of human GABARAPL2, and was termed Gabarapl2 by Mouse Gene Nomenclature Committee. The putative protein of Gabarapl2 has a calculated molecular weight of 13 700 and an isoelectric point of 8.56. It was also predicted to contain

two protein kinase C phosphorylation sites and one tyrosine kinase phosphorylation site. **Northern** hybridization showed that Gabarapl2 was expressed as a single 1.35 kb transcript, with high levels in brain, thymus, **lung, heart, kidney**, and liver, and low in pancreas, testis, small intestine, colon, and stomach. CONCLUSION: A novel mouse Gabarapl2 gene was cloned and identified.

L32 ANSWER 13 OF 78 MEDLINE DUPLICATE 6
ACCESSION NUMBER: 2001261706 MEDLINE
DOCUMENT NUMBER: 21201248 PubMed ID: 11304808
TITLE: Identification of genes differentially expressed in benign prostatic hyperplasia.
AUTHOR: DiLella A G; Toner T J; Austin C P; Connolly B M
CORPORATE SOURCE: Departments of Pharmacology, Merck Research Laboratories, P.O. Box 4, West Point, PA 19486.. tony_dilella@merck.com
SOURCE: JOURNAL OF HISTOCHEMISTRY AND CYTOCHEMISTRY, (2001 May) 49 (5) 669-70.
Journal code: 9815334. ISSN: 0022-1554.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010521
Last Updated on STN: 20010521
Entered Medline: 20010517

AB Differences between benign prostatic hyperplasia (BPH) and normal **prostate** tissue at the level of mRNA expression provide an opportunity to identify candidate genes for this disease. A cDNA subtraction procedure was used to isolate differentially expressed genes in BPH. The subtraction was done by solution hybridization of BPH cDNA against excess normal **prostate** cDNA. We identified known, **EST**, and novel genes by sequence and **database** analysis of the subtracted cDNAs. Several of these cDNAs were used as probes in **Northern** blotting analysis to confirm over-expression of their corresponding mRNAs in BPH tissues. One highly upregulated sequence of interest shared identity with a known mRNA encoding human NELL2, a protein

containing epidermal growth factor-like domains. NELL2 was not previously reported to be expressed in **prostate** and may code for a novel prostatic growth factor. In situ hybridization analysis of hyperplastic **prostate** specimens demonstrated that NELL2 mRNA expression is

predominantly localized in basal cells of the epithelium. Disease-related changes in the levels of NELL2 may contribute to alterations in epithelial-stromal homeostasis in BPH. (J Histochem Cytochem 49:669-670, 2001)

L32 ANSWER 14 OF 78 MEDLINE DUPLICATE 7
ACCESSION NUMBER: 2001414085 MEDLINE
DOCUMENT NUMBER: 21356311 PubMed ID: 11463335
TITLE: Identification of PEX5p-related novel peroxisome-targeting signal 1 (PTS1)-binding proteins in mammals.
AUTHOR: Amery L; Sano H; Mannaerts G P; Snider J; Van Looy J; Fransen M; Van Veldhoven P P
CORPORATE SOURCE: Katholieke Universiteit Leuven, Campus Gasthuisberg (O/N), Departement Moleculaire Celbiologie, Afdeling Farmacologie, Herestraat 49, B-3000 Leuven, Belgium.
SOURCE: BIOCHEMICAL JOURNAL, (2001 Aug 1) 357 (Pt 3) 635-46. Journal code: 2984726R. ISSN: 0264-6021.
PUB. COUNTRY: England; United Kingdom
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB032591; GENBANK-AB032592; GENBANK-AB032593; GENBANK-AJ245503
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010903
Last Updated on STN: 20010903
Entered Medline: 20010830

AB Based on peroxin protein 5 (Pex5p) homology searches in the expressed **sequence tag database** and sequencing of large full-length cDNA inserts, three novel and related human cDNAs were identified. The brain-derived cDNAs coded for two related proteins that differ only slightly at their N-terminus, and exhibit 39.8% identity to human PEX5p. The shorter liver-derived cDNA coded for the C-terminal tetratricopeptide repeat-containing domain of the brain cDNA-encoded proteins. Since these three proteins specifically bind to various C-terminal peroxisome-targeting signals in a manner indistinguishable from Pex5p and effectively compete with Pex5p in an in vitro peroxisome-targeting signal 1 (PTS1)-binding assay, we refer to them as 'Pex5p-related proteins' (Pex5Rp). In contrast to Pex5p, however, human PEX5Rp did not bind to Pex14p or to the RING finger motif of Pex12p, and could not restore PTS1 protein import in Pex5(-/-) mouse fibroblasts. Immunofluorescence analysis of epitope-tagged PEX5Rp in Chinese hamster **ovary** cells suggested an exclusively cytosolic localization. **Northern**-blot analysis showed that the PEX5R gene, which is localized to chromosome 3q26.2--3q27, is expressed preferentially in brain. Mouse PEX5Rp was also delineated. In addition, experimental evidence established that the closest-related yeast homologue, YMR018wp, did not bind PTS1. Based on its subcellular localization and binding properties, Pex5Rp may function as a regulator in an early step of the PTS1 protein import process.

L32 ANSWER 15 OF 78 MEDLINE DUPLICATE 8
ACCESSION NUMBER: 2001493705 MEDLINE
DOCUMENT NUMBER: 21427669 PubMed ID: 11536302
TITLE: GDEP, a new gene differentially expressed in normal prostate and prostate cancer.
AUTHOR: Olsson P; Bera T K; Essand M; Kumar V; Duray P; Vincent J; Lee B; Pastan I
CORPORATE SOURCE: Laboratory of Molecular Biology, Division of Basic

of Sciences, National Cancer Institute, National Institutes

Health, Bethesda, Maryland 20892-4255, USA.

SOURCE: PROSTATE, (2001 Sep 15) 48 (4) 231-41.
Journal code: 8101368. ISSN: 0270-4137.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200110

ENTRY DATE: Entered STN: 20010906

Last Updated on STN: 20011008

Entered Medline: 20011004

AB BACKGROUND: The **database** of human expressed **sequence tags** (dbEST) is a potential source for the identification of tissue specific genes. The **database** contains sequences that originate from cDNA libraries from different tissues cell types and tumors. METHODS: Computer based analysis identified a cluster of sequence homologous **ESTs**, containing **ESTs** derived only from human **prostate** cDNA libraries. The tissue specificity was examined by multiple tissue RNA dot blots and RT-PCR. The new RNA transcript was characterized using **northern** blot analysis, RACE-PCR, and a ribonuclease protection assay. RESULTS: We have identified

a gene differentially expressed in **prostate** using **EST database** analysis and experimental studies. We name the gene GDEP for gene differentially expressed in **prostate**. The major GDEP transcript is about 520 bp long. GDEP RNA was detected in nine **prostate** tissue samples, four normal and five cancer. Expression in **prostate** epithelial cells was established by in situ hybridization. Weak expression was detected in the **prostate** cancer cell line LNCaP. In vitro transcription/translation indicate that the RNA encodes a small 34 amino acid protein. The major transcript consists of two exons with one large intron (> 15 kb). The GDEP gene was mapped to chromosome 4q21.1 by radiation hybrid mapping. CONCLUSIONS: Our data proves that tissue specific genes can be identified by **EST database** mining. The **prostate** specificity of GDEP expression indicates that GDEP may be useful in the diagnosis or treatment

of **prostate** cancer. Published 2001 Wiley-Liss, Inc.

L32 ANSWER 16 OF 78

MEDLINE

DUPLICATE 9

ACCESSION NUMBER: 2001357671 MEDLINE

DOCUMENT NUMBER: 21311632 PubMed ID: 11418238

TITLE: Identification of a new fibroblast growth factor receptor, FGFR5.

AUTHOR: Sleeman M; Fraser J; McDonald M; Yuan S; White D; Grandison

P; Kumble K; Watson J D; Murison J G
CORPORATE SOURCE: Genesis Research and Development Corporation Ltd., 1 Fox Street, Parnell, Auckland, New Zealand.

SOURCE: GENE, (2001 Jun 27) 271 (2) 171-82.
Journal code: 7706761. ISSN: 0378-1119.

PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AF321300; GENBANK-AF321301

ENTRY MONTH: 200108

ENTRY DATE: Entered STN: 20010827

Last Updated on STN: 20010827

Entered Medline: 20010823

AB A novel fibroblast growth factor receptor (FGFR), designated FGFR5, was identified from an **EST database** of a murine lymph node stromal cell cDNA library. The **EST** has approximately 32% identity to the extracellular domain of FGFR1-4. Library screening with this **EST** identified two full-length alternative transcripts which we designated as FGFR5 beta and FGFR5 gamma. The main difference between these transcripts is that FGFR5 beta contains three extracellular Ig domains whereas FGFR5 gamma contains only two. A unique feature of FGFR5 is that it does not contain an intracellular tyrosine kinase domain.

Predictive structural modelling of the extracellular domain of FGFR5 gamma suggested that it was a member of the I-set subgroup of the Ig-superfamily, consistent with the known FGFRs. **Northern** analysis of mouse and human FGFR5 showed detectable mRNA in a broad range of tissues, including **kidney**, brain and **lung**. Genomic sequencing identified four introns but identified no alternative transcripts containing a tyrosine kinase domain. Extracellular regions of FGFR5 beta and 5 gamma were cloned in-frame with the Fc fragment of human IgG(1) to generate recombinant non-membrane bound protein. Recombinant FGFR5 beta Fc and R5 gamma Fc demonstrated specific binding to the ligand FGF-2, but not FGF-7 or EGF. However, biological data suggest that FGF-2 binding to these proteins is with lower affinity than its cognate receptor FGFR2C. The above data indicate that this receptor should be considered as the fifth member of the FGFR family.

L32 ANSWER 17 OF 78

MEDLINE

DUPLICATE 10

ACCESSION NUMBER: 2001235758 MEDLINE

DOCUMENT NUMBER: 21142404 PubMed ID: 11245989

TITLE: cDNA cloning, mapping and expression of the mouse propionyl

CoA carboxylase beta (pccb), the gene for human type II propionic acidemia.

AUTHOR: Schrick J J; Lingrel J B

CORPORATE SOURCE: Department of Molecular Genetics, Microbiology and Biochemistry, University of Cincinnati, Cincinnati OH 45267, USA.. jerry.lingrel@uc.edu

CONTRACT NUMBER: HL41496 (NHLBI)

SOURCE: GENE, (2001 Feb 7) 264 (1) 147-52.

Journal code: 7706761. ISSN: 0378-1119.

PUB. COUNTRY: Netherlands

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AF327060

ENTRY MONTH: 200105

ENTRY DATE: Entered STN: 20010517

Last Updated on STN: 20010517

Entered Medline: 20010503

AB Propionyl CoA carboxylase (PCC) is a mitochondrial, biotin-dependent enzyme involved in the catabolism of amino acids, odd-chained fatty acids and other metabolites. PCC is composed of two equal subunits, alpha and beta, which are encoded by two separate genes at two distinct human loci. Mutations of either gene in humans results in propionic acidemia (PA). To identify the mouse cDNA for the propionyl CoA carboxylase beta-subunit (pccb), we have screened the mouse **EST database** using the human sequence. The murine mRNA transcript is approximately 2.3 kb, nearly 500 bps larger than the human approximately 1.8 kb transcript. A

PAC genomic DNA clone from the mouse was also isolated and used to generate probes and PCR primers for mapping the pccb locus in the mouse. Both the C57Bl/6J^{Ei} and Spret/^{Ei} alleles for regions flanking the pccb gene were sequenced to identify RFLPs. The Jackson Laboratory BSS and BSB backcross panel DNAs were then analyzed using a DdeI polymorphism placing the pccb locus on mouse chromosome 9. **Northern** blots of adult tissue show that the pccb gene is broadly expressed in the mouse. The approximately 2.3 kb transcript is most abundantly expressed in the **kidney**, liver, small intestine and stomach tissues.

L32 ANSWER 18 OF 78 MEDLINE DUPLICATE 11
 ACCESSION NUMBER: 2001272086 MEDLINE
 DOCUMENT NUMBER: 21238674 PubMed ID: 11340635
 TITLE: PRAC: A novel small nuclear protein that is specifically expressed in human prostate and colon.
 AUTHOR: Liu X F; Olsson P; Wolfgang C D; Bera T K; Duray P; Lee B; Pastan I
 CORPORATE SOURCE: Laboratory of Molecular Biology, Division of Basic Sciences, National Cancer Institute, National Institutes of Health, Bethesda, Maryland, USA.
 SOURCE: PROSTATE, (2001 May 1) 47 (2) 125-31.
 Journal code: 8101368. ISSN: 0270-4137.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200105
 ENTRY DATE: Entered STN: 20010529
 Last Updated on STN: 20010529
 Entered Medline: 20010521

AB BACKGROUND: The **database** of human Expressed **Sequence Tags** (dbEST) provides a potential source for identification of tissue-specific genes. This **database** contains sequences that originate from cDNA libraries from particular tumors, organs or cell types. In this report, we have used the **EST database** to identify PRAC, a novel gene specifically expressed in human **Prostate**, **prostate** cancer, Rectum And distal Colon.
 METHODS: Using a computer based analysis, a cluster of sequence homologous **ESTs** was identified which contained **ESTs** derived only from human **prostate** cDNA libraries. The tissue specificity was examined by multiple tissue RNA dot blots and RT-PCR. The PRAC transcript and protein was identified using **Northern** blot analysis, RACE-PCR, primer extension, and western blot. RESULTS: PRAC encode a 382 nucleotide RNA found in **prostate**, rectum, distal colon, and in three **prostate** cancer cell lines; LNCaP, PC-3 and DU145. This transcript encodes a 6 kDa nuclear protein. The PRAC gene is located on chromosome 17 at position 17q21, about 4 kbp downstream from the homeodomain Hoxb-13 gene. CONCLUSIONS: Our data proves that the **EST database** can be a useful tool for discovery of **prostate**-specific genes. The nuclear localization, identification of potential phosphorylation sites, and possible cotranscription with the Hoxb-13 gene suggest that PRAC may have a regulatory role in the nucleus.
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L32 ANSWER 19 OF 78 MEDLINE DUPLICATE 12
 ACCESSION NUMBER: 2001528245 MEDLINE
 DOCUMENT NUMBER: 21458557 PubMed ID: 11574155
 TITLE: Discovery and mapping of ten novel G protein-coupled receptor genes.

AUTHOR: Lee D K; Nguyen T; Lynch K R; Cheng R; Vanti W B; Arkhitko O; Lewis T; Evans J F; George S R; O'Dowd B F
 CORPORATE SOURCE: Department of Pharmacology, University of Toronto, Toronto, Ontario, M5S 1A8, Canada.
 SOURCE: GENE, (2001 Sep 5) 275 (1) 83-91.
 Journal code: 7706761. ISSN: 0378-1119.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF4111107; GENBANK-AF4111108; GENBANK-AF4111109;
 GENBANK-AF4111110; GENBANK-AF4111111; GENBANK-AF4111112;
 GENBANK-AF4111113; GENBANK-AF4111114; GENBANK-AF4111115;
 GENBANK-AF4111116; GENBANK-AF4111117
 ENTRY MONTH: 200112
 ENTRY DATE: Entered STN: 20011001
 Last Updated on STN: 20020122
 Entered Medline: 20011213

AB We report the identification, cloning and tissue distributions of ten novel human genes encoding G protein-coupled receptors (GPCRs) GPR78, GPR80, GPR81, GPR82, GPR93, GPR94, GPR95, GPR101, GPR102, GPR103 and a pseudogene, psi GPR79. Each novel orphan GPCR (oGPCR) gene was discovered using customized searches of the GenBank high-throughput genomic sequences

database with previously known GPCR-encoding sequences. The expressed genes can now be used in assays to determine endogenous and pharmacological ligands. GPR78 shared highest identity with the oGPCR gene

GPR26 (56% identity in the transmembrane (TM) regions). psi GPR79 shared highest sequence identity with the P2Y(2) gene and contained a frame-shift

truncating the encoded receptor in TM5, demonstrating a pseudogene. GPR80 shared highest identity with the P2Y(1) gene (45% in the TM regions), while GPR81, GPR82 and GPR93 shared TM identities with the oGPCR genes HM74 (70%), GPR17 (30%) and P2Y(5) (40%), respectively. Two other novel GPCR genes, GPR94 and GPR95, encoded a subfamily with the genes encoding the UDP-glucose and P2Y(12) receptors (sharing >50% identities in the TM regions). GPR101 demonstrated only distant identities with other GPCR genes and GPR102 shared identities with GPR57, GPR58 and PNR (35-42% in the TM regions). GPR103 shared identities with the neuropeptide FF 2, neuropeptide Y2 and galanin GalR1 receptors (34-38% in the TM regions). **Northern** analyses revealed GPR78 mRNA expression in the pituitary and placenta and GPR81 expression in the pituitary. A search of the GenBank **databases** with the GPR82 sequence retrieved an identical sequence in an expressed **sequence tag (EST)** partially encoding GPR82 from human colonic tissue. The GPR93 sequence retrieved an identical, human **EST** sequence from human primary tonsil B-cells and an **EST** partially encoding mouse GPR93 from small intestinal tissue. GPR94 was expressed in the frontal cortex, caudate putamen and thalamus of brain while GPR95 was expressed in the human **prostate** and rat stomach and fetal tissues. GPR101 revealed mRNA transcripts in caudate putamen and hypothalamus. GPR103

mRNA signals were detected in the cortex, pituitary, thalamus, hypothalamus, basal forebrain, midbrain and pons.

L32 ANSWER 20 OF 78 MEDLINE DUPLICATE 13
 ACCESSION NUMBER: 2002018676 MEDLINE
 DOCUMENT NUMBER: 21337971 PubMed ID: 11444019
 TITLE: cDNA of a novel mRNA expressed predominantly in mouse

kidney.
AUTHOR: Kawamura T; Kuroda N; Kimura Y; Lazoura E; Okada N; Okada H
CORPORATE SOURCE: Department of Molecular Biology, Nagoya City University School of Medicine, Mizuho-cho, Mizuho-ku, Nagoya, 467-8601, Japan.
SOURCE: BIOCHEMICAL GENETICS, (2001 Feb) 39 (1-2) 33-42.
Journal code: 0126611. ISSN: 0006-2928.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20020121
Last Updated on STN: 20020121
Entered Medline: 20011205

AB We examined embryonic carcinoma (EC) cells for a potential prototype molecule of C3, the third component of complement. PCR primers, corresponding to the base sequence derived from the C3 cDNA of several species, were used for PCR amplification of the EC cell cDNA. All the PCR products obtained had the same sequence and showed no sequence homology

to

C3. Subsequently, cDNA clones were isolated from a mouse liver cDNA library using the PCR product as a probe. Unexpectedly, neither the base sequence of the cDNA clones nor the amino acid sequence deduced from the cDNA showed homology to C3, although partial homology was observed to a number of sequences from **EST databases**. We designated this new clone NCU-G1. **Northern** hybridization experiments revealed that NCU-G1 is expressed constitutively not only in the mouse fetus but also in various mouse tissues, and is most abundant in the **kidney** cortex.

L32 ANSWER 21 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:288231 BIOSIS
DOCUMENT NUMBER: PREV200100288231
TITLE: Molecular cloning of NELIN, a putative human cytoskeleton regulation gene.
AUTHOR(S): Zhao Yong; Wei Ying-Jie; Cao Hui-Qing; Ding Jin-Feng (1)
CORPORATE SOURCE: (1) Molecular Medicine Center for Cardiovascular Diseases, Fu Wai Heart Hospital and Cardiovascular Institute, Peking Union Medical College and Chinese Academy of Medical Sciences, Beijing, 100037: jinfengd@yahoo.com China
SOURCE: Shengwu Huaxue yu Shengwu Wuli Xuebao, (2001) Vol. 33, No. 1, pp. 19-24. print.
ISSN: 0582-9879.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: Chinese; English

AB For searching cardiovascular-associated genes and investigating their expression profiles, human adult **heart** and aorta cDNA libraries were constructed, and a novel gene from adult **heart** cDNA library was isolated based on large-scale **ESTs** (expressed **sequence tags**) sequencing (GenBank accession number AF114264). The 2 736 bp clone contains one 1 344 bp open reading frame extending from 412 to 1 755. We named it NELIN (nexilin-like protein) because it shares high similarity with the rat nexilin. NELIN was expression-restricted in **heart**, skeletal muscle, artery and vein by **Northern** blot and RT-PCR analyses, and mapped to chromosome 1p31-1p32 by **database** analyses. Based on domain structure, NELIN could regulate the formations of stress fibers, focal adhesion and its signaling complex, and even participates in the signal transduction in

FAs(focal adhesions).

L32 ANSWER 22 OF 78 MEDLINE DUPLICATE 14
ACCESSION NUMBER: 2000483169 MEDLINE
DOCUMENT NUMBER: 20445994 PubMed ID: 10990492
TITLE: Isolation and expression of PASK, a serine/threonine kinase, during rat embryonic development, with special emphasis on the pancreas.
AUTHOR: Miao N; Fung B; Sanchez R; Lydon J; Barker D; Pang K
CORPORATE SOURCE: Ontogeny, Inc., Cambridge, Massachusetts 02138-1118, USA.
SOURCE: JOURNAL OF HISTOCHEMISTRY AND CYTOCHEMISTRY, (2000 Oct) 48 (10) 1391-400.
Journal code: 9815334. ISSN: 0022-1554.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200010
ENTRY DATE: Entered STN: 20001019
Last Updated on STN: 20020420
Entered Medline: 20001010
AB We report the isolation and characterization of a serine/threonine kinase expressed during rat pancreas development. This kinase was cloned as part of a general screen using degenerate oligonucleotides to map expression of kinases and receptors during the course of pancreatic development. Sequence analysis showed it to be a member of the ste20-like serine/threonine kinase family. **Northern** blotting analysis against both fetal and adult tissues showed two transcripts, one of 2 kb and the other of 4 kb. The ratio of transcript expression varied with the tissue. In situ hybridization analysis showed that this gene is expressed in the early gut and pancreatic epithelium. By embryonic Day 15, the transcript is localized to cells that will eventually become exocrine in nature. In situ hybridization analysis also demonstrated high levels of expression in the choroid plexus, the developing myocardium, **kidney**, CNS, dorsal root ganglia, and testes. In addition, a search of the **EST database** revealed a related human kinase not previously described.

L32 ANSWER 23 OF 78 MEDLINE DUPLICATE 15
ACCESSION NUMBER: 2000432844 MEDLINE
DOCUMENT NUMBER: 20247020 PubMed ID: 10784614
TITLE: B cell- and monocyte-activating chemokine (BMAC), a novel non-ELR alpha-chemokine.
AUTHOR: Sleeman M A; Fraser J K; Murison J G; Kelly S L; Prestidge R L; Palmer D J; Watson J D; Kumble K D
CORPORATE SOURCE: Genesis Research and Development Corp. Ltd, PO Box 50, Auckland, New Zealand.
SOURCE: INTERNATIONAL IMMUNOLOGY, (2000 May) 12 (5) 677-89.
Journal code: 8916182. ISSN: 0953-8178.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF044196; GENBANK-AF073957; GENBANK-AF144754
ENTRY MONTH: 200009
ENTRY DATE: Entered STN: 20000928
Last Updated on STN: 20000928
Entered Medline: 20000921
AB A novel alpha-chemokine, designated KS1, was identified from an **EST database** of a murine immature keratinocyte cDNA

library. The **EST** has 94% similarity to a recently cloned human gene, **BRAK**, that has no demonstrated function. **Northern** analysis of mouse and human genes showed detectable mRNA in brain, intestine, muscle and **kidney**. Tumour panel blots showed that **BRAK** was down-regulated in cervical adenocarcinoma and uterine leiomyoma, but was up-regulated in breast invasive ductal carcinoma. **KS1** bound specifically to B cells and macrophages, as well as two B cell lines, **CESS** and **A20**,

and

a monocyte line, **THP-1**. **KS1** showed no binding to naive or activated T cells. In addition, **KS1** stimulated the chemotaxis of **CESS** and **THP-1** cells but not T cells. The s.c. injection of **KS1** creates a mixed inflammatory response in **Nude** and **C3H/HeJ** mice. The above data indicates that **KS1** and its human homologue represents a novel non-ELR alpha-chemokine that may have important roles in trafficking of B cells and monocytes. We propose the name B cell- and monocyte-activating chemokine (**BMAC**) for this molecule to reflect the described biological functions.

L32 ANSWER 24 OF 78 MEDLINE DUPLICATE 16
ACCESSION NUMBER: 2000404486 MEDLINE
DOCUMENT NUMBER: 20334634 PubMed ID: 10874211
TITLE: Isolation and characterization of human **NBL4**, a gene involved in the beta-catenin/tcf signaling pathway.
AUTHOR: Ishiguro H; Furukawa Y; Daigo Y; Miyoshi Y; Nagasawa Y; Nishiwaki T; Kawasoe T; Fujita M; Satoh S; Miwa N; Fujii Y;
Nakamura Y
CORPORATE SOURCE: Laboratory of Molecular Medicine, Human Genome Center, Institute of Medical Science, The University of Tokyo, Minato-ku, Tokyo 108-8639, Japan.
SOURCE: JAPANESE JOURNAL OF CANCER RESEARCH, (2000 Jun) 91 (6) 597-603.
Journal code: 8509412. ISSN: 0910-5050.
PUB. COUNTRY: Japan
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB030240; GENBANK-D30788; GENBANK-U13673
ENTRY MONTH: 200008
ENTRY DATE: Entered STN: 20000901
Last Updated on STN: 20000922
Entered Medline: 20000818
AB beta-Catenin, a key regulator of cellular proliferation, is often mutated in various types of human cancer. To investigate cellular responses related to the beta-catenin signaling pathway, we applied a differential display method using mouse cells transfected with an activated form of mutant beta-catenin. This analysis and subsequent **northern-blot** hybridization confirmed that expression of a murine gene encoding **NBL4** (novel band 4.1-like protein 4) was up-regulated by activation of beta-catenin. To examine a possible role of **NBL4** in cancer, we isolated the human homologue of the murine **NBL4** gene by matching **mNBL4** against the human **EST** (expressed sequence tag) database followed by 5' rapid amplification of cDNA ends (5'RACE). The cDNA of **hNBL4** encoded a protein of 598 amino acids that shared 87% identity in amino acid sequence with murine **NBL4** and 71% with zebrafish **NBL4**. A 2.2-kb **hNBL4** transcript was expressed in all human tissues examined with high levels of expression in brain, liver, thymus and peripheral blood leukocytes and low levels of expression in **heart**, **kidney**, testis and colon. We determined its chromosomal localization at 5q22 by fluorescence in situ hybridization. Expression of **hNBL4** was significantly reduced when beta-catenin was depleted in **SW480** cells, a human cancer cell line that constitutionally accumulates

beta-catenin. The results support the view that NBL4 is an important component of the beta-catenin / Tcf pathway and is probably related to determination of cell polarity or proliferation.

L32 ANSWER 25 OF 78 MEDLINE DUPLICATE 17
ACCESSION NUMBER: 2000294863 MEDLINE
DOCUMENT NUMBER: 20294863 PubMed ID: 10833435
TITLE: Mouse and human GTPBP2, newly identified members of the GP-1 family of GTPase.
AUTHOR: Kudo H; Senju S; Mitsuya H; Nishimura Y
CORPORATE SOURCE: Division of Immunogenetics, Kumamoto University Graduate School of Medical Sciences, Kumamoto, Japan.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2000 Jun 7) 272 (2) 456-65.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF168891; GENBANK-AF168990
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 20000720
Last Updated on STN: 20001027
Entered Medline: 20000710

AB We earlier identified the GTPBP1 gene which encodes a putative GTPase structurally related to peptidyl elongation factors. This finding was the result of a search for genes, the expression of which is induced by interferon-gamma in a macrophage cell line, THP-1. In the current study, we probed the expressed **sequence tag database** with the deduced amino acid sequence of GTPBP1 to search for partial cDNA clones homologous to GTPBP1. We used one of the partial cDNA clones to screen a mouse brain cDNA library and identified a novel gene, mouse GTPBP2, encoding a protein consisting of 582 amino acids and carrying GTP-binding motifs. The deduced amino acid sequence of mouse GTPBP2 revealed 44.2% similarity to mouse GTPBP1. We also cloned a human homologue of this gene from a cDNA library of the human T cell line, Jurkat. GTPBP2 protein was found highly conserved between human and mouse (over 99% identical), thereby suggesting a fundamental role of this molecule across species. On **Northern** blot analysis of various mouse tissues, GTPBP2 mRNA was detected in brain, thymus, **kidney** and skeletal muscle, but was scarce in liver. Level of expression of GTPBP2 mRNA was enhanced by interferon-gamma in THP-1 cells, HeLa cells, and thioglycollate-elicited mouse peritoneal macrophages. In addition, we determined the chromosomal localization of GTPBP1 and GTPBP2 genes in human and mouse. The GTPBP1 gene was mapped to mouse chromosome 15, region E3, and human chromosome 22q12-13.1, while the GTPBP2 gene is located in mouse chromosome 17, region C-D, and human chromosome 6p21-12.
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L32 ANSWER 26 OF 78 MEDLINE DUPLICATE 18
ACCESSION NUMBER: 2000211281 MEDLINE
DOCUMENT NUMBER: 20211281 PubMed ID: 10745026
TITLE: A novel karyopherin-beta homolog is developmentally and hormonally regulated in fetal lung.
AUTHOR: Zhang C; Sweezey N B; Gagnon S; Muskat B; Koehler D; Post M; Kaplan F
CORPORATE SOURCE: Departments of Human Genetics and Pediatrics, and Montreal Children's Hospital Research Institute, McGill University, Montreal, Quebec, Canada.
SOURCE: AMERICAN JOURNAL OF RESPIRATORY CELL AND MOLECULAR BIOLOGY,

(2000 Apr) 22 (4) 451-9.
Journal code: 8917225. ISSN: 1044-1549.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF110195
ENTRY MONTH: 200005
ENTRY DATE: Entered STN: 20000606
Last Updated on STN: 20000606
Entered Medline: 20000524

AB To investigate molecular mechanisms of **lung** organogenesis, we used representational difference analysis to search for glucocorticoid-inducible genes in developing **lung** in a fetal rat model. Messenger RNA prepared from fetal and adult rat **lung** was used to prepare "representative amplicons." Adult-**lung** complementary DNA (cDNA) amplicons were used as "driver" in successive rounds of subtractive hybridization/amplification to isolate target fetal **lung**-specific cDNAs. A single clone, which was conserved and had near-perfect homology to eight human/rodent expressed **sequence tags**, was used as template for 5' and 3' rapid amplification of cDNA ends and SPICE (system for polymerase chain reaction amplification

of
cDNA ends) reactions to obtain the 3.6-kb cDNA, LGL2 (Genbank, AF 110195) encoding a deduced polypeptide (lgl2) of 963 amino acids. **Northern** analysis confirmed that LGL2 is differentially expressed in fetal **lung** (maximal during the pseudoglandular stage, gestational Days 14 to 16), induced by glucocorticoid, and enriched in epithelium relative to the mesenchyme. LGL2 was also detected in human fetal **lung** at gestational Week 16 as well as in human and rat fetal brain, **heart**, intestine, and **kidney**. We mapped LGL2 to chromosome 1p33-34.2. Comparison with sequences in the genome **database** identified lgl2 as a member of the karyopherin-beta family of nuclear import proteins, with greatest homology to transportin SR. Maximal expression of LGL2 in the pseudoglandular stage of development is coordinate with that of key transcription factors that regulate prominent signal transduction pathways
in fetal **lung** organogenesis. We propose a role for lgl2 in nuclear import of transcription factors that regulate signal transduction during fetal **lung** development.

L32 ANSWER 27 OF 78 MEDLINE DUPLICATE 19
ACCESSION NUMBER: 2001033192 MEDLINE
DOCUMENT NUMBER: 20490014 PubMed ID: 11032736
TITLE: cDNA representational difference analysis of human neutrophils stimulated by GM-CSF.
AUTHOR: Yousefi S; Cooper P R; Mueck B; Potter S L; Jarai G
CORPORATE SOURCE: Novartis Horsham Research Centre, Wimblehurst Road, Horsham, West Sussex, RH12 5AB, United Kingdom.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2000 Oct 22) 277 (2) 401-9.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200011
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001130

AB Neutrophils are the first cell type to migrate out of the vascular space

and into the inflammatory site during an acute inflammation. However, in chronic inflammatory diseases, such as chronic obstructive pulmonary disease (COPD), a lack of clearance of neutrophils, imbalance between inflammatory mediators produced by neutrophils and their natural inhibitors make these cells a potential cause of tissue destruction in lung disease. Neutrophilic inflammation is generally characterised by high levels of local expression of activating cytokines (e.g., GM-CSF).

Only a few studies have been published so far that have investigated the expression of genes preferentially expressed in activated neutrophils.

The isolation of such genes, however, can lead to a better understanding of inflammatory disease and the identification of potential novel therapeutic targets or markers of the disease. We performed representational difference analysis of cDNA, a sensitive PCR-based subtractive enrichment procedure, and isolated 12 genes, 1 **EST** clone, and 3 sequences not represented in the public **databases**. Differential expression for 9 of these clones was confirmed by **Northern** hybridisation. Of the above nine transcripts three were chosen and shown to be up-regulated in neutrophils cocultured with stimulated primary human bronchial epithelial cells using a semiquantitative RT-PCR approach.

Among the known genes identified were HM-74, CIS1, Cathepsin C, alpha-enolase, CD44, and the gene Translocation Three Four (TTF), most of them previously

not known to be involved in GM-CSF induced neutrophil activation. Along with its tissue and cellular distribution we also derived the complete cDNA sequence and genomic structure of CIS1 using an in silico approach. In addition, we also report the initial characterisation of a novel gene, P1-89 that is primarily expressed in granulocytes and is up-regulated in activated cells. Our results identify several important genes associated with neutrophil activation and can lead to a better understanding of the molecular mechanisms of neutrophilic inflammations.
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L32 ANSWER 28 OF 78 MEDLINE DUPLICATE 20
ACCESSION NUMBER: 2000231760 MEDLINE
DOCUMENT NUMBER: 20231760 PubMed ID: 10767556
TITLE: cDNA cloning of acyl-CoA desaturase homologs in the silkworm, Bombyx mori.
AUTHOR: Yoshiga T; Okano K; Mita K; Shimada T; Matsumoto S
CORPORATE SOURCE: Laboratory of Molecular Entomology and Baculovirology, RIKEN, Hirosawa 2-1, Wako, Saitama, Japan.
SOURCE: GENE, (2000 Apr 4) 246 (1-2) 339-45.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF157627; GENBANK-AF182405; GENBANK-AF182406
ENTRY MONTH: 200005
ENTRY DATE: Entered STN: 20000613
Last Updated on STN: 20000613
Entered Medline: 20000531

AB We have isolated two acyl-CoA desaturase clones from a pheromone gland cDNA library by using the **EST** (expressed **sequence tag**) **database** of Bombyx mori. The putative acyl-CoA desaturases encoded by the clones desat 1 (2029bp) and desat 2 (2341bp) have 98% identity, and both proteins show 61% identities to Trichoplusia ni acyl-CoA Delta(11) desaturase. The deduced amino acid sequences

conserve well the histidine clusters that are catalytically essential for acyl-CoA desaturase activity. **Northern** blot and RT-PCR analyses revealed that both transcripts of desat 1 and desat 2 were expressed predominantly in the pheromone gland. Both transcripts detected 3 days before adult eclosion dramatically increased a day before adult eclosion, keeping the mRNA levels high even after eclosion. These results, combined with the fact that Delta(11) and Delta(10, 12) desaturation of palmitate is a key step to synthesize pheromone in *B. mori*, suggest that the desaturases encoded by desat 1 and desat 2 are involved in either or both of the desaturation steps in the pheromone biosynthetic pathway of *B. mori*. The mRNA levels of desat 1 and desat 2 were not affected by decapitation or injection of the pheromone biosynthesis activating neuropeptide (PBAN) into the adult female moth, suggesting that the transcription of desat 1 and desat 2 is not regulated by PBAN. In addition to the clones in the pheromone gland, eight other clones encoding the

same

Delta(9) desaturase homolog were found in an embryonic cDNA library by searching from the **EST database** of *B. mori*. The deduced amino acid sequence from one of the clones (desat 3) shows 79% identity to *T. ni* Delta(9) desaturase but only 52% identity to the desaturases in the pheromone gland of *B. mori*. **Northern** blot analysis showed that the mRNA corresponding to the desat 3 was detected

in

the **ovary** and fat body, but not in the pheromone gland.

Abundance of the Delta(9) desaturase clones (eight out of the 762

randomly

sequenced clones) in the library prepared from diapause-destined embryos (40h after oviposition) suggests that the Delta(9) desaturase encoded by desat 3 plays an important role in embryonic development in *B. mori*.

L32 ANSWER 29 OF 78

MEDLINE

ACCESSION NUMBER: 2001323800 MEDLINE

DOCUMENT NUMBER: 20541296 PubMed ID: 11092749

TITLE: Identification and expression analysis of C3orf1, a novel human gene homologous to the *Drosophila* RP140-upstream gene.

AUTHOR: Escarceller M; Pluvinet R; Sumoy L; Estivill X

CORPORATE SOURCE: Medical and Molecular Genetics Center, Institut de Recerca Oncologica, Hospital Duran i Reynals, Barcelona, Spain.

SOURCE: DNA SEQUENCE, (2000) 11 (3-4) 335-8.

Journal code: 9107800. ISSN: 1042-5179.

PUB. COUNTRY: Switzerland

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AF210057

ENTRY MONTH: 200106

ENTRY DATE: Entered STN: 20010611

Last Updated on STN: 20010611

Entered Medline: 20010607

AB We have isolated C3orf1, a novel gene on human chromosome 3 showing homology to the *Drosophila* RP140-upstream gene. When mutated, RP140-upstream causes lethality in flies through an unknown mechanism, perhaps by interfering with transcription of the RP140 RNA polymerase subunit. The human C3orf1 gene encodes a predicted membrane protein of 32.2 kDa with four transmembrane domains without any other known motifs. **Northern** blot analysis showed generalized expression of C3orf1, enhanced in **heart** and skeletal muscle. **EST database** searching revealed the existence of a homologue gene in mouse. Thus, the C3orf1 gene is conserved and may perform an essential function in all tissues in mammals.

L32 ANSWER 30 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:311511 BIOSIS
DOCUMENT NUMBER: PREV200100311511
TITLE: Two unique genes cloned from differentially expressed ESTs after induction of K562 cells with sodium butyrate.
AUTHOR(S): Mitchell, T. (1); Plonczynski, M.; Hardy, C. L.; Safaya, S.; Steinberg, M. H.
CORPORATE SOURCE: (1) Pediatric Hematology/Oncology, University of Mississippi Medical Center, Jackson, MS USA
SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 1, pp. 235a. print.
Meeting Info.: 42nd Annual Meeting of the American Society of Hematology San Francisco, California, USA December 01-05, 2000 American Society of Hematology
. ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

AB We studied the temporal changes in gene expression in K562 cells at intervals from 2-to 48-h following induction of differentiation with sodium butyrate, using differential display-PCR and gene expression arrays. Globin synthesis was verified by the activity of a transduced A-globin gene promoter, and an average 62-fold increase in -globin gene expression was observed during induction. This high through-put gene screening approach allowed the preparation of a partial profile of over 100 genes induced by butyrate. From this profile two novel genes, named D12 and P30, which resulted from two unique **ESTs** were "cloned" from available **databases**. Differential expression of these two gene fragments was confirmed by **Northern** blot analysis and semi-quantitative PCR. D12 was characterized by mRNA of approximately 1.8 kb, and P30 was characterized by mRNAs of approximately 2.6 and 4.0 kb resulting from either alternative mRNA splicing, alternative transcription start sites or other mRNA processing. Some of the other properties of these genes were included. The TRP (tertratricopeptide) genes are active in processes such as transcription and mitosis. The expression of these two genes is unrelated to known genes and their expression is not restricted to erythroid cells. D12 is expressed primarily in brain and P30 is expressed in **heart**, skeletal muscle, **kidney** and placenta. Although the function of these novel genes in erythroid maturation is unclear, a variety of regulatory proteins is required for transcription of -globin and fetal hemoglobin in K562 cells. Their identification under these defined conditions may serve to relate previously undescribed pathways to the transcriptional cascades that are active in erythroid differentiation.

L32 ANSWER 31 OF 78 MEDLINE DUPLICATE 21
ACCESSION NUMBER: 2001040426 MEDLINE
DOCUMENT NUMBER: 20435298 PubMed ID: 10978524
TITLE: Murine cDNA encoding a novel type I HSP40/DNAJ homolog, mmDjA4(1).
AUTHOR: Hata M; Ohtsuka K
CORPORATE SOURCE: Cell Stress Biology Research Group, Aichi Cancer Center Research Institute, Chikusa-ku, 464-8681, Nagoya, Japan.
SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (2000 Sep 7) 1493 (1-2) 208-10.
Journal code: 0217513. ISSN: 0006-3002.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB032401
ENTRY MONTH: 200012
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001207

AB We have cloned a cDNA encoding a novel type I HSP40/DNAJ protein from the mouse **EST database**, and designated it mmDjA4 (Mus musculus type I DnaJ homolog 4). This cDNA encodes 397 amino acid residues

whose sequence shows 67 and 51% identity with the previously identified murine Hsj2 and mDj3, respectively. The sequence of mmDjA4 contains the four repeats of CxxCxGxG motif which are characteristic of type I HSP40/DNAJ proteins, and a CaaX prenylation motif at the carboxy terminus.

Northern blot analysis showed that mmDjA4 is specifically expressed in mouse testis and **heart**. This is the fourth member of the mammalian type I HSP40/DNAJ family to be identified.

L32 ANSWER 32 OF 78 MEDLINE DUPLICATE 22
ACCESSION NUMBER: 2001012409 MEDLINE
DOCUMENT NUMBER: 20461778 PubMed ID: 10858550
TITLE: Cloning, expression and functional characterization of rat napsin.
AUTHOR: Schauer-Vukasinovic V; Wright M B; Breu V; Giller T
CORPORATE SOURCE: F. Hoffmann-La Roche Ltd., Pharma Division, Preclinical Research, Grenzacherstrasse 124, CH-4070 Basel, Switzerland.
SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (2000 Jun 21) 1492 (1) 207-10.
Journal code: 0217513. ISSN: 0006-3002.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200010
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001031

AB A full-length cDNA clone coding for rat napsin was identified by homology search of the ZooSeq rat **EST database** (Incyte).

Northern blot analysis revealed high expression of napsin mRNA transcripts in **kidney**, **lung** and spleen. Western blot analysis showed that rat napsin is expressed in **kidney** as a 50-kDa, highly glycosylated, monomeric protein. Lysates prepared from human embryonic **kidney** cells (HEK293) transfected with rat napsin showed increased enzymatic activity which was inhibited by pepstatin.

L32 ANSWER 33 OF 78 MEDLINE DUPLICATE 23
ACCESSION NUMBER: 2000397938 MEDLINE
DOCUMENT NUMBER: 20299143 PubMed ID: 10837915
TITLE: Molecular cloning and characterisation of GPR74 a novel G-protein coupled receptor closest related to the Y-receptor family.
AUTHOR: Parker R M; Copeland N G; Eyre H J; Liu M; Gilbert D J; Crawford J; Couzens M; Sutherland G R; Jenkins N A; Herzog H
CORPORATE SOURCE: Garvan Institute of Medical Research, Neurobiology Program,

St. Vincent's Hospital, 384 Victoria Street, Darlinghurst,
NSW 2010, Sydney, Australia.
SOURCE: BRAIN RESEARCH. MOLECULAR BRAIN RESEARCH, (2000 May 5) 77
(2) 199-208.
Journal code: 8908640. ISSN: 0169-328X.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200008
ENTRY DATE: Entered STN: 20000824
Last Updated on STN: 20000824
Entered Medline: 20000811

AB A novel gene product, GPR74, with homology to the seven
transmembrane-domain receptor superfamily, has been cloned. GPR74 has
been identified from the expressed **sequence tags** (**EST**) **database**. Subsequent PCR amplification of that
sequence and screening of a human **heart** cDNA library led to the
isolation of a 1.7-kb cDNA clone encoding a protein of 408 amino acids.
GPR74 shows highest amino acid identity (33%) to the human neuropeptide
Y-receptor subtype Y2. The human and mouse genes for GPR74 have been
isolated and their exon-intron structures determined. In both species the
gene consists of four exons spanning around 20 kb with the exon-intron
borders being 100% conserved. **Northern** analysis of various human
tissues reveals highest levels of mRNA expression in brain and
heart. In situ hybridisation analysis of rat brain tissue confirms
this result and identifies the hippocampus and amygdala nuclei as the
brain areas with particular high expression of GPR74 mRNA. Fluorescence
in situ hybridisation, PCR analysis on a radiation hybrid panel and
interspecific mouse backcross mapping have localised the genes to human
chromosome 4q21 and mouse chromosome 5. Expression of the human GPR74
cDNA as a GFP-fusion protein in various cell lines reveals the inability of
the recombinant receptor protein to reach the cell surface. This is
consistent with the lack of NPY specific binding in these cells and suggests that
unknown factors are required for a full functional receptor complex.

L32 ANSWER 34 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:299307 BIOSIS
DOCUMENT NUMBER: PREV200100299307
TITLE: Overexpression of ribosomal proteins in chronic
lymphocytic leukemia identified by subtractive hybridization.
AUTHOR(S): Witzens, Mathias (1); Krackhardt, Angela M. (1); Harig,
Sabine (1); Donovan, John W. (1); Gribben, John G. (1)
CORPORATE SOURCE: (1) Adult Oncology, Dana-Farber Cancer Institute, Boston,
MA USA
SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 2, pp.
168b. print.
Meeting Info.: 42nd Annual Meeting of the American Society
of Hematology San Francisco, California, USA December
01-05, 2000 American Society of Hematology
. ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Chronic lymphocytic leukemia (CLL) is the most common form of leukemia.

Although CLL is relatively indolent, it is incurable with current therapies. The idiotype can elicit an autologous T and B cell immune response. However, these responses are relatively weak and the idiotype has to be determined individually in each patient. To identify new tumor associated antigens in B cell malignancies that could serve as a target antigen for immunotherapy, we performed an analysis of a subtracted cDNA library. The library was constructed by subtraction of mRNA from healthy

B
cells (driver) from mRNA of primary CLL tumor cells (tester). Tumor specific cDNA sequences were isolated by subtracting the driver cDNA from the tester cDNA. The remaining cDNA fragments were PCR amplified, cloned and sequenced. 120 sequences were analysed. As expected, we found sequences coding for MHC molecules, since driver and tester mRNA were derived from different individuals, confirming the quality of the constructed library. Interestingly, in the remaining tumor specific sequences 9 ribosomal proteins (S2, S6, S9, S10, S15, L12, L13, L18 and L24) were identified. In addition to their overexpression in CLL, systematic analysis of **EST databases** revealed expression of these proteins in wide panel of various human tumors, including lung, pancreatic, prostate, esophagus, renal and colon cancer as well as lymphoma. Using **Northern Blot**, we confirmed that the ribosomal protein S2 is overexpressed in CLL tumor cells when compared with healthy PBMC. The expression of ribosomal proteins in a broad variety of malignancies indicates an important role

of these proteins in the developement and maintenance of the malignant state.

However, in spite of the overexpression of ribosomal proteins in CLL, the immune system does not generate a significant antitumor response. To examine whether cellular immune tolerance towards tumors expressing ribosomal proteins can be overcome, we used two independent bioinformatic algorithms to predict for HLA class I binding immunogenic peptides. We identified 3 decamer peptides with high prediction scores for binding to HLA-A*0201 within the 221 amino acid long open reading frame of the S2 sequence. Numerous other peptides with high prediction scores for binding to HLA-A*0201 could also be identified in the remaining ribosomal proteins. Ongoing studies are characterizing the immunogenicity of these peptides for both allogeneic and autologous CD8+ T cell responses and will

determine the ability of peptide stimulated CD8+ T cells to lyse primary tumor cells that overexpress ribosomal proteins.

L32 ANSWER 35 OF 78 MEDLINE
ACCESSION NUMBER: 2000123885 MEDLINE
DOCUMENT NUMBER: 20123885 PubMed ID: 10631317
TITLE: Caveolin-1 isoforms are encoded by distinct mRNAs.
Identification Of mouse caveolin-1 mRNA variants caused by alternative transcription initiation and splicing.
AUTHOR: Kogo H; Fujimoto T
CORPORATE SOURCE: Department of Anatomy and Molecular Cell Biology, Nagoya University School of Medicine, Showa-ku, Nagoya, Japan..
hkogo@med.nagoya-u.ac.jp
SOURCE: FEBS LETTERS, (2000 Jan 14) 465 (2-3) 119-23.
Journal code: 0155157. ISSN: 0014-5793.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200002
ENTRY DATE: Entered STN: 20000309

Last Updated on STN: 20000309

Entered Medline: 20000218

AB By searching the **EST database** with the known cDNA sequence encoding alpha-caveolin-1 (full-length: FL), we found a variant having a hitherto unknown sequence in place of the first exon (5'-end variant: 5'V). The expression level of 5'V mRNA was equivalent to that of FL mRNA. The entire sequences of FL and 5'V mRNA were determined by 3'- and 5'-RACE analysis; their sizes were 2484 bp and 2533 bp, respectively, and the sequences were identical except for the region of the first exon. By **Northern blotting**, FL and 5'V mRNAs showed the same tissue distribution, and were intensely expressed in the **lung**, **heart**, and skeletal muscle. Analyzing the protein production from these mRNAs using green fluorescent protein as a tag, we found FL mRNA to produce the alpha-isoform predominantly, but to form little beta-isoform. The production of the beta-isoform from 5'V mRNA was also demonstrated.

By sequence analysis of the first intron of the caveolin-1 gene, a TATA box was found at 28 bp upstream of the transcription initiation site for 5'V mRNA. This is the first demonstration of caveolin-1 mRNA variants generated by alternative transcription initiation, and it indicates that the two isoforms of caveolin-1 are produced from two distinct mRNAs.

L32 ANSWER 36 OF 78 MEDLINE DUPLICATE 24
ACCESSION NUMBER: 2000412228 MEDLINE
DOCUMENT NUMBER: 20314386 PubMed ID: 10854696
TITLE: Mouse receptor-activity-modifying proteins 1, -2 and -3: amino acid sequence, expression and function.
AUTHOR: Husmann K; Sexton P M; Fischer J A; Born W
CORPORATE SOURCE: Research Laboratory for Calcium Metabolism, Departments of Orthopaedic Surgery and Medicine, Zurich, Switzerland.. khusmann@balgrist.unizh.ch
SOURCE: MOLECULAR AND CELLULAR ENDOCRINOLOGY, (2000 Apr 25) 162 (1-2) 35-43.
Journal code: 7500844. ISSN: 0303-7207.
PUB. COUNTRY: Ireland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200008
ENTRY DATE: Entered STN: 20000907
Last Updated on STN: 20000907
Entered Medline: 20000828

AB The calcitonin receptor-like receptor (CRLR) requires novel receptor-activity-modifying proteins (RAMPs) for its function as an adrenomedullin (ADM) or a calcitonin (CT) gene-related peptide (CGRP) receptor. Here, mouse cDNA clones representing expressed **sequence tags (ESTs)** in the GenEMBL **database** have been identified. They encode for proteins with 70, 68 and 84% amino acid sequence identity with respect to human RAMP1, -2 and -3. On **Northern blot** analysis of polyA(+) RNA mouse RAMP1 (mRAMP1) encoding mRNA with an apparent size of 0.8 kb was predominantly observed in embryonic and adult brain and **lung** and in adult skeletal muscle. Mouse RAMP2 encoding 0.8 and 1.2 kb mRNA were recognized in all tissues analyzed with the highest levels in embryonic brain, **lung** and gut and in adult **heart**, **lung**, skeletal muscle and brain. A single 1.2 kb mRAMP3 encoding transcript was mainly expressed in embryonic and adult brain. In COS-7 cells co-expressing rat CRLR (rCRLR) and mRAMP1, [125I]alphaCGRP binding was inhibited by ralphaCGRP(8-37), ralphaCGRP and rbetaCGRP with IC(50) of 1.4+/-0.5, 4.5+/-0.6 and 7+/-0.3 nM, respectively. CyclicAMP accumulation was maximally stimulated tenfold by rbetaCGRP and ralphaCGRP with EC(50) of 0.65+/-0.67 and 0.86+/-0.6

nM.

In the same cells co-expressing rCRLR and mRAMP2, binding of [125I]rADM was displaced by rADM and rADM(20-50) with IC(50) of 1.9+/-0.5 and 3.4+/-1.4 nM, respectively, and a maximal sevenfold stimulation of cAMP accumulation was observed with rADM with an EC(50) of 0.82+/-0.85 nM. In the cells co-expressing rCRLR and mRAMP3, [125I]alphaCGRP binding was inhibited by ralphaCGRP(8-37), rbetaCGRP, ralphaCGRP, rADM and rADM(20-50) with IC(50) between 4 and 22 nM. cAMP accumulation was stimulated by rADM with an EC(50) of 5.1+/-2.7 nM that was 12-fold and 11-fold lower than that of ralphaCGRP and rbetaCGRP. In conclusion, mouse RAMP1, -2 and -3 exhibit high amino acid sequence homology to the corresponding human RAMPs. Co-expression of rCRLR with mRAMP1, -2 or -3 in COS-7 cells revealed distinct CGRP-, ADM- or ADM/CGRP receptors.

L32 ANSWER 37 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2002:223827 BIOSIS

DOCUMENT NUMBER: PREV200200223827

TITLE: Cloning and functional characterization of a cation-Cl cotransporter interacting protein.

AUTHOR(S): Isenring, Paul (1); Gagnon, Edith (1); Caron, Luc (1)

CORPORATE SOURCE: (1) Groupe de Nephrologie de L'Hotel-Dieu de Quebec, Departement de Medecine, Faculte de Medecine, Universite Laval, Quebec, PQ Canada

SOURCE: Journal of the American Society of Nephrology, (September, 2000) Vol. 11, No. Program and Abstract Issue, pp.

30A-31A.

<http://www.jasn.org/>. print.

Meeting Info.: 33rd Annual Meeting of the American Society of Nephrology and the 2000 Renal Week Toronto, Ontario, Canada October 10-16, 2000

ISSN: 1046-6673.

DOCUMENT TYPE: Conference

LANGUAGE: English

AB The cation-Cl cotransporters (CCC) mediate the coupled movement of Na and/or K to that of Cl across the plasmalemma of animal cells. In polarized tissues, cation-Cl cotransport is involved in net transepithelial water and salt movement, and in non-polarized tissues, cation-Cl cotransport modulates the water and the electrolyte content of cells. To date, the CCC family comprises two branches of homologous membrane proteins. One branch includes the Na-K-Cl cotransporters (NKCC1 and 2) and the Na-Cl cotransporter (NCC1), and the other branch, the K-Cl cotransporters (KCC1, 2, 3, and 4). Here, we have isolated the first member of a third CCC family branch. This member was first identified in human and mouse expressed **sequence tag (EST)** **databases** as a 500-bp sequence homologous to a region in the carboxy-terminus of the CCCs. We isolated corresponding cDNAs from a human

heart cDNA library, and the full-length clone, termed WO3.3, was found to encode a 914-residue polypeptide having a calculated molecular mass of 96.2 kDa. Overall, WO3.3 shares apprx25% identity in amino acid sequence with each of the known CCCs. Sequence analyses predict a 12-transmembrane domain (tm) region, two N-linked glycosylation sites between tm5 and tm6, and a large intracellular carboxy-terminus containing

protein kinase C phosphorylation sites. **Northern** blot analysis uncovers a apprx3.7-kb transcript present in muscle, placenta, brain, and **kidney**. With regard to function, WO3.3 expressed either in HEK-293 cells or *Xenopus laevis* oocytes does not increase Rb-, Na- and Cl-coupled transport during 5-min or 6-hour fluxes, respectively. In the oocyte, however, WO3.3 specifically inhibits human NKCC1-mediated 86Rb flux. In addition, coimmunoprecipitation studies using lysates from

WO3.3-transfected HEK-293 cells suggest a direct interaction of WO3.3 with endogenous NKCC. Thus, we have cloned and characterized the first putative heterologous CCC interacting protein (CIP) known at present. CIP1 may be part of a novel family of proteins that modifies the activity or kinetics of CCCs through heterodimer formation.

L32 ANSWER 38 OF 78 MEDLINE
ACCESSION NUMBER: 2001700700 MEDLINE
DOCUMENT NUMBER: 21616802 PubMed ID: 11741232
TITLE: Human proton/oligopeptide transporter (POT) genes: identification of putative human genes using bioinformatics.
AUTHOR: Botka C W; Wittig T W; Graul R C; Nielsen C U; Higaka K; Amidon G L; Sadee W
CORPORATE SOURCE: Department of Biopharmaceutical Sciences, University of California San Francisco, San Francisco CA 94143-0446, USA.
SOURCE: AAPS PharmSci, (2000) 2 (2) E16.
Journal code: 100897065. ISSN: 1522-1059.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20011220
Last Updated on STN: 20020208
Entered Medline: 20020207

AB The proton-dependent oligopeptide transporters (POT) gene family currently consists of approximately 70 cloned cDNAs derived from diverse organisms. In mammals, two genes encoding peptide transporters, *PeptT1* and *PeptT2* have been cloned in several species including humans, in addition to a rat histidine/peptide transporter (*rPHT1*). Because the *Candida elegans* genome contains five putative POT genes, we searched the available protein and nucleic acid **databases** for additional mammalian/human POT genes, using iterative BLAST runs and the human expressed **sequence tags (EST) database**. The apparent human orthologue of *rPHT1* (expression largely confined to rat brain and retina) was represented by numerous **ESTs** originating from many tissues. Assembly of these **ESTs** resulted in a contiguous sequence covering approximately 95% of the suspected coding region. The contig sequences and analyses revealed the presence of several possible splice variants of *hPHT1*. A second closely related human **EST**-contig displayed high identity to a recently cloned mouse cDNA encoding cyclic adenosine monophosphate (cAMP)-inducible 1 protein (gi:4580995). This contig served to identify a PAC clone containing deduced exons and introns of the likely human orthologue (termed *hPHT2*). **Northern** analyses with **EST** clones indicated that *hPHT1* is primarily expressed in skeletal muscle and spleen, whereas *hPHT2* is found in spleen, placenta, lung, leukocytes, and heart. These results suggest considerable complexity of the human POT gene family, with relevance to the absorption and distribution of cephalosporins and other peptoid drugs.

L32 ANSWER 39 OF 78 MEDLINE DUPLICATE 25
ACCESSION NUMBER: 2000282814 MEDLINE
DOCUMENT NUMBER: 20282814 PubMed ID: 10820484
TITLE: Development of a prostate cDNA microarray and statistical

gene expression analysis package.
AUTHOR: Carlisle A J; Prabhu V V; Elkahloun A; Hudson J; Trent J
M;

Linehan W M; Williams E D; Emmert-Buck M R; Liotta L A;
Munson P J; Krizman D B

CORPORATE SOURCE: Laboratory of Pathology, National Cancer Institute,
Rockville, Maryland, USA.

SOURCE: MOLECULAR CARCINOGENESIS, (2000 May) 28 (1) 12-22.
Journal code: 8811105. ISSN: 0899-1987.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200006

ENTRY DATE: Entered STN: 20000616

Last Updated on STN: 20000616

Entered Medline: 20000606

AB A cDNA microarray comprising 5184 different cDNAs spotted onto nylon
membrane filters was developed for **prostate** gene expression
studies. The clones used for arraying were identified by cluster analysis
of > 35 000 **prostate** cDNA library-derived expressed
sequence tags (ESTs) present in the dbEST
database maintained by the National Center for Biotechnology
Information. Total RNA from two cell lines, **prostate** line 8.4
and melanoma line UACC903, was used to make radiolabeled probe for filter
hybridizations. The absolute intensity of each individual cDNA spot was
determined by phosphorimager scanning and evaluated by a bioinformatics
package developed specifically for analysis of cDNA microarray
experimentation. Results indicated 89% of the genes showed intensity
levels above background in **prostate** cells compared with only 28%
in melanoma cells. Replicate probe preparations yielded results with
correlation values ranging from $r = 0.90$ to 0.93 and coefficient of
variation ranging from 16 to 28%. Findings indicate that among others,
the
keratin 5 and vimentin genes were differentially expressed between these
two divergent cell lines. Follow-up **northern** blot analysis
verified these two expression changes, thereby demonstrating the
reliability of this system. We report the development of a cDNA
microarray
system that is sensitive and reliable, demonstrates a low degree of
variability, and is capable of determining verifiable gene expression
differences between two distinct human cell lines. This system will prove
useful for differential gene expression analysis in **prostate**
-derived cells and tissue.

L32 ANSWER 40 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:88451 BIOSIS

DOCUMENT NUMBER: PREV200100088451

TITLE: Cloning and functional characterization of a novel
beta-adrenergic-like receptor from *Drosophila*

melanogaster.

AUTHOR(S): Yu, E. J.; Kennedy, K.; Chatwin, H. M.; Reale, V.; Evans,
P. D.

SOURCE: Society for Neuroscience Abstracts, (2000) Vol. 26, No.
1-2, pp. Abstract No.-343.7. print.
Meeting Info.: 30th Annual Meeting of the Society of
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Society for Neuroscience
. ISSN: 0190-5295.

DOCUMENT TYPE: Conference

LANGUAGE: English

SUMMARY LANGUAGE: English

AB The functional role of the small amounts of the catecholamine, norepinephrine (NE), present in the insect nervous system has been an enigma for many years and has been overshadowed by the successes achieved in studies on the functional roles of octopamine and dopamine receptors in insect nervous systems (see Evans, 1980, Adv. Insect Physiol., 15:317-473; Roeder, 1994, Comp.Biochem.Physiol., 107C:1-12).

Here

we report on the cloning and functional characterization of a novel G-protein coupled receptor from *Drosophila melanogaster* that has structural homology with vertebrate beta-adrenergic receptors. We originally identified part of the sequence of this receptor from a *Drosophila* **EST database**. We then obtained the full coding sequence of the receptor using PCR on *Drosophila* head mRNA. The open reading frame encodes a receptor of 322 amino acids with a predicted molecular weight of 36.5kDa. The protein has seven transmembrane domains as revealed by hydropathy plot and many other conserved features of

GPCRs.

Sequence comparisons reveal that it has the highest sequence homology with

vertebrate beta-adrenergic receptors. **Northern** blot analysis of poly(A)+RNA from adult body parts indicates that the receptor is expressed

as a single transcript of 3.7kb in heads but not bodies, consistent with a

functional role in the nervous system. The receptor shows high expression in poly(A)+RNA from embryos and adults but not from larvae. When expressed

in *Xenopus* oocytes, either alone or along with the promiscuous G-protein, Galpha-16, we could find no evidence for coupling of the receptor to either calcium or cyclic AMP based second messenger pathways. However, when stably expressed in Chinese Hamster **Ovary** cells, a NE induced increase in cyclic AMP levels could be detected in some cell lines.

L32 ANSWER 41 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:97103 BIOSIS

DOCUMENT NUMBER: PREV200100097103

TITLE: A new electroneutral member of Na/HCO₃ cotransporter (NBC) family cloned from human brain (NBCn2).

AUTHOR(S): Grichtchenko, I. I. (1); Choi, I.; Boron, W. F.

CORPORATE SOURCE: (1) Yale Univ Med Sch, New Haven, CT USA

SOURCE: Society for Neuroscience Abstracts, (2000) Vol. 26, No. 1-2, pp. Abstract No.-306.7. print.

Meeting Info.: 30th Annual Meeting of the Society of Neuroscience New Orleans, LA, USA November 04-09, 2000
Society for Neuroscience
. ISSN: 0190-5295.

DOCUMENT TYPE: Conference

LANGUAGE: English

SUMMARY LANGUAGE: English

AB We obtained the full-length sequence of the human NBCn2 (GENBANK AF069512),

a new electroneutral member of Na⁺/HCO₃ cotransporter (NBC) family. We cloned it by searching the **EST database** against rkNBC, screening a Lambda ZAPII cDNA library from human frontal cortex (gift of Dr. N. Johnston, John Hopkins University) with **EST** clone, and then using 5' RACE. NBCn2 is 56% identical to the electrogenic rkNBC and 78% identical to electroneutral NBCn1. By **Northern** blotting, the NBCn2 mRNA signal is robust in all regions of human brain and also in testis; moderate in **kidney**, pancreas and **ovary**; and

weak in spinal cord, **prostate**, small intestine, colon and peripheral blood (leukocytes). We used voltage and pH-sensitive microelectrodes to study the function of NBCn2 expressed in *Xenopus* oocytes. Switching the external buffer from HEPES to CO₂/HCO₃ did not elicited a change in membrane potential (V_m), but (after the initial CO₂-induced acidification) caused pHi to increase at a rate of 8 ± 3 x 10⁻⁵pH unit/s (n= 9) in NBCn2-expressing cells. DIDS (500 μM) slowed the pHi recovery by >90%. Na⁺ removal slowed and usually reversed the pHi recovery (probably reflecting reversal of the transporter). In the absence of Na⁺, removing Cl⁻ did not change the pHi trajectory, ruling out Na⁺-driven Cl⁻/HCO₃ exchange. Thus, our data show that NBCn2 is an electroneutral Na/HCO₃ cotransporter. (Support: NIH R01 NS18400 & NKF).

L32 ANSWER 42 OF 78 MEDLINE DUPLICATE 26
 ACCESSION NUMBER: 1999376996 MEDLINE
 DOCUMENT NUMBER: 99376996 PubMed ID: 10446133
 TITLE: Cloning and functional expression of a human Na(+) and Cl(-)-dependent neutral and cationic amino acid transporter
 AUTHOR: Sloan J L; Mager S
 CORPORATE SOURCE: Department of Cell and Molecular Physiology and the Curriculum in Neurobiology, University of North Carolina, Chapel Hill, North Carolina 27599, USA.
 SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1999 Aug 20) 274 (34) 23740-5.
 PUB. COUNTRY: United States
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF151978; GENBANK-AF161714
 ENTRY MONTH: 199909
 ENTRY DATE: Entered STN: 19990921
 Last Updated on STN: 19990921
 Entered Medline: 19990909
 AB A Na(+)-dependent neutral and cationic amino acid transport system (B(0+)) plays an important role in many cells and tissues; however, the molecular basis for this transport system is still unknown. To identify new transporters, the expressed **sequence tag database** was queried, and cDNA fragments with sequence similarity to the Na(+)/Cl(-)-dependent neurotransmitter transporter family were identified. Based on these sequences, rapid amplification of cDNA ends of human mammary gland cDNA was used to obtain a cDNA of 4.5 kilobases (kb). The open reading frame encodes a 642-amino acid protein named amino acid transporter B(0+). Human ATB(0+) (hATB(0+)) is a novel member of the Na(+)/Cl(-)-dependent neurotransmitter transporter family with the highest sequence similarity to the glycine and proline transporters. **Northern** blot analysis identified transcripts of approximately 4.5 kb and approximately 2 kb in the **lung**. Another tissue survey suggests expression in the trachea, salivary gland, mammary gland, stomach, and pituitary gland. Electrophysiology and radiolabeled amino acid uptake measurements were used to functionally characterize the transporter expressed in *Xenopus* oocytes. hATB(0+) was found to transport both neutral and cationic amino acids, with the highest affinity for hydrophobic amino acids and the lowest affinity for proline. Amino acid transport was Na(+) and Cl(-)-dependent and was attenuated in the presence

of 2-aminobicyclo-[2.2.1]-heptane-2-carboxylic acid, a system B(0+) inhibitor. These characteristics are consistent with system B(0+) amino acid transport. Thus, hATB(0+) is the first cloned B(0+) amino acid transporter.

L32 ANSWER 43 OF 78 MEDLINE
ACCESSION NUMBER: 1999253969 MEDLINE
DOCUMENT NUMBER: 99253969 PubMed ID: 10318827
TITLE: Molecular cloning and tissue-specific expression of a novel murine laminin gamma3 chain.
AUTHOR: Iivanainen A; Morita T; Tryggvason K
CORPORATE SOURCE: Division of Matrix Biology, Department of Medical Biochemistry and Biophysics, Karolinska Institute, S-17177 Stockholm, Sweden.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1999 May 14) 274 (20) 14107-11.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF079520
ENTRY MONTH: 199906
ENTRY DATE: Entered STN: 19990628
Last Updated on STN: 19990628
Entered Medline: 19990617
AB A novel laminin gamma3 chain was identified from the expressed **sequence tag** data base at the National Center for Biotechnology Information. A complete cDNA derived peptide sequence reveals a 1592-amino acid-long primary translation product, including a tentative 33-amino acid-long signal peptide. Comparison with the laminin gamma1 chain predicts that the two polypeptides have equal spatial dimensions.
In addition, the well conserved domains VI and III(LE4) predict that gamma3 containing laminins are able to integrate to the laminin network and also via nidogen connect to other protein networks in the basement membranes. Combination of **Northern** analysis and in situ hybridization experiments indicate that expression of the gamma3 chain is highly tissue- and cell-specific, being significantly strong in capillaries and arterioles of **kidney** as well as in interstitial Leydig cells of testis.

L32 ANSWER 44 OF 78 MEDLINE DUPLICATE 27
ACCESSION NUMBER: 1999386883 MEDLINE
DOCUMENT NUMBER: 99386883 PubMed ID: 10456937
TITLE: Molecular cloning and characterization of rat genes encoding homologues of human beta-defensins.
AUTHOR: Jia H P; Mills J N; Barahmand-Pour F; Nishimura D; Mallampali R K; Wang G; Wiles K; Tack B F; Bevins C L; McCray P B Jr
CORPORATE SOURCE: Department of Pediatrics, University of Iowa College of Medicine, Iowa City, Iowa, USA.
CONTRACT NUMBER: AI-32234 (NIAID)
HL61234 (NHLBI)
P50 HL-61234-01 (NHLBI)
+
SOURCE: INFECTION AND IMMUNITY, (1999 Sep) 67 (9) 4827-33.
Journal code: 0246127. ISSN: 0019-9567.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF068860; GENBANK-AF068861
ENTRY MONTH: 199910
ENTRY DATE: Entered STN: 19991014
Last Updated on STN: 19991014
Entered Medline: 19991005

AB beta-Defensins are cationic peptides with broad-spectrum antimicrobial activity that may play a role in mucosal defenses of several organs. They have been isolated in several species, and in humans, two beta-defensins have been identified. Here, we report the identification of two genes encoding beta-defensin homologues in the rat. Partial cDNAs were found by searching the expressed-**sequence-tag database**, and primers were designed to generate full-length mRNA coding sequences.

One gene was highly similar to the human beta-defensin-1 (HBD-1) gene and mouse beta-defensin-1 gene at both the nucleic acid and amino acid levels and was termed rat beta-defensin-1 (RBD-1). The other gene, named RBD-2, was homologous to the HBD-2 and bovine tracheal antimicrobial peptide (TAP) genes. The predicted prepropeptides were strongly cationic, were 69 and 63 residues in length for RBD-1 and RBD-2, respectively, and contained

the six-cysteine motif characteristic of beta-defensins. The beta-defensin

genes mapped closely on rat chromosome 16 and were closely linked to the alpha-defensins genes, suggesting that they are part of a gene cluster, similar to the organization reported for humans. **Northern blot** analysis showed that both RBD-1 and RBD-2 mRNA transcripts were approximately 0.5 kb in length; RBD-1 mRNA was abundantly transcribed in the rat **kidney**, while RBD-2 was prevalent in the **lung**. Reverse transcription-PCR indicated that RBD-1 and RBD-2 mRNAs were distributed in a variety of other tissues. In the **lung**, RBD-1 mRNA expression localized to the tracheal epithelium while RBD-2 was expressed in alveolar type II cells. In conclusion, we characterized two novel beta-defensin homologues in the rat. The rat may be a useful model to investigate the function and contribution of beta-defensins to host defense in the **lung**, **kidney**, and other tissues.

L32 ANSWER 45 OF 78 MEDLINE

ACCESSION NUMBER: 1999400797 MEDLINE
DOCUMENT NUMBER: 99400797 PubMed ID: 10471358
TITLE: Chromosomal, in silico and in vitro expression analysis of cardiovascular-based genes encoding zinc finger proteins.
AUTHOR: Dai K S; Liew C C
CORPORATE SOURCE: The Cardiac Gene Unit, Institute of Medical Science
Department of Laboratory Medicine and Pathobiology,
University of Toronto, Ontario, Canada.
SOURCE: JOURNAL OF MOLECULAR AND CELLULAR CARDIOLOGY, (1999 Sep)
31

(9) 1749-69.
Journal code: 0262322. ISSN: 0022-2828.

PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199910
ENTRY DATE: Entered STN: 19991014
Last Updated on STN: 19991014
Entered Medline: 19991004

AB Three hundred and sixty expressed **sequence tags** (**ESTs**) from human **heart** cDNA libraries corresponding to one hundred and twenty six unique zinc finger proteins (ZFPs) were annotated and classified into seven types of ZFPs as reported previously. Among these 126 cvbZFPs (cardiovascular-based ZFPs), the C(2)H(2)-type and the C(2)C(2)-type are the two major ZFP types which account for more than 80% of ZFP genes present in the cardiovascular system. The expression patterns of 11 randomly selected ZFP genes (at least one for each type) in normal fetal, adult and hypertrophic adult **hearts**, respectively, were determined using reverse transcriptase-polymerase chain reaction (RT-PCR) analysis. The results suggest that ZFPs may be involved in the processes of either developmental control (downregulated or upregulated expression) or basic cellular functional regulation (constant expression). Interestingly, PAF-1 (peroxisome assembly factor-1), a C(3)HC(4)-type ZFP (RING domain-containing ZFP) showing a downregulated expression pattern in normal tissues was found to be upregulated in hypertrophic adult **heart**, suggesting a possible role for this fetal gene in the pathogenesis of cardiac hypertrophy. In silico **Northern** analysis of 15 tissues showed that over 90% of cvbZFPs demonstrate widespread tissue distribution, suggesting the vast majority of ZFPs are functionally shared among tissues. The potential importance of transcriptional repressors in cardiovascular development and disease, such as HFHZ, was supported by the observation that one-third (39 of 126) of cvbZFPs possess this function. Of these, 26 are C(2)H(2)-type and the remaining 13 included 8 C(2)C(2)-type, 1 C(3)HC(4)-type, 1 C(2)HC(4)C(HD)-type, 2 C(3)H-type and 1 combination type. Of particular interest was the observation that ZFPs which contain a KRAB domain are the major subtype present (51.3% of the total repressors in cvbZFPs). Chromosomal distribution analysis showed that mapping loci of cvbZFP genes are concentrated on chromosomes 1, 3, 6, 8, 10, 11, 12, 19 and X. In particular, chromosome 19 appears to be enriched in ZFP genes with C(2)H(2)-type as the predominant type present. Overall, this report provides a fundamental initial step toward understanding the potential role of ZFPs in regulating cardiac development and disease. Copyright 1999 Academic Press.

L32 ANSWER 46 OF 78 MEDLINE
 ACCESSION NUMBER: 1999445952 MEDLINE
 DOCUMENT NUMBER: 99445952 PubMed ID: 10514543
 TITLE: Cloning and expression analyses of down-regulated cDNA C6-2A in human esophageal cancer.
 AUTHOR: Wu K; Xu Z; Wang M; Xu X; Han Y; Cao Y; Wang R; Sun Y; Wu M
 CORPORATE SOURCE: National Laboratory of Molecular Oncology, Department of Cell Biology, Cancer Institute, Chinese Academy of Medical Sciences and Peking Union Medical college, Beijing 100021 P.R.China.. wangmr@pubem.cicams.ac.cn
 SOURCE: CHUNG-HUA I HSUEH I CHUAN HSUEH TSA CHIH, (1999 Oct) 16 (5)
 325-7.
 Journal code: 9425197. ISSN: 1003-9406.
 PUB. COUNTRY: China
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: Chinese
 FILE SEGMENT: Priority Journals

ENTRY MONTH: 199911
ENTRY DATE: Entered STN: 20000111
Last Updated on STN: 20000111
Entered Medline: 19991118

AB OBJECTIVE: To clone genes associated with the genesis of human esophageal cancer. METHODS: Identifying missing or low expressing cDNAs in human esophageal cancer tissues by mRNA differential display and examining its mRNA expression in 4 human cancer cell lines, 9 fetal tissues and other matched esophageal cancer tissues by **Northern** blot, dot blot and RT-PCR. RESULTS: One cDNA fragment named C6-2A, was cloned and sequenced. There was no identical sequence with C6-2A in BLASTN **database**; but in querying Genbank **EST**, the authors found that C6-2A was identical with ne27b03.s1NCI-CGAP-C03 humans sapiens cDNA clone IMAGE:898541 3' and zv30g07.rl Soares **ovary** tumor NbHOT homo sapiens cDNA clone 755196. 6/6 esophageal cancer tissues in **Northern** blot and 7/8 in dot blot did not or slightly express C6-2A. RT-PCR analysis showed that C6-2A was expressed much lower in

17/20

esophageal cancer tissues than adjacent microscopically normal mucosa, highly expressed in fetal esophageal mucosa, **skin**, cerebrum, placenta; moderately expressed in fetal stomach and liver, but not detected in fetal **heart**, small intestine and **kidney**. CONCLUSION: The high frequency of deletion of decreased expression of C6-2A in esophageal cell lines and human esophageal cancer tissues suggested that C6-2A might be involved in the carcinogenesis of esophagus.

L32 ANSWER 47 OF 78 MEDLINE DUPLICATE 28
ACCESSION NUMBER: 1999137667 MEDLINE
DOCUMENT NUMBER: 99137667 PubMed ID: 9950961
TITLE: Cloning of the human kidney PAH transporter: narrow substrate specificity and regulation by protein kinase C.
AUTHOR: Lu R; Chan B S; Schuster V L
CORPORATE SOURCE: Departments of Medicine, Physiology and Biophysics, Albert Einstein College of Medicine, Bronx, New York 10461, USA.
CONTRACT NUMBER: DK-49688 (NIDDK)
SOURCE: AMERICAN JOURNAL OF PHYSIOLOGY, (1999 Feb) 276 (2 Pt 2) F295-303.
Journal code: 0370511. ISSN: 0002-9513.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990413
Last Updated on STN: 19990413
Entered Medline: 19990330

AB Conserved from fish to mammals, renal proximal tubule organic anion secretion plays an important role in drug and xenobiotic elimination. Studies with the model substrate p-aminohippurate (PAH) have suggested that a basolateral PAH/alpha-ketoglutarate exchanger imports diverse organic substrates into the proximal tubule prior to apical secretion. cDNAs encoding PAH transporters have been cloned recently from rat and flounder. Here we report the cloning of a highly similar human PAH transporter (hPAHT) from human **kidney**. By **Northern** blot analysis and **EST database** searching, hPAHT mRNA was detected in **kidney** and brain. PCR-based monochromosomal somatic cell hybrid mapping placed the hPAHT gene on chromosome 11. When expressed transiently in vitro, hPAHT catalyzed time-dependent and saturable [3H]PAH uptake (Km of approximately 5 microM). Preincubation with unlabeled alpha-ketoglutaric or with glutaric acid stimulated tracer

PAH uptake, and preincubation with unlabeled PAH stimulated tracer alpha-ketoglutarate uptake, results that are consistent with PAH/alpha-ketoglutarate exchange. Several structurally diverse organic anions cis-inhibited PAH uptake. Like rat OAT1 organic anion transporter, hPAHT was inhibited by furosemide, indomethacin, probenecid, and alpha-ketoglutarate. Unlike OAT1, hPAHT was not inhibited by prostaglandins or methotrexate (MTX). Moreover, tracer PGE2 and MTX were not transported, indicating that the substrate specificity for transport by hPAHT is not broad. PAH uptake was inhibited by phorbol 12-myristate 13-acetate (PMA) in a dose- and time-dependent fashion, but not by the inactive 4alpha-phorbol-12,13 didecanoate. PMA-induced inhibition was blocked by staurosporine. Thus the protein kinase C-mediated inhibition of basolateral organic anion entry previously reported in intact tubules is likely due, at least in part, to direct modulation of the PAH/alpha-ketoglutarate exchanger.

L32 ANSWER 48 OF 78 MEDLINE DUPLICATE 29
 ACCESSION NUMBER: 2000035822 MEDLINE
 DOCUMENT NUMBER: 20035822 PubMed ID: 10571045
 TITLE: Cloning of the human phospholipase A2 activating protein (hPLAP) gene on the chromosome 9p21 melanoma deleted region.
 AUTHOR: Ruiz A; Nadal M; Puig S; Estivill X
 CORPORATE SOURCE: Medical and Molecular Genetics Center-IRO, Hospital Duran i Reynals, L'Hospitalet de Llobregat, Barcelona, Catalonia, Spain.
 SOURCE: GENE, (1999 Oct 18) 239 (1) 155-61.
 Journal code: 7706761. ISSN: 0378-1119.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AJ238243
 ENTRY MONTH: 199912
 ENTRY DATE: Entered STN: 20000113
 Last Updated on STN: 20000113
 Entered Medline: 19991210
 AB Cutaneous malignant melanoma (CMM) is a common **skin** cancer. About 50% of CMM sporadic tumours have lost one copy of the chromosome 9p21 region. To identify genes involved in the initiation and/or progression of CMM we have characterised the 9p21 melanoma deleted region and screened the human expressed **sequence tag** (**EST**) **databases** (dbEST) to search for expressed genes. We have identified the gene that encodes the human orthologue of the rat phospholipase A2 activating protein (PLAP). PLAP was considered a potential candidate to be involved in malignant melanoma because it maps to the critical region for CMM and because the PLA2 gene has been identified as a modifier of the APC gene, responsible for the adenomatous polyposis phenotype in the mouse. PLAP encodes a protein of 738 amino acids and has a high DNA (90%) and protein (97%) sequence similarity with the rat and mouse PLAP protein. PLAP has a region of WD40 repeats in the amino-terminus, which allows us to include this protein in the superfamily of beta-transducin proteins. **Northern** blot hybridisation gave a fragment of 4.5 kb, with higher expression in **heart** compared to other tissues. PLAP was localised at chromosome 9p21, between marker AFM218xg11 and TEK. SSCP analysis of the coding region of PLAP revealed no variants in the studied samples, but one of six CMM samples analysed by

RT-PCR showed specific inactivation of PLAP. Despite PLAP's important role in mediating several cellular responses and its localisation to the chromosome 9p21 region deleted in CMM, it is unlikely that point mutations or deletions in the coding region of PLAP are responsible for the initiation or progression of CMM. Further studies on PLAP inactivation should be performed to clarify its potential involvement in CMM.

L32 ANSWER 49 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2000:96075 BIOSIS
DOCUMENT NUMBER: PREV200000096075
TITLE: Caveolin-1 isoforms are encoded by distinct mRNAs: Identification of mouse caveolin-1 mRNA variants caused by alternative transcription initiation and splicing.
AUTHOR(S): Kogo, Hiroshi (1); Fujimoto, Toyoshi
CORPORATE SOURCE: (1) Department of Anatomy and Molecular Cell Biology, Nagoya University School of Medicine, Showa-ku, Nagoya, 466-8550 Japan
SOURCE: FEBS Letters, (Jan. 14, 1999) Vol. 464, No. 2-3, pp. 119-123.
ISSN: 0014-5793.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

AB By searching the **EST database** with the known cDNA sequence encoding alpha-caveolin-1 (full-length: FL), we found a variant having a hitherto unknown sequence in place of the first exon (5'-end variant: 5'V). The expression level of 5'V mRNA was equivalent to that of FL mRNA. The entire sequences of FL and 5'V mRNA were determined by 3'- and 5'-RACE analysis; their sizes were 2484 bp and 2533 bp, respectively, and the sequences were identical except for the region of the first exon. By **Northern blotting**, FL and 5'V mRNAs showed the same tissue distribution, and were intensely expressed in the **lung**, **heart**, and skeletal muscle. Analyzing the protein production from these mRNAs using green fluorescent protein as a tag, we found FL mRNA to produce the alpha-isoform predominantly, but to form little beta-isoform. The production of the beta-isoform from 5'V mRNA was also demonstrated.

By sequence analysis of the first intron of the caveolin-1 gene, a TATA box was found at 28 bp upstream of the transcription initiation site for 5'V mRNA. This is the first demonstration of caveolin-1 mRNA variants generated by alternative transcription initiation, and it indicates that the two isoforms of caveolin-1 are produced from two distinct mRNAs.

L32 ANSWER 50 OF 78 MEDLINE DUPLICATE 30
ACCESSION NUMBER: 1999326186 MEDLINE
DOCUMENT NUMBER: 99326186 PubMed ID: 10395968
TITLE: Identification and characterization of the mouse cDNA encoding acyl-CoA: dihydroxyacetone phosphate acyltransferase.
AUTHOR: Ofman R; Hogenhout E M; Wanders R J
CORPORATE SOURCE: Department of Clinical Chemistry and Pediatrics, University of Amsterdam, Academic Medical Centre, Meibergdreef 9, 1105 AZ, Amsterdam, The Netherlands.
SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (1999 Jul 9) 1439 (1) 89-94.
Journal code: 0217513. ISSN: 0006-3002.
PUB. COUNTRY: Netherlands

Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF110769
 ENTRY MONTH: 199908
 ENTRY DATE: Entered STN: 19990820
 Last Updated on STN: 19990820
 Entered Medline: 19990811

AB We used the amino acid sequence of human acyl-CoA: dihydroxyacetone phosphate acyltransferase (DHAPAT) as bait to screen the **database** of expressed **sequence tags** (dbEST) and identified several partial mouse cDNA clones showing high identity. Primers were selected based on the dbEST sequences and used for amplification of this transcript from cDNA prepared from mouse **skin** fibroblasts. The complete nucleotide sequence was then determined and revealed an open reading frame (ORF) of 2034 bp encoding a protein consisting of 678 amino acids with a calculated molecular mass of 76870. The deduced amino acid sequence showed high identity (80%) with that of human DHAPAT and also revealed a typical peroxisomal targeting signal type 1 (PTS1) at its extreme carboxy-terminus (alanine-lysine-leucine, AKL). Definitive evidence that this cDNA indeed codes for DHAPAT was obtained by heterologous expression in the yeast *Saccharomyces cerevisiae*. **Northern** blot analysis revealed high expression of DHAPAT especially in mouse **heart**, liver and testis.

L32 ANSWER 51 OF 78 MEDLINE DUPLICATE 31
 ACCESSION NUMBER: 1998283984 MEDLINE
 DOCUMENT NUMBER: 98283984 PubMed ID: 9618465
 TITLE: Cloning and characterization of human protease-activated receptor 4.
 AUTHOR: Xu W F; Andersen H; Whitmore T E; Presnell S R; Yee D P; Ching A; Gilbert T; Davie E W; Foster D C
 CORPORATE SOURCE: Department of Biochemistry, University of Washington, Box 357350, Seattle, WA 98195-7350, USA.
 CONTRACT NUMBER: HL16919 (NHLBI)
 SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1998 Jun 9) 95 (12) 6642-6. Journal code: 7505876. ISSN: 0027-8424.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF055917
 ENTRY MONTH: 199807
 ENTRY DATE: Entered STN: 19980716
 Last Updated on STN: 19980716
 Entered Medline: 19980709

AB Protease-activated receptors 1-3 (PAR1, PAR2, and PAR3) are members of a unique G protein-coupled receptor family. They are characterized by a tethered peptide ligand at the extracellular amino terminus that is generated by minor proteolysis. A partial cDNA sequence of a fourth member of this family (PAR4) was identified in an expressed **sequence tag database**, and the full-length cDNA clone has been isolated from a lymphoma Daudi cell cDNA library. The ORF codes for a seven transmembrane domain protein of 385 amino acids with 33% amino acid sequence identity with PAR1, PAR2, and PAR3. A putative protease cleavage site (Arg-47/Gly-48) was identified within the extracellular amino terminus. COS cells transiently transfected with PAR4 resulted in the formation of intracellular inositol triphosphate when treated with either thrombin or trypsin. A PAR4 mutant in which the Arg-47 was replaced with

Ala did not respond to thrombin or trypsin. A hexapeptide (GYPGQV) representing the newly exposed tethered ligand from the amino terminus of PAR4 after proteolysis by thrombin activated COS cells transfected with either wild-type or the mutant PAR4. **Northern** blot showed that PAR4 mRNA was expressed in a number of human tissues, with high levels being present in **lung**, pancreas, thyroid, testis, and small intestine. By fluorescence in situ hybridization, the human PAR4 gene was mapped to chromosome 19p12.

L32 ANSWER 52 OF 78 MEDLINE DUPLICATE 32
 ACCESSION NUMBER: 1998308497 MEDLINE
 DOCUMENT NUMBER: 98308497 PubMed ID: 9644627
 TITLE: cDNA cloning and expression of a novel family of enzymes with calcium-independent phospholipase A2 and lysophospholipase activities.
 AUTHOR: Portilla D; Crew M D; Grant D; Serrero G; Bates L M; Dai G;
 Sasner M; Cheng J; Buonanno A
 CORPORATE SOURCE: Department of Internal Medicine, University of Arkansas for
 Medical Sciences, Little Rock 72205-7199, USA.
 CONTRACT NUMBER: R01 DK52926 (NIDDK)
 R29 DK46914 (NIDDK)
 SOURCE: JOURNAL OF THE AMERICAN SOCIETY OF NEPHROLOGY, (1998 Jul) 9
 (7) 1178-86.
 Journal code: 9013836. ISSN: 1046-6673.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AA074652; GENBANK-AA106432; GENBANK-AA111418;
 GENBANK-AA138125; GENBANK-AA153793; GENBANK-AA174687;
 GENBANK-AA176126; GENBANK-AA186013; GENBANK-AA200741;
 GENBANK-AA204477; GENBANK-AA232315; GENBANK-AA238823;
 GENBANK-AA243609; GENBANK-AA260891; GENBANK-AA261500;
 GENBANK-AA262396; GENBANK-AA272267; GENBANK-H04075;
 GENBANK-H29141; GENBANK-H88463; GENBANK-H93729;
 GENBANK-R12332; GENBANK-R20112; GENBANK-R59445;
 GENBANK-R75944; GENBANK-U97146; GENBANK-U97147;
 GENBANK-U97148; GENBANK-W35748; GENBANK-W35757
 ENTRY MONTH: 199810
 ENTRY DATE: Entered STN: 19981021
 Last Updated on STN: 19981021
 Entered Medline: 19981015
 AB Previous studies have suggested that activation of calcium-independent PLA2 (CaIPLA2) is an early event in cell death after hypoxic injury in proximal tubule cells. An approximately 28-kD CaIPLA2 with preferential activity toward plasmalogen phospholipids has been recently purified from rabbit **kidney** cortex (D. Portilla and G. Dai, J Biol Chem 271, 15,451-15,457, 1996). Their report describes the cloning of a full-length rat cDNA encoding CaIPLA2, using sequences derived from the purified rabbit **kidney** cortex enzyme. In addition, cDNA from rabbit **kidney** that encode the rabbit homologue of the enzyme and a closely related isoform were isolated. The rat cDNA is predicted to encode
 an approximately 24-kD protein, and each cDNA contains the sequence G-F-S-Q-G, which fits the active site consensus sequence G-X-S-X-G of carboxylesterases. Several lines of evidence (DNA sequence comparison, Southern blot analysis, and examination of the expressed **sequence tag database**) show that CaIPLA2 enzymes are encoded by a

multigene family in rats, mice, rabbits, and humans. **Northern** analysis of various tissues from the rat indicated that the CaIPLA2 gene is ubiquitously expressed, with highest mRNA abundance observed in the **kidney** and small intestine. The rat CaIPLA2 cDNA, when expressed in a baculovirus expression system, and the purified rabbit **kidney** cortex protein exhibit both CaIPLA2 and lysophospholipase activities. The cloned CaIPLA2 cDNA are expected to aid in understanding the role of CaIPLA2 in cell death after hypoxic/ischemic cell injury.

L32 ANSWER 53 OF 78 MEDLINE DUPLICATE 33
ACCESSION NUMBER: 1998384536 MEDLINE
DOCUMENT NUMBER: 98384536 PubMed ID: 9716656
TITLE: Cloning and tissue expression of the mouse ortholog of AIM1, a betagamma-crystallin superfamily member.
AUTHOR: Teichmann U; Ray M E; Ellison J; Graham C; Wistow G; Meltzer P S; Trent J M; Pavan W J
CORPORATE SOURCE: Laboratory for Genetic Disease Research, National Human Genome Research Institute, National Institutes of Health, 49 Convent Drive MSC4472, Bethesda, Maryland 20892-4472, USA.
SOURCE: MAMMALIAN GENOME, (1998 Sep) 9 (9) 715-20.
Journal code: 9100916. ISSN: 0938-8990.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199905
ENTRY DATE: Entered STN: 19990601
Last Updated on STN: 19990601
Entered Medline: 19990517

AB We report the isolation of the murine ortholog of AIM1, a human gene whose expression is associated with the reversal of tumorigenicity in an experimental model of melanoma. Mouse and human AIM1 are more than 90% identical in amino acid sequence in the betagamma-crystallin repeats and the C-terminal domain, and more than 75% identical in the extended N-terminal domain. Consistent with the isolated cDNA representing the authentic AIM1 ortholog, linkage analysis localized mouse Aim1 to proximal mouse Chromosome (Chr) 10 in a conserved linkage group with genes localized to human Chr band 6q21. Searches of **EST databases** identified a second AIM1-like gene in both mouse and human, suggesting the existence of a gene family. **Northern** analysis demonstrates Aim1 is expressed most abundantly in adult **skin, lung, heart, liver, and kidney** and is temporally regulated during embryogenesis. Aim1 is expressed highly in the shaft region of the hair follicles and the presumptive ectoderm, but not at detectable levels in melanocytes or melanocyte precursor cells.

L32 ANSWER 54 OF 78 MEDLINE DUPLICATE 34
ACCESSION NUMBER: 1999103632 MEDLINE
DOCUMENT NUMBER: 99103632 PubMed ID: 9888557
TITLE: Cloning and expression of a novel tissue specific 17beta-hydroxysteroid dehydrogenase.
AUTHOR: Li K X; Smith R E; Krozowski Z S
CORPORATE SOURCE: Laboratory of Molecular Hypertension, Baker Medical Research Institute, Melbourne, Australia.
SOURCE: ENDOCRINE RESEARCH, (1998 Aug-Nov) 24 (3-4) 663-7.
Journal code: 8408548. ISSN: 0743-5800.

PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199904
 ENTRY DATE: Entered STN: 19990426
 Last Updated on STN: 19990426
 Entered Medline: 19990413

AB The 11beta-hydroxysteroid dehydrogenases (11betaHSD) modulate intracellular glucocorticoid levels, with 11betaHSD1 converting cortisone to cortisol mainly in the liver, and 11betaHSD2 performing the reverse reaction in sodium transporting epithelia and placenta. We have attempted to expand the 11betaHSD subfamily by isolating homologous cDNA's. Expressed **Sequence Tag databases** were screened with segments of the 11betaHSD1 enzyme amino acid sequence and Pan1b identified as a new member of the short chain alcohol dehydrogenase superfamily. **Northern** blot analysis of total RNA from human tissues showed a single band at 1.9 kb and a tissue specific pattern of expression with high levels in the liver, adrenal carcinoma, **lung** and small intestine, and much lower levels in the **kidney**, **heart** and placenta. Expression studies in a Chinese hamster **ovary** cell line (CHOP) showed that Pan1b did not metabolize glucocorticoids. However, preliminary studies on a range of substrates revealed that Pan1b acted as a dehydrogenase on 17beta-hydroxysteroids, although further kinetic analysis was confounded by large amounts of endogenous oxidoreductase activity in CHOP cells. These studies suggest the existence of a novel human 17betaHSD enzyme.

L32 ANSWER 55 OF 78 MEDLINE DUPLICATE 35
 ACCESSION NUMBER: 1999059684 MEDLINE
 DOCUMENT NUMBER: 99059684 PubMed ID: 9841866
 TITLE: Molecular characterization and expression of the gene for mouse NAD+:arginine ecto-mono(ADP-ribosyl)transferase, Art1.
 AUTHOR: Braren R; Glowacki G; Nissen M; Haag F; Koch-Nolte F
 CORPORATE SOURCE: Institute for Immunology, University Hospital, Martinistr. 52, D-20246 Hamburg, Germany.
 SOURCE: BIOCHEMICAL JOURNAL, (1998 Dec 15) 336 (Pt 3) 561-8. Journal code: 2984726R. ISSN: 0264-6021.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AJ132040; GENBANK-AJ132042; GENBANK-AJ132043; GENBANK-AJ132044
 ENTRY MONTH: 199902
 ENTRY DATE: Entered STN: 19990311
 Last Updated on STN: 20000303
 Entered Medline: 19990225

AB Mono(ADP-ribosyl)transferases regulate the function of target proteins by attaching ADP-ribose to specific amino acid residues in the proteins. We have characterized the gene for mouse arginine-specific ADP-ribosyltransferase, Art1. Southern blot analyses indicate that Art1 is a single-copy gene. **Northern** blot and reverse transcription-PCR analyses demonstrate prominent expression of Art1 in cardiac and skeletal muscle, and lower levels in spleen, **lung**, liver and fetal tissues. While human ART1 is not represented in the public expressed **sequence tag (EST) database**, the **database** contains 14 mouse Art1 **ESTs**. The Art1 gene encompasses four exons spanning 20 kb of genomic DNA. The deduced amino

acid sequence of Art1 exhibits the characteristic features of a glycosylphosphatidylinositol-anchored membrane protein. It shows 75-77% sequence identity with its orthologues from the human and rabbit, and 33-34% identity with its paralogues from the mouse, Art2-1 and Art2-2. Separate exons encode the N- and C-terminal signal peptides, and a single long exon encodes the entire predicted native polypeptide chain. We expressed Art1 in 293T cells as a recombinant fusion protein with the Fc portion of human IgG1. This soluble protein exhibits enzyme activities characteristic of arginine-specific ADP-ribosyltransferases. The availability of the Art1 gene provides the basis for applying transgene and knockout technologies to further probe the function of this gene product.

L32 ANSWER 56 OF 78 MEDLINE
 ACCESSION NUMBER: 1998259838 MEDLINE
 DOCUMENT NUMBER: 98259838 PubMed ID: 9597550
 TITLE: The expanding beta 4-galactosyltransferase gene family: messages from the databanks.
 AUTHOR: Lo N W; Shaper J H; Pevsner J; Shaper N L
 CORPORATE SOURCE: Department of Pharmacology and Molecular Sciences, Kennedy Krieger Institute, Baltimore, MD, USA.
 CONTRACT NUMBER: CA45799 (NCI)
 SOURCE: GLYCOBIOLOGY, (1998 May) 8 (5) 517-26.
 Journal code: 9104124. ISSN: 0959-6658.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF038660; GENBANK-AF038661; GENBANK-AF038662; GENBANK-AF038663; GENBANK-AF038664
 ENTRY MONTH: 199808
 ENTRY DATE: Entered STN: 19980903
 Last Updated on STN: 20000303
 Entered Medline: 19980825

AB From a systematic search of the UniGene and dbEST databanks, using human beta 4-galactosyltransferase (beta 4GalT-I), which is recognized to function in lactose biosynthesis, as the query sequence, we have identified five additional gene family members denoted as beta 4GalT-II, -III, -IV, -V, and -VI. Complementary DNA clones containing the complete coding regions for each of the five human homologs were obtained or generated by a PCR-based strategy (RACE) and sequenced. Relative to beta 4GalT-I, the percent sequence identity at the amino acid level between the individual family members, ranges from 33% (beta 4GalT-VI) to 55% (beta 4GalT-II). The highest sequence identity between any of the homologs is between beta 4GalT-V and beta 4GalT-VI (68%). beta 4GalT-II is the ortholog of the chicken beta 4GalT-II gene, which has been demonstrated to encode an alpha-lactalbumin responsive beta 4-galactosyltransferase (Shaper et al.; J. Biol. Chem., 272, 31389-31399, 1997). As established by Northern analysis, beta 4GalT-II and -IV show the most restricted pattern of tissue expression. High steady state levels of beta 4GalT-II mRNA are seen only in fetal brain and adult heart, muscle, and pancreas; relatively high levels of beta 4GalT-VI mRNA are seen only in adult brain. When the corresponding mouse EST clone for each of the beta 4GalT family members was used as the hybridization probe for Northern analysis of murine mammary tissue, transcription of only the beta 4GalT-I gene could be detected in the lactating mammary gland. These observations support the conclusion that among the six known beta 4GalT family members in the mammalian genome, that have been generated

the through multiple gene duplication events of an ancestral gene(s), only
beta 4GalT-I ancestral lineage was recruited for lactose biosynthesis
during the evolution of mammals.

L32 ANSWER 57 OF 78 MEDLINE DUPLICATE 36
ACCESSION NUMBER: 1998440830 MEDLINE
DOCUMENT NUMBER: 98440830 PubMed ID: 9753662
TITLE: Carnitine biosynthesis: identification of the cDNA
encoding human gamma-butyrobetaine hydroxylase.
AUTHOR: Vaz F M; van Gool S; Ofman R; Ijlst L; Wanders R J
CORPORATE SOURCE: Department of Clinical Chemistry and Pediatrics, Academic
Medical Center, University of Amsterdam, The Netherlands.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1998
Sep 18) 250 (2) 506-10.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF082868
ENTRY MONTH: 199811
ENTRY DATE: Entered STN: 19990106
Last Updated on STN: 20000303
Entered Medline: 19981105
AB gamma-Butyrobetaine hydroxylase (EC 1.14.11.1) is the last enzyme in the
biosynthetic pathway of L-carnitine and catalyzes the formation of
L-carnitine from gamma-butyrobetaine, a reaction dependent on
alpha-ketoglutarate, Fe²⁺, and oxygen. We report the purification of the
protein from rat liver to apparent homogeneity, which allowed N-terminal
sequencing using Edman degradation. The obtained amino acid sequence was
used to screen the expressed **sequence tag**
database and led to the identification of a human cDNA containing
an open reading frame of 1161 base pairs encoding a polypeptide of 387
amino acids with a predicted molecular weight of 44.7 kDa. Heterologous
expression of the open reading frame in the yeast *Saccharomyces*
cerevisiae
confirmed that the cDNA encodes the human gamma-butyrobetaine
hydroxylase.
Northern blot analysis showed gamma-butyrobetaine hydroxylase
expression in **kidney** (high), liver (moderate), and brain (very
low), while no expression could be detected in the other investigated
tissues.

L32 ANSWER 58 OF 78 MEDLINE DUPLICATE 37
ACCESSION NUMBER: 1998149982 MEDLINE
DOCUMENT NUMBER: 98149982 PubMed ID: 9480748
TITLE: FAHL4, a new gene encoding long-chain acyl-CoA synthetase
4, is deleted in a family with Alport syndrome,
elliptocytosis, and mental retardation.
AUTHOR: Piccini M; Vitelli F; Bruttini M; Poher B R; Jonsson J J;
Villanova M; Zollo M; Borsani G; Ballabio A; Renieri A
CORPORATE SOURCE: Genetica Medica, Policlinico le Scotte, 53100 Siena,
Italy.
SOURCE: GENOMICS, (1998 Feb 1) 47 (3) 350-8.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-Y12777; GENBANK-Y13058
ENTRY MONTH: 199804
ENTRY DATE: Entered STN: 19980416
Last Updated on STN: 19980416
Entered Medline: 19980408

AB We observed a family in which two boys were diagnosed with Alport syndrome, elliptocytosis, and mental retardation and carried a large deletion of the Xq22.3-q23 region, encompassing the COL4A5 gene. This suggests the possibility of a new contiguous gene syndrome. In an attempt to characterize the genes contributing to this complex phenotype, we have isolated a gene encoding a new long-chain acyl-CoA synthetase (FACL4 or LACS4) from the region deleted in these patients. Among several **ESTs** identified by searching the human gene map database maintained at the National Center for Biotechnology Information, using

the

map position as a query, only one was deleted in the patients. RACE products containing the entire ORF were subsequently generated. **Northern** blot analysis showed a 5-kb mRNA expressed in several tissues except for liver and lung. Brain shows a longer transcript, possibly reflecting the use of a brain-specific upstream ATG start codon. FACL4 encodes a predicted protein product of 670 amino acids (711 in brain), with a remarkable level of conservation compared to the rat acyl-CoA synthetases ACS4 and brain-specific ACS3 protein sequences. We are investigating the possibility that the absence of this enzyme may play a role in the development of mental retardation or other signs associated with Alport syndrome in the family.
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L32 ANSWER 59 OF 78 MEDLINE DUPLICATE 38
ACCESSION NUMBER: 1998248992 MEDLINE
DOCUMENT NUMBER: 98248992 PubMed ID: 9587421
TITLE: Identification of a novel human glutathione S-transferase using bioinformatics.
AUTHOR: Liu S; Stoesz S P; Pickett C B
CORPORATE SOURCE: Schering-Plough Research Institute, Kenilworth, New Jersey 07033, USA.
SOURCE: ARCHIVES OF BIOCHEMISTRY AND BIOPHYSICS, (1998 Apr 15) 352 (2) 306-13.
JOURNAL CODE: 0372430. ISSN: 0003-9861.
PUB. COUNTRY: United States
JOURNAL; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF025887
ENTRY MONTH: 199806
ENTRY DATE: Entered STN: 19980611
Last Updated on STN: 19980611
Entered Medline: 19980603

AB In searching the expressed **sequence tag (EST)** data-base of GenBank with coding sequences of 11 known human glutathione

S-transferases in conjunction with bioinformatic analysis, we have identified five **ESTs** that encode a new human glutathione S-transferase (GST) designated GST A4. The cDNA clone (I.M.A.G.E. Consortium cDNA Clone ID 515157) had an insert length of 1279 bp and contains an open reading frame of 666 bp, which encodes a protein of 222 amino acid residues. The GST A4 protein is identical in length to human GST A1 and A2 and is 54% identical to human GST A1 and A2. Sequence comparison with other human GSTs suggests that it is a new GST belonging to the alpha class GSTs. **Northern** blot analysis and **EST** database searches have demonstrated that the GST A4 mRNA is

expressed at a high level in brain, placenta, and skeletal muscle and much lower in **lung** and liver. Analysis of the sequence tagged site (STS) **database** indicated that the GST A4 gene is located on chromosome 6. This STS represents a previously unidentified transcript further confirming the novelty of the new sequence.

L32 ANSWER 60 OF 78 MEDLINE DUPLICATE 39
ACCESSION NUMBER: 1998081868 MEDLINE
DOCUMENT NUMBER: 98081868 PubMed ID: 9419370
TITLE: Discovery of three genes specifically expressed in human prostate by expressed sequence tag **database** analysis.
AUTHOR: Vasmatzis G; Essand M; Brinkmann U; Lee B; Pastan I
CORPORATE SOURCE: Laboratory of Molecular Biology, Division of Basic Sciences, National Cancer Institute, National Institutes of Health, Building 37/4E16, 37 Convent Drive, MSC 4255, Bethesda, MD 20892-4255, USA.
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1998 Jan 6) 95 (1) 300-4. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199802
ENTRY DATE: Entered STN: 19980226
Last Updated on STN: 19980226
Entered Medline: 19980218
AB A procedure is described to discover genes that are specifically expressed in human **prostate**. The procedure involves searching the expressed **sequence tag (EST)** **database** for genes that have many related **EST** sequences from human **prostate** cDNA libraries but none or few from nonprostate human libraries. The selected candidate **EST** clones were tested by RNA dot blots to examine tissue specificity and by **Northern** blots to examine the transcript size of the corresponding mRNA. The computer analysis identified 15 promising genes that were previously unidentified. When seven of these were examined in an RNA hybridization experiment, three were found to be **prostate** specific. The genes identified could be useful in the targeted therapy of **prostate** cancer. The procedure can easily be applied to discover genes specifically expressed in other organs or tumors.

L32 ANSWER 61 OF 78 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1999:1087 BIOSIS
DOCUMENT NUMBER: PREV199900001087
TITLE: Nucleotide sequences Hmob3 and Hmob33 from human medulla oblongata complementary DNA clone library: Chromosome localization and features of structure and expression.
AUTHOR(S): Dergunova, L. V.; Vladychenskaya, I. P.; Polukarova, L. G.;
Raevskaya, N. M.; Lelikova, G. P.; Limborskaya, S. A.
CORPORATE SOURCE: Inst. Mol. Genet., Russ. Acad. Sci., Moscow 123182 Russia
SOURCE: Molekulyarnaya Biologiya (Moscow), (March-April, 1998) Vol. 32, No. 2, pp. 249-254.
ISSN: 0026-8984.
DOCUMENT TYPE: Article

LANGUAGE: Russian

SUMMARY LANGUAGE: Russian

AB Differential screening was used to obtain nucleotide sequences Hmob3 and Hmob33 (1420 and 1567 respectively) from human medulla oblongata DNA clone

library. The sequences were actively transcribed in various fragments of the brain. **Northern** hybridization of DNA from these clones with mRNA from other human tissues showed that transcripts were absent in the **kidney**, uterine wall and skeletal muscle. Comparison of clone nucleotide sequence with sequences deposited in **databases** GenBank and HCD revealed a series of highly homologous short expressed **sequence tags (EST)**. The anonymity of **EST** and the absence of substantial Hmob3 and Hmob33 homology with known genes indicates that they belong to new genes not described earlier.

Hmob3 and Hmob33 were localized on human chromosomes 5 and 10 respectively, using DNA panels of hybrid somatic cells and in situ hybridization.

L32 ANSWER 62 OF 78 MEDLINE DUPLICATE 40
ACCESSION NUMBER: 1998201609 MEDLINE
DOCUMENT NUMBER: 98201609 PubMed ID: 9524256
TITLE: A novel 52 kDa protein induces apoptosis and concurrently activates c-Jun N-terminal kinase 1 (JNK1) in mouse C3H10T1/2 fibroblasts.
AUTHOR: Sun L; Liu Y; Fremont M; Schwarz S; Siegmann M; Matthies R;
Jost J P
CORPORATE SOURCE: Friedrich Miescher Institute, Basel, Switzerland.
SOURCE: GENE, (1998 Feb 27) 208 (2) 157-66.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF029071
ENTRY MONTH: 199805
ENTRY DATE: Entered STN: 19980514
Last Updated on STN: 20000303
Entered Medline: 19980504

AB A 52 kDa protein (p52) was purified from chicken embryos and its corresponding cDNA was cloned. The p52 cDNA is 1768 bp long and has an open reading frame of 465 amino acids. The sequence of the p52 cDNA shows significant homology with mouse and human cDNAs from the **EST database**, so do the deduced amino acid sequences, indicating the existence of human and mouse homologues of p52. **Northern** blot hybridization showed that the p52 mRNA was expressed in a wide range of embryonic and adult tissues. There was more p52 mRNA in embryonic **heart** and liver than in the brain or muscle. The adult testis had the highest level of p52 mRNA, whereas adult liver had the lowest. Expression of p52 in mouse C3H10T1/2 fibroblasts caused apoptotic cell death, upregulation of transcription factor c-Jun and activation of c-Jun N-terminal kinase 1 (JNK1). In addition, expression of Bcl-2, but not of the dominant negative mutant JNK1, can block the p52-mediated apoptosis. These results indicate that p52 may represent a new cell-death protein inducing apoptosis and activating JNK1 through different pathways.

L32 ANSWER 63 OF 78 MEDLINE DUPLICATE 41
ACCESSION NUMBER: 1999077694 MEDLINE
DOCUMENT NUMBER: 99077694 PubMed ID: 9858711
TITLE: A novel growth differentiation factor-9 (GDF-9) related

factor is co-expressed with GDF-9 in mouse oocytes during folliculogenesis.

AUTHOR: Laitinen M; Vuojolainen K; Jaatinen R; Ketola I; Aaltonen J; Lehtonen E; Heikinheimo M; Ritvos O

CORPORATE SOURCE: Department of Bacteriology and Immunology, Haartman Institute, P.O. Box 21, University of Helsinki, FIN-00014, Helsinki, Finland.. mplaitin@cc.helsinki.fi

SOURCE: MECHANISMS OF DEVELOPMENT, (1998 Nov) 78 (1-2) 135-40.
Journal code: 9101218. ISSN: 0925-4773.

PUB. COUNTRY: Ireland

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AJ010259

ENTRY MONTH: 199903

ENTRY DATE: Entered STN: 19990316
Last Updated on STN: 20000303
Entered Medline: 19990304

AB Growth differentiation factor-9 (GDF-9) is a transforming growth factor-b (TGF-b) family member which is expressed in the oocytes in mouse **ovaries** (McGrath, S.A., Esquela, A.F., Lee, S.J., 1995. Oocyte-specific expression of growth/differentiation factor-9. Mol. Endocrinol. 9, 131-136). GDF-9 is indispensable for normal folliculogenesis since female mice deficient for the GDF-9 gene are infertile due to an arrest of follicular growth at the primary follicle stage (Dong, J., Albertini, D.F., Nishimori, K., Kumar, T.R., Lu, N., Matzuk, M.M., 1996. Growth differentiation factor-9 is required during early ovarian folliculogenesis. Nature 383, 531-535). We searched the GenBank Expressed **Sequence Tag (EST)** **database** with the mouse GDF-9 cDNA sequence, and identified from a mouse 2-cell embryo library an **EST** cDNA that encodes a putative member of the TGF-b superfamily, and named it as GDF-9B. **Northern** blot hybridization analyses of mouse **ovaries** revealed a single transcript of approximately 4.0 kilobases (kb) for GDF-9B and of 2.0 kb for GDF-9. We cloned by reverse transcription-polymerase chain reaction from mouse ovarian RNA a partial 821-base pair GDF-9B cDNA that spans the sequence encoding the putative mature region of GDF-9B. The COOH-terminal region of GDF-9B appears to be 53% homologous to GDF-9. Moreover, like GDF-9, GDF-9B lacks the cysteine residue needed for the covalent dimerization of several TGF-b family members. Using in situ hybridization analysis, we demonstrate that GDF-9B and GDF-9 mRNAs are co-localized in the oocyte. We also show that GDF-9B and GDF-9 genes are co-ordinately expressed during follicular development.

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L32 ANSWER 64 OF 78 MEDLINE DUPLICATE 42

ACCESSION NUMBER: 1998234542 MEDLINE

DOCUMENT NUMBER: 98234542 PubMed ID: 9570947

TITLE: Divergently transcribed overlapping genes expressed in liver and kidney and located in the 11p15.5 imprinted domain.

AUTHOR: Cooper P R; Smilnich N J; Day C D; Nowak N J; Reid L H; Pearsall R S; Reece M; Prawitt D; Landers J; Housman D E; Winterpacht A; Zabel B U; Pelletier J; Weissman B E; Shows T B; Higgins M J

CORPORATE SOURCE: Department of Human Genetics, Roswell Park Cancer Institute, Buffalo, New York 14263, USA.

CONTRACT NUMBER: CA63176 (NCI)
CA63333 (NCI)
HG00333 (NHGRI)

SOURCE: GENOMICS, (1998 Apr 1) 49 (1) 38-51.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AC001228; GENBANK-AF087428
ENTRY MONTH: 199806
ENTRY DATE: Entered STN: 19980708
Last Updated on STN: 20000512
Entered Medline: 19980625

AB Human chromosomal band 11p15.5 has been shown to contain genes involved in

the development of several pediatric and adult tumors and in Beckwith-Wiedemann syndrome (BWS). Overlapping P1 artificial chromosome clones from this region have been used as templates for genomic sequencing

in an effort to identify candidate genes for these disorders. PowerBLAST identified several matches with expressed **sequence tags** (**ESTs**) from fetal brain and liver cDNA libraries.

Northern blot analysis indicated that two of the genes identified by these **ESTs** encode transcripts of 1-1.5 kb with predominant expression in fetal and adult liver and **kidney**. With RT-PCR and RACE, full-length transcripts were isolated for these two genes, with the largest open reading frames encoding putative proteins of 253 and 424 amino acids. **Database** comparison of the predicted amino acid sequence of the larger transcript indicated homology to integral membrane organic cation transporters; hence, we designate this gene ORCTL2

(organic cation transporter-like 2). An expressed sequence polymorphism provided evidence that the ORCTL2 gene exhibits "leaky" imprinting in both human fetal **kidney** and human fetal liver. The mouse orthologue (Orctl2) was identified, and a similar polymorphism was used to demonstrate maternal-specific expression of this gene in fetal liver from interspecific F1 mice. The predicted protein of the smaller gene showed

no significant similarity in the **database**. **Northern** and RACE analyses suggest that this gene may have multiple transcription

start sites. Determination of the genomic structure in humans indicated that

the 5'-end of this transcript overlaps in divergent orientation with the

first two exons of ORCTL2, suggesting a possible role for antisense regulation of one gene by the other. We, therefore, provisionally name this second transcript ORCTL2S (ORCTL2-antisense). The expression patterns of these genes and the imprinted expression of ORCTL2 are suggestive of a possible role in the development of Wilms tumor (WT) and hepatoblastoma. Although SSCP analysis of 62 WT samples and 10 BWS patients did not result in the identification of any mutations in ORCTL2 or ORCTL2S; it will be

important to examine their expression pattern in tumors and BWS patients, since epigenetic alteration at these loci may play a role in the etiology of these diseases.

L32 ANSWER 65 OF 78

MEDLINE

DUPLICATE 43

ACCESSION NUMBER: 1998077364 MEDLINE

DOCUMENT NUMBER: 98077364 PubMed ID: 9416882

TITLE: A genome-based resource for molecular cardiovascular medicine: toward a compendium of cardiovascular genes.

AUTHOR: Hwang D M; Dempsey A A; Wang R X; Rezvani M; Barrans J D; Dai K S; Wang H Y; Ma H; Cukerman E; Liu Y Q; Gu J R;

Zhang

CORPORATE SOURCE: J H; Tsui S K; Waye M M; Fung K P; Lee C Y; Liew C C
 Department of Laboratory Medicine, Centre for
 Cardiovascular Research, The Toronto Hospital, University
 of Toronto, Ontario, Canada.
 SOURCE: CIRCULATION, (1997 Dec 16) 96 (12) 4146-203.
 Journal code: 0147763. ISSN: 0009-7322.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
 ENTRY MONTH: 199801
 ENTRY DATE: Entered STN: 19980130
 Last Updated on STN: 20000303
 Entered Medline: 19980122

AB BACKGROUND: Large-scale partial sequencing of cDNA libraries to generate expressed **sequence tags (ESTs)** is an effective means of discovering novel genes and characterizing transcription patterns in different tissues. To catalogue the identities and expression levels of genes in the cardiovascular system, we initiated large-scale sequencing and analysis of human cardiac cDNA libraries. METHODS AND RESULTS: Using automated DNA sequencing, we generated 43,285 **ESTs** from human **heart** cDNA libraries. An additional 41,619 **ESTs** were retrieved from public **databases**, for a total of 84,904 **ESTs** representing more than 26 million nucleotides of raw cDNA sequence data from 13 independent cardiovascular system-based cDNA libraries. Of these, 55% matched to known genes in the Genbank/EMBL/DDBJ **databases**, 33% matched only to other **ESTs**, and 12% did not match to any known sequences (designated cardiovascular system-based **ESTs**, or CVbESTs). **ESTs** that matched to known genes were classified according to function, allowing for detection of differences in general transcription patterns between various tissues and developmental stages of the cardiovascular system. In silico **Northern** analysis of known gene matches identified widely expressed cardiovascular genes as well as genes putatively exhibiting greater tissue specificity or developmental stage specificity. More detailed analysis identified 48 genes potentially overexpressed in cardiac hypertrophy, at least 10 of which were previously documented as differentially expressed. Computer-based chromosomal localizations of 1048 cardiac **ESTs** were performed to further assist in the search for disease-related genes. CONCLUSIONS: These data represent the most extensive compilation of cardiovascular gene expression information to date. They further demonstrate the untapped potential of genome research for investigating questions related to cardiovascular biology and represent a first-generation genome-based resource for molecular cardiovascular medicine.

L32 ANSWER 66 OF 78 MEDLINE DUPLICATE 44
 ACCESSION NUMBER: 97312490 MEDLINE
 DOCUMENT NUMBER: 97312490 PubMed ID: 9168931
 TITLE: Molecular cloning and expression analysis of rat Rgs12 and Rgs14.
 AUTHOR: Snow B E; Antonio L; Suggs S; Gutstein H B; Siderovski D P
 CORPORATE SOURCE: Quantitative Biology Laboratory, Amgen Institute, Toronto, Ontario, Canada.
 SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1997 Apr 28) 233 (3) 770-7.
 Journal code: 0372516. ISSN: 0006-291X.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U92279; GENBANK-U92280
ENTRY MONTH: 199706
ENTRY DATE: Entered STN: 19970716
Last Updated on STN: 20000303
Entered Medline: 19970630

AB We report the cloning of two novel rat regulators of G-protein signaling (RGS) cDNAs using a degenerate PCR strategy. The rRgs12 and rRgs14 cDNAs encode predicted polypeptides of 1387 and 544 amino acids, respectively. We have also identified the human orthologue of rRgs12 by alignment of cosmid sequences in the **database** which map the human RGS12 gene to chromosome 4p16.3. Furthermore, we identified human **ESTs** with high homology to rRgs14 which map to human chromosome 5qter. **Northern** blot analysis indicates that rRgs14 is expressed at high levels in brain, lung, and spleen, whereas rRgs12 is expressed at high levels in brain and lung and lower levels in testis, heart, and spleen. Analysis of the predicted rRGS12 and rRGS14 polypeptides indicates that they are closely related and possess regions of homology outside of the conserved RGS domain. We have also identified conserved regions in RGS12 which are similar to protein domains found in mouse rhophilin and coiled-coil proteins suggesting possible interactions with ras-like G-proteins.

L32 ANSWER 67 OF 78 MEDLINE DUPLICATE 45

ACCESSION NUMBER: 1998004295 MEDLINE
DOCUMENT NUMBER: 98004295 PubMed ID: 9346309
TITLE: Characterisation of macrophage inflammatory
protein-5/human

CC cytokine-2, a member of the macrophage-inflammatory-protein family of chemokines.

AUTHOR: Coulin F; Power C A; Alouani S; Peitsch M C; Schroeder J M;

Moshizuki M; Clark-Lewis I; Wells T N

CORPORATE SOURCE: Geneva Biomedical Research Institute, Switzerland.

SOURCE: EUROPEAN JOURNAL OF BIOCHEMISTRY, (1997 Sep 1) 248 (2) 507-15.

Journal code: 0107600. ISSN: 0014-2956.

PUB. COUNTRY: GERMANY: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-Z70293; SWISSPROT-Q16663

ENTRY MONTH: 199711

ENTRY DATE: Entered STN: 19971224

Last Updated on STN: 19971224

Entered Medline: 19971121

AB A human monocyte-activating CC chemokine has been identified based on sequences in an expressed **sequence tag (EST)** cDNA **database**. The protein shows highest sequence identity to the macrophage inflammatory protein (MIP) group of chemokines, particularly MIP-3 (76.7%) and MIP-1alpha (75.4%), and has been named MIP-5. Model building confirms that the protein has a similar three dimensional structure to other chemokines, but has an additional third disulphide bond. **Northern** blot analysis and reverse-transcriptase PCR show that the mRNA for MIP-5 is expressed at a high levels in liver, intestine and in lung leukocytes. MIP-5 induces chemotaxis of human monocytes, T-lymphocytes and, to a lesser degree, eosinophils at nanomolar concentrations; it has no effect on neutrophil migration. In receptor-binding assays, MIP-5 shows IC50 values of 12 nM for competition with 125I-MIP-1alpha for binding to CC-chemokine receptor

(CCR)1, and 2.5 nM for competition with 125I-MCP-3 for binding to CCR3.
It

shows no ability to compete with ligand for binding to the two interleukin (IL)-8 receptors (CXC-chemokine receptors 1 and 2) or to CCR2, CCR4 or CCR5. Consistent with this binding data, MIP-5 was only able to induce calcium fluxes in CHO cells stably transfected with CCR1 or CCR3.

L32 ANSWER 68 OF 78 MEDLINE DUPLICATE 46
ACCESSION NUMBER: 1998110580 MEDLINE
DOCUMENT NUMBER: 98110580 PubMed ID: 9441748
TITLE: Analysis of a human gene homologous to rat ventral prostate.1 protein.
AUTHOR: Peacock R E; Keen T J; Inglehearn C F
CORPORATE SOURCE: Molecular Medicine Unit, St James University Hospital, Leeds, United Kingdom.
SOURCE: GENOMICS, (1997 Dec 15) 46 (3) 443-9.
JOURNAL code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF007189
ENTRY MONTH: 199803
ENTRY DATE: Entered STN: 19980319
Last Updated on STN: 19980319
Entered Medline: 19980309
AB We report on the analysis of a human gene homologous to the rat ventral prostate.1 protein (RVP.1), which is transcriptionally induced in the regressing rat prostate after castration. EST database searching and Northern blotting reveal that this is one of at least four different members of a gene family in the human genome that produce transcripts of 3.4, 2.4, 1.9, and 1.2 kb, expressed in a wide range of tissues. Three other members of this gene family have already been mapped to chromosomes 7q, 17p, and 22q and reported either as anonymous ESTs or as full-length clones. We have now characterized a fourth member (assigned the gene name C7orf1 by GDB) and localized it also to chromosome 7q. C7orf1 is almost identical over much of its length to the reported ORF of RVP.1 while the other family members are more divergent from RVP.1. The genomic sequence of C7orf1 is intron-less, is spanned by a CpG low-methylation island, and has two noncoding, nonpolymorphic STR regions immediately adjacent to the open reading frame, one 5' and one 3'. The presence of a NotI restriction site in the coding sequence results in a deficiency in the IMAGE cDNA libraries, as a result of which the 3' end of the gene is not in the EST databases. The putative 220-amino-acid protein shows 89% identity to the amino terminus of rat RVP.1. Like rat RVP.1, it has four hydrophobic potential membrane-spanning regions, but it lacks 60 amino acid residues at its carboxyl terminus relative to rat RVP.1. Nevertheless, gene-specific primers from this transcript amplified a product in human cDNAs from several different tissues; its size corresponds to the 1.2-kb transcript seen on a Northern blot, and identical ESTs from several different tissues exist in the databases. It therefore seems likely that C7orf1 is the closest human homologue of rat RVP.1.

L32 ANSWER 69 OF 78 MEDLINE DUPLICATE 47
ACCESSION NUMBER: 97213770 MEDLINE
DOCUMENT NUMBER: 97213770 PubMed ID: 9060459
TITLE: Monocyte chemotactic protein-4: tissue-specific expression

and signaling through CC chemokine receptor-2.
 AUTHOR: Godiska R; Chantry D; Raport C J; Schweickart V L; Trong H L; Gray P W
 CORPORATE SOURCE: ICOS Corporation, Bothell, Washington 98021, USA.
 SOURCE: JOURNAL OF LEUKOCYTE BIOLOGY, (1997 Mar) 61 (3) 353-60.
 Journal code: 8405628. ISSN: 0741-5400.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-U59808
 ENTRY MONTH: 199704
 ENTRY DATE: Entered STN: 19970414
 Last Updated on STN: 19970414
 Entered Medline: 19970403

AB Chemokines constitute a family of low-molecular-weight proteins that attract or activate a variety of cell types, including leukocytes, endothelial cells, and fibroblasts. An electronic search of the GenBank Expressed **Sequence Tags database** uncovered a partial cDNA sequence with homology to the chemokine monocyte chemotactic protein-1 (MCP-1). Isolation of the full-length clone revealed that it encodes the chemokine MCP-4, an eosinophil chemoattractant recently described by Ugucioni et al. [J. Exp. Med. 183, 2379-2384]. Recombinant MCP-4 was expressed in mammalian cells and purified by heparin-Sepharose chromatography. Sequencing the amino terminus of this protein corroborated the reported sequence of recombinant MCP-4 produced in insect cells. As shown by calcium flux assays, MCP-4 activated the cloned G protein-coupled receptor CCR-2, which also recognizes MCP-1 and MCP-3. **Northern** hybridization indicated that MCP-4 is constitutively expressed at high levels in the small intestine, colon, and **lung**. This expression profile is consistent with its role as a chemoattractant for eosinophils, which can be rapidly mobilized to the **lung** or intestine in response to invading pathogens. In marked contrast to MCP-1, MCP-4 was not induced in cell lines treated with pro-inflammatory stimuli such as lipopolysaccharide or tumor necrosis factor alpha.

L32 ANSWER 70 OF 78 MEDLINE DUPLICATE 48
 ACCESSION NUMBER: 97399181 MEDLINE
 DOCUMENT NUMBER: 97399181 PubMed ID: 9255310
 TITLE: Identification of a novel transcript up-regulated in a clinically aggressive prostate carcinoma.
 AUTHOR: Chuaqui R F; Englert C R; Strup S E; Vocke C D; Zhuang Z; Duray P H; Bostwick D G; Linehan W M; Liotta L A; Emmert-Buck M R
 CORPORATE SOURCE: Laboratory of Pathology, National Cancer Institute, Bethesda, Maryland, USA.
 SOURCE: UROLOGY, (1997 Aug) 50 (2) 302-7.
 Journal code: 0366151. ISSN: 0090-4295.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199709
 ENTRY DATE: Entered STN: 19970922
 Last Updated on STN: 19970922
 Entered Medline: 19970908
 AB OBJECTIVES: To identify differentially expressed genes in tumor cells of patients with **prostate** cancer by means of tissue microdissection

and targeted differential display. METHODS: RNA was recovered from pure populations of microdissected normal epithelium and invasive tumor from frozen tissue sections of a radical prostatectomy specimen. Reverse transcription-polymerase chain reaction (PCR) using arbitrary and zinc finger PCR primers was performed. RESULTS: A 130-base pair product was identified that appeared selectively in the tumor sample. DNA sequence analysis revealed it to be a clone from the expressed **sequence tag database** (GenBank accession R00504). Microdissection of normal epithelium and the corresponding invasive tumor was subsequently performed on a test panel of 10 **prostate** carcinoma specimens. Comparison of R00504 levels in normal epithelium and invasive carcinoma, using beta-actin as an internal control, showed the transcript to be substantially overexpressed in 5 of 10 carcinomas. **Northern** blotting revealed R00504 to be a 2.6-kilobase gene. CONCLUSIONS: A novel transcript up-regulated in an aggressive **prostate** carcinoma was identified using degenerate zinc finger primers in microdissected tissue samples. The approach used in this study may be helpful in quantitative comparison of known genes and identification of novel genes in microdissected human tissue samples.

L32 ANSWER 71 OF 78 MEDLINE DUPLICATE 49
 ACCESSION NUMBER: 97289529 MEDLINE
 DOCUMENT NUMBER: 97289529 PubMed ID: 9144434
 TITLE: cDNA cloning and tissue-specific expression of a novel basic helix-loop-helix/PAS protein (BMAL1) and identification of alternatively spliced variants with alternative translation initiation site usage.
 AUTHOR: Ikeda M; Nomura M
 CORPORATE SOURCE: Department of Physiology, Saitama Medical School, Moroyama, Japan.. mikeda@saitama-med.ac.jp
 SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1997 Apr 7) 233 (1) 258-64. Journal code: 0372516. ISSN: 0006-291X.
 PUB. COUNTRY: United States
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AB000812; GENBANK-AB000813; GENBANK-AB000814; GENBANK-AB000815; GENBANK-AB000816; GENBANK-D89722
 ENTRY MONTH: 199706
 ENTRY DATE: Entered STN: 19970612
 Last Updated on STN: 20000303
 Entered Medline: 19970605
 AB Basic helix-loop-helix (bHLH)/PAS proteins, such as Sim, act as transcriptional factors, playing a critical role in the control of central nervous system (CNS) development. To isolate novel bHLH/PAS factors in the CNS an iterative search of a **database** for expressed **sequence tags (ESTs)** resulted in the location of several bHLH/PAS protein-like sequences. The rapid amplification of cDNA end (RACE) method was applied to isolate full-length cDNAs of these **ESTs**. Several 5' and 3' terminal sequences were isolated using primers derived from an **EST** from the human brain cDNA library. The predicted novel factor polypeptide had bHLH and PAS domains that were highly homologous with those of Ah receptor nuclear translocator (Arnt) and Arnt2. Combination of the isolated cDNA fragments revealed the existence of several alternatively spliced variants. The distribution of the novel bHLH/PAS factor message was analyzed by **Northern** blot

hybridization. This detected only one transcript, which was 2.9 kb in size. Strong hybridization was found in the brain, skeletal muscle and **heart**. Expression of the novel bHLH/PAS factor, brain and muscle Arnt-like protein 1 (BMAL1), was different from that of Arnt and Arnt2, suggesting that BMAL1 has a different function in the CNS and muscle than Arnt and Arnt2.

L32 ANSWER 72 OF 78 MEDLINE DUPLICATE 50
 ACCESSION NUMBER: 97306278 MEDLINE
 DOCUMENT NUMBER: 97306278 PubMed ID: 9162095
 TITLE: Cloning of a new human gene with short consensus repeats using the **EST database**.
 AUTHOR: Nangaku M; Shankland S J; Kurokawa K; Bomsztyk K; Johnson R
 J; Couser W G
 CORPORATE SOURCE: Division of Nephrology, Box 356 521, University of Washington, Seattle, WA, USA.
 CONTRACT NUMBER: DK02142 (NIDDK)
 DK34198 (NIDDK)
 DK43422 (NIDDK)
 +
 SOURCE: IMMUNOGENETICS, (1997) 46 (2) 99-103.
 Journal code: 0420404. ISSN: 0093-7711.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199707
 ENTRY DATE: Entered STN: 19970805
 Last Updated on STN: 19970805
 Entered Medline: 19970723

AB The complement system, which provides many of the effector functions of humoral immunity and inflammation, is tightly regulated by various complement regulatory proteins. The most common structural feature of these proteins is a motif called short consensus repeat (SCR). In order to identify a new human complement regulatory protein, we performed a similarity search using SCR on the expressed **sequence tag (EST) database** and found a partial sequence of a new human gene. Using a probe containing this partial sequence, we obtained a full-length cDNA of this gene from a human umbilical vein endothelial cell (HUVEC) library. The sequencing reaction demonstrated an open reading frame of 1383 nucleotides coding for a 461 amino acid polypeptide with a deduced relative molecular mass of 51 000. Structural analysis showed that the protein has three SCRs with one transmembrane domain. A characteristic feature of these SCR was that they have six conserved cysteines per repeat instead of the usual four. Therefore, we named this cDNA THECY (three hexa-cysteine motifs). A six cysteine motif is a characteristic feature of selectins. We used **northern blot** analysis to show that a 2.0 kilobase (kb) transcript was ubiquitously present in most organs studied, and the mRNA was most abundant in the **heart**. In conclusion, we discovered a member of a new class of membrane-bound SCR-containing molecules using the **EST database**. Utilization of the **EST database** may be useful in the search for other new immunological proteins. The function of this gene remains to be elucidated.

L32 ANSWER 73 OF 78 MEDLINE
 ACCESSION NUMBER: 96279170 MEDLINE
 DOCUMENT NUMBER: 96279170 PubMed ID: 8663127
 TITLE: Molecular cloning and functional expression of the K-C1

cotransporter from rabbit, rat, and human. A new member of the cation-chloride cotransporter family.

AUTHOR: Gillen C M; Brill S; Payne J A; Forbush B 3rd
 CORPORATE SOURCE: Department of Cellular and Molecular Physiology, Yale University School of Medicine, New Haven, Connecticut 06520, USA.
 CONTRACT NUMBER: DK09219 (NIDDK)
 SOURCE: DK47661 (NIDDK)
 JOURNAL OF BIOLOGICAL CHEMISTRY, (1996 Jul 5) 271 (27) 16237-44.
 Journal code: 2985121R. ISSN: 0021-9258.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-U05958; GENBANK-U07547; GENBANK-U07549; GENBANK-U20973; GENBANK-U20975; GENBANK-U30246; GENBANK-U55053; GENBANK-U55054; GENBANK-U55815; GENBANK-U55816
 ENTRY MONTH: 199608
 ENTRY DATE: Entered STN: 19960911
 Last Updated on STN: 19980206
 Entered Medline: 19960829

AB We report the cloning, sequence analysis, tissue distribution, and functional expression of the K-Cl cotransport protein, KCC1. KCC1 was identified by searching the human expressed **sequence tag** data base, based on the expectation that it would be distantly related to the Na-K-Cl cotransporter. Rabbit KCC1 (rbKCC1) and rat KCC1 (rtKCC1) were

cloned by screening rabbit **kidney** and rat brain cDNA libraries using homologous cDNA probes. Human KCC1 (hKCC1) was obtained from I.M.A.G.E. clones and in part by reverse transcription-polymerase chain reaction; it exhibits 97% identity with rbKCC1. KCC1 encodes a 1085-residue polypeptide with substantial sequence homology (24-25% identity) to the bumetanide-sensitive Na-K-Cl cotransporter (NKCC or BSC) and the thiazide-sensitive Na-Cl cotransporter (NCC or TSC). Hydropathy analysis of KCC1 indicates structural homology to NKCC, including 12 transmembrane domains, a large extracellular loop with potential N-linked glycosylation sites, and cytoplasmic N- and C-terminal regions. **Northern** blot analysis revealed a ubiquitously expressed 3.8-kilobase transcript. Much of the genomic sequence of hKCC1 is in the data base, and the gene has been previously localized to 16q22.1 (Larsen, F., Solheim, J., Kristensen, T., Kolsto, A. B., and Prydz, H. (1993) Hum. Mol. Genet. 2, 1589-1595). Epitope-tagged rbKCC1 was stably expressed in human embryonic **kidney** (HEK 293) cells, resulting in production of a approximately 150-kDa glycoprotein. The initial rate of 86Rb efflux from cells expressing rbKCC1 was more than 7 times greater than efflux from control cells and was inhibited by 2 mM furosemide; 86Rb efflux was stimulated by cell swelling. Uptake of 86Rb into rbKCC1 cells after a 15-min pretreatment with 1 mM N-ethylmaleimide was dependent on external chloride but not on external sodium, and was inhibited by furosemide with a Ki of approximately 40 microM and by bumetanide with a Ki of approximately 60 microM. These data demonstrate that the KCC1 cDNAs encode a widely expressed K-Cl cotransporter with the characteristics of the K-Cl transporter that has been characterized in red cells.

L32 ANSWER 74 OF 78

MEDLINE

DUPLICATE 51

ACCESSION NUMBER: 97114072 MEDLINE

DOCUMENT NUMBER: 97114072 PubMed ID: 8955891

TITLE: Isolation of a developmentally-regulated expressed
sequence tag from bladder tissue using the mRNA differential display.

AUTHOR: Chaqour B; Howard P S; Macarak E J

CORPORATE SOURCE: University of Pennsylvania, School of Dental Medicine,
Department of Anatomy & Histology, Philadelphia 19104,
USA.

CONTRACT NUMBER: DK45419 (NIDDK)
DK48215 (NIDDK)

SOURCE: BIOCHEMISTRY AND MOLECULAR BIOLOGY INTERNATIONAL, (1996
Nov) 40 (5) 1011-6.
Journal code: 9306673. ISSN: 1039-9712.

PUB. COUNTRY: Australia
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-R41901; GENBANK-R57591

ENTRY MONTH: 199703

ENTRY DATE: Entered STN: 19970313
Last Updated on STN: 19970313
Entered Medline: 19970306

AB In order to gain insight into the molecular and cellular events that govern the structural and the functional properties in developing organs, we have conducted a study to identify genes that have a temporally-restricted expression in the **bladder** wall during fetal development. We utilized the mRNA differential display technique and compared the pattern of gene expression during the first, the second and the third trimester of gestation. We cloned and sequenced a cDNA fragment (bld-10) which was expressed during the second and third trimester but consistently absent during the first trimester. The bld-10 sequence is not related to any known gene in the GenBank **database** but has significant homology (89%) with human expressed **sequence tag (EST)** that has been cloned from human fetal **heart** and brain libraries. When used in **Northern-blot** hybridization as a probe, the fragment bld-10 generates two hybridization signals of 3.1 and 4.0 kb, that are minimally expressed during the first trimester of gestation and upregulated in the second and third trimester. Differential expression of this gene may be responsible for some of the profound changes which occur during organ development.

L32 ANSWER 75 OF 78 MEDLINE DUPLICATE 52

ACCESSION NUMBER: 96380169 MEDLINE

DOCUMENT NUMBER: 96380169 PubMed ID: 8788182

TITLE: Expression and characterization of a novel human sperm membrane protein.

AUTHOR: Liu Q Y; Wang L F; Miao S Y; Catterall J F

CORPORATE SOURCE: Population Council, Center for Biomedical Research, New York, New York 10021, USA.

CONTRACT NUMBER: HD 13541 (NICHD)

SOURCE: BIOLOGY OF REPRODUCTION, (1996 Feb) 54 (2) 323-30.
Journal code: 0207224. ISSN: 0006-3363.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-S83157

ENTRY MONTH: 199610

ENTRY DATE: Entered STN: 19961106

Last Updated on STN: 19980206
Entered Medline: 19961022

AB A cDNA fragment (HSD-1) coding for part of a human sperm membrane protein (hSMP-1) was previously isolated from a human testis cDNA expression library, with the serum from an infertile patient used as a probe. By rescreening human testis cDNA libraries with the HSD-1 insert and using rapid amplification of cDNA ends, the complete cDNA of 2482 bp was identified and sequenced. An open reading frame of 1572 bp encodes 523 amino acid residues with a computed molecular mass of 55.08 kDa. This protein sequence does not match any other sequence in the **databases**, indicating that it represents a novel sperm antigen. **Northern** blot analysis of human and rat testis poly(A) mRNA detected a band of approximately 2.5 kb in both species. Reverse transcriptase polymerase chain reaction analysis showed that hSMP-1 mRNA was present in human testis but was not in either **kidney** or liver. When the cDNA was expressed in Escherichia coli under the control of the T7 promoter, the expressed protein accumulated to a level of about 50% of the total cellular protein. The expressed protein, which contained an N-terminal poly(his) **sequence tag**, was purified by chromatography on an nitrilo-tri-acetic acid affinity resin.

Approximately

10 mg of pure protein was obtained from a 500-ml culture, purified, and used as antigen to generate a polyclonal antiserum in rabbits. Western blot analysis of human sperm extracts showed a single specific band at 55.5 kDa. Immunofluorescence data showed that hSMP-1 was localized to the head of human sperm. The fluorescent staining formed a cap-shaped pattern that was similar in morphology to the human sperm acrosome. The availability of large amounts of recombinant hSMP-1 and its antiserum

will

facilitate studies on the function and expression of the protein during spermatogenesis and the assessment of its potential value as a contraceptive immunogen.

L32 ANSWER 76 OF 78 MEDLINE DUPLICATE 53
ACCESSION NUMBER: 97131607 MEDLINE
DOCUMENT NUMBER: 97131607 PubMed ID: 8977118
TITLE: Characterization of a human gene related to genes encoding somatostatin receptors.
AUTHOR: Kolakowski L F Jr; Jung B P; Nguyen T; Johnson M P; Lynch K
CORPORATE SOURCE: R; Cheng R; Heng H H; George S R; O'Dowd B F
Department of Pharmacology, University of Texas Health Science Center at San Antonio, 78284, USA.
SOURCE: FEBS LETTERS, (1996 Dec 2) 398 (2-3) 253-8.
Journal code: 0155157. ISSN: 0014-5793.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U71092; GENBANK-U77953
ENTRY MONTH: 199701
ENTRY DATE: Entered STN: 19970219
Last Updated on STN: 20000303
Entered Medline: 19970131

AB We report the identification of a gene, named SLC-1(1), encoding a novel
G protein-coupled receptor (GPCR). A customized search procedure of a **database** of expressed **sequence tags** (dbEST) retrieved a human cDNA sequence that partially encoded a GPCR. A genomic DNA fragment identical to the cDNA was obtained and used to screen a library to isolate the full-length coding region of the gene. This gene

was intronless in its open reading frame, and encoded a receptor of 402 amino acids, and shared -40% amino acid identity in the transmembrane (TM) regions to the five known human somatostatin receptors. **Northern** blot analysis revealed that SLC-1 is expressed in human brain regions, including the forebrain and hypothalamus. Expression in the rat was highest in brain, followed by **heart**, **kidney**, and **ovary**. Expression of SLC-1 in COS-7 cells failed to show specific binding to radiolabelled Tyr1-somatostatin-14, naloxone, bremazocine, 1,3-di(2-tolyl)-guanidine (DTG), or haloperidol. A repeat polymorphism of the form (CA)_n was discovered in the 5'-untranslated region (UTR) of the gene and SLC-1 was mapped to chromosome 22, q13.3.

L32 ANSWER 77 OF 78 MEDLINE DUPLICATE 54
 ACCESSION NUMBER: 96299762 MEDLINE
 DOCUMENT NUMBER: 96299762 PubMed ID: 8661126
 TITLE: Construction of a normalized directionally cloned cDNA library from adult heart and analysis of 3040 clones by partial sequencing.
 AUTHOR: Tanaka T; Ogiwara A; Uchiyama I; Takagi T; Yazaki Y; Nakamura Y
 CORPORATE SOURCE: Laboratory of Molecular Medicine, Institute of Medical Science, University of Tokyo, 4-6-1 Shirokanedai, Minato-ku, Tokyo, 108, Japan.
 SOURCE: GENOMICS, (1996 Jul 1) 35 (1) 231-5.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-C02623; GENBANK-C02624; GENBANK-C02625;
 GENBANK-C02626; GENBANK-C02627; GENBANK-C02628;
 GENBANK-C02629; GENBANK-C02630; GENBANK-C02631;
 GENBANK-C02632; GENBANK-C02633; GENBANK-C02634;
 GENBANK-C02635; GENBANK-C02636; GENBANK-C02637;
 GENBANK-C02638; GENBANK-C02639; GENBANK-C02640;
 GENBANK-C02641; GENBANK-C02642; GENBANK-C02643;
 GENBANK-C02644; GENBANK-C02645; GENBANK-C02646;
 GENBANK-C02647; GENBANK-C02648; GENBANK-C02649;
 GENBANK-C02650; GENBANK-C02651; GENBANK-C02652; +
 ENTRY MONTH: 199609
 ENTRY DATE: Entered STN: 19961015
 Last Updated on STN: 19961015
 Entered Medline: 19960930

AB Large-scale sequencing of clones from cDNA libraries derived from specific tissues is a rapid and efficient way of discovering novel genes expressed in those tissues. However, because the **heart** is continually contracting and relaxing, it strongly expresses muscle-contractile genes and/or mitochondrial genes, a bias that reduces the efficiency of this method. To improve the efficiency of identifying novel genes expressed in the **heart**, we constructed a normalized directionally cloned cDNA library from adult **heart** and partially sequenced 3040 clones. Comparisons of these sequence data with known DNA sequences in the **database** revealed that 57.1% of the clones matched human genes already known, 23.4% were identical or almost identical to human expressed **sequence tags (ESTs)**, 14.2% bore no significant homology to any sequences in the **database**, and 1.2% represented repetitive sequences. The remaining 4.1% showed some homology with known genes, and **Northern** blot analysis of several clones

in this category revealed that most of them were expressed mainly in the **heart** and skeletal muscle. After redundancy was excluded, the 3040 clones accounted for 1395 distinctive **ESTs**, 446 of which exhibited no match to any known sequence. Our results suggest that our normalized library is less redundant than standard libraries and is a useful resource for cataloging genes expressed in the **heart**.

L32 ANSWER 78 OF 78 MEDLINE DUPLICATE 55
 ACCESSION NUMBER: 96128239 MEDLINE
 DOCUMENT NUMBER: 96128239 PubMed ID: 8543061
 TITLE: Human ClpP protease: cDNA sequence, tissue-specific expression and chromosomal assignment of the gene.
 AUTHOR: Bross P; Andresen B S; Knudsen I; Kruse T A; Gregersen N
 CORPORATE SOURCE: Center for Medical Molecular Biology, Aarhus University Hospital, Denmark.
 SOURCE: FEBS LETTERS, (1995 Dec 18) 377 (2) 249-52.
 Journal code: 0155157. ISSN: 0014-5793.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-D17510; GENBANK-J05534; GENBANK-L07793;
 GENBANK-L28807; GENBANK-L38581; GENBANK-U16135;
 GENBANK-X04465; GENBANK-X15901; GENBANK-X54484;
 GENBANK-X86563; GENBANK-Z00044; GENBANK-Z49073;
 GENBANK-Z50853
 ENTRY MONTH: 199602
 ENTRY DATE: Entered STN: 19960227
 Last Updated on STN: 20020420
 Entered Medline: 19960213

AB We identified three overlapping human expressed **sequence tags** with significant homology to the E. coli ClpP amino sequence by screening the EMBL nucleotide **database**. With this sequence information we applied 5' and 3'-rapid amplification of cDNA ends (RACE) to amplify and sequence human clpP cDNA in two overlapping fragments. The open reading frame encodes a 277 amino acid long precursor polypeptide. Two ClpP specific motifs surrounding the active site residues are present and extensive homology to ClpP's from other organisms was observed. **Northern** blotting showed high relative expression levels of clpP mRNA in skeletal muscle, intermediate levels in **heart**, liver and pancreas, and low levels in brain, placenta, **lung** and **kidney**. By analysis of human/rodent cell hybrids the human clpP gene was assigned to chromosome 19.

=>
 => d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
 19:04:09
 ON 08 JUL 2002

L1 13496 S EST
 L2 34 S L1(S) (NO#(W)CORRELAT?)
 L3 21 DUP REM L2 (13 DUPLICATES REMOVED)
 L4 3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
 L5 1972 S L4(S) (PROTEIN OR PEPTIDE)
 L6 1748 S L5(S) (EXPRESS?)
 L7 775 S L6(S)DATABASE#
 L8 355 DUP REM L7 (420 DUPLICATES REMOVED)

L9 96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN)
 L10 47 S L8(S) GENBANK
 L11 87 S L8(S) (HEART OR BONE OR BRAIN)
 L12 137 S L11 OR L9
 L13 1 S L12 AND (NO#(W) EXPRESS?)
 L14 67 S L12(S) (TRANSCRI?)
 L15 86 S L8(S) NORTHERN
 L16 50 S L1(S) (NO#(2W) CORRELAT?)
 L17 16 S L16 NOT L2
 L18 12 DUP REM L17 (4 DUPLICATES REMOVED)
 L19 54 S L1(S) (NO#(3W) CORRELAT?)
 L20 0 S L19 NOT L1
 L21 20 S L19 NOT L2
 L22 4 S L21 NOT L16

FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002

L23 13496 S EST OR (SEQUENCE(W) TAG#)
 L24 234 S L23 AND DATABASE#/TI
 L25 0 S L24 AND (NO(3W) CORRELAT?)
 L26 234 S L24(S) DATABASE#
 L27 2221 S L23(S) DATABASE#
 L28 4 S L27(S) (NO#(3W) CORRELAT?)
 L29 1174 S L23(S) (BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVA)
 L30 310 S L29(S) NORTHERN
 L31 133 S L30 AND DATABASE#
 L32 78 DUP REM L31 (55 DUPLICATES REMOVED)

=> s l23(s) (predict? or anticipat?)
 L33 1072 L23(S) (PREDICT? OR ANTICIPAT?)

=> s l33 and database#/ti
 L34 22 L33 AND DATABASE#/TI

=> dup rem l34
 PROCESSING COMPLETED FOR L34
 L35 13 DUP REM L34 (9 DUPLICATES REMOVED)

=> d ibib abs tot

L35	ANSWER 1 OF 13	MEDLINE	DUPLICATE 1
ACCESSION NUMBER:	2002229697	MEDLINE	
DOCUMENT NUMBER:	21963940	PubMed ID: 11966884	
TITLE:	Leveraging genomic databases : from an Aedes albopictus mosquito cell line to the malaria vector Anopheles gambiae via the Drosophila genome project.		
AUTHOR:	Eccleston E D; Gerenday Anna; Fallon Ann M		
CORPORATE SOURCE:	ThermoFinnigan Protein Chemistry Unit, MicroChemical Facility, Academic Health Center, University of Minnesota, St. Paul, MN 55108, USA.		
CONTRACT NUMBER:	AI 36258 (NIAID) AI 43971 (NIAID)		
SOURCE:	INSECT MOLECULAR BIOLOGY, (2002 Apr) 11 (2) 187-95. Journal code: 9303579. ISSN: 0962-1075.		
PUB. COUNTRY:	England: United Kingdom Journal; Article; (JOURNAL ARTICLE)		
LANGUAGE:	English		
FILE SEGMENT:	Priority Journals		
ENTRY MONTH:	200207		
ENTRY DATE:	Entered STN: 20020423 Last Updated on STN: 20020704 Entered Medline: 20020703		

AB An important justification for genome sequencing efforts is the **anticipation** that data from model organisms will provide a framework for the more rapid analysis of other, less studied genomes. In this investigation, we sequenced an internal region of 25 amino acids from a 52 kDa protein that was differentially expressed in 20-hydroxyecdysone-treated *Aedes albopictus* cells in culture. Within the GenBank non-mouse and non-human expressed **sequence tag (EST)** database, this "Aedes peptide" uncovered a putative homology to hypothetical translation products from *Anopheles gambiae*, *Caenorhabditis elegans* and *Drosophila melanogaster*. The hypothetical translation product from *D. melanogaster*, which included 462 amino acids, uncovered five expressed **sequence tags (ESTs)** from the malaria vector, *Anopheles gambiae*. When the *Anopheles ESTs* were aligned against the hypothetical *Drosophila* protein, we found that in aggregate they covered 324 amino acids, with gaps measuring 19, 30, and 87 amino acids. To approximate the complete amino acid sequence, gaps between translation products from *Anopheles ESTs* were replaced with corresponding amino acids from *Drosophila* to arrive at a calculated mass of 51 104 and a pI of 5.84 for the mosquito protein, consistent with the position of the *Ae. albopictus* protein on two-dimensional polyacrylamide gels. Finally, tandem mass spectrometry of a tryptic digest of the 52 kDa *Ae. albopictus* protein revealed 33 peptides with masses within 1 Dalton of those **predicted** from an in silico digestion of the reconstructed *Anopheles* protein. In addition to providing the first direct evidence that a hypothetical protein in *Drosophila* is in fact translated, this analysis provides a general approach for maximizing recovery, from existing databases, of information that can facilitate prioritization of efforts among several candidate proteins.

L35 ANSWER 2 OF 13 MEDLINE DUPLICATE 2
 ACCESSION NUMBER: 2002004287 MEDLINE
 DOCUMENT NUMBER: 21624809 PubMed ID: 11752289
 TITLE: PALS db: Putative Alternative Splicing **database**.
 AUTHOR: Huang Y-H; Chen Y-T; Lai J-J; Yang S-T; Yang U-C
 CORPORATE SOURCE: Bioinformatics Program, National Yang-Ming University, No. 155, Sec. 2, Li-Noun Street, Taipei, Taiwan 11221, Republic of China.
 SOURCE: NUCLEIC ACIDS RESEARCH, (2002 Jan 1) 30 (1) 186-90. Journal code: 0411011. ISSN: 1362-4962.
 PUB. COUNTRY: England: United Kingdom
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200201
 ENTRY DATE: Entered STN: 20020102
 Last Updated on STN: 20020125
 Entered Medline: 20020121
 AB PALS db is a collection of Putative Alternative Splicing information from 19 936 human UniGene clusters and 16 615 mouse UniGene clusters. Alternative splicing (AS) sites were **predicted** by using the longest messenger RNA (mRNA) sequence in each UniGene cluster as the reference sequence. This sequence was aligned with related sequences in UniGene and dbEST to reveal the AS. This information was presented with six features: (i) literature aliases were used to improve the result of a gene name search; (ii) the quality of a **prediction** can be easily judged from the color-coded similarity and the scaled length of an

alignment; (iii) we have clustered those **EST** sequences that support the same AS site together to enhance the users' confidence on a **prediction**; (iv) the users can also set up the alignment criteria interactively to recover false negatives; (v) tissue distribution can be displayed by placing the mouse cursor over an alignment; (vi) gene features will be analyzed at foreign sites by submitting the selected

mRNA

or its encoded protein as a query. Using these features, the users cannot only discover putative AS sites in silico, but also make new observations by combining AS information with tissue distributions or with gene features. PALS db is available at <http://palsdb.ym.edu.tw/>.

L35 ANSWER 3 OF 13 MEDLINE DUPLICATE 3

ACCESSION NUMBER: 2002081897 MEDLINE
DOCUMENT NUMBER: 21666988 PubMed ID: 11808872
TITLE: **Database** and analysis system for cDNA clones obtained from full-length enriched cDNA libraries.
AUTHOR: Nishikawa Tetsuo; Ota Toshio; Kawai Yuri; Ishii Shizuko; Saito Kaoru; Yamamoto Jun-ichi; Wakamatsu Ai; Ozawa Masashi; Suzuki Yutaka; Sugano Sumio; Isogai Takao
CORPORATE SOURCE: Helix Research Institute, Chiba, Japan.
SOURCE: In Silico Biol, (2002) 2 (1) 5-18.
Journal code: 9815902. ISSN: 1386-6338.
PUB. COUNTRY: Netherlands
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200206
ENTRY DATE: Entered STN: 20020128
Last Updated on STN: 20020623
Entered Medline: 20020621

AB We have developed an efficient sequence-analysis system and a database system for clones obtained from full-length enriched cDNA libraries made by using the oligo-capping method. We developed a semi-automatic analysis system for 5'- and 3'-end sequences. It pre-processes raw sequences (vector cut and accurate-sequence region extraction), clusters the sequences, searches for similarities through public databases, annotates completeness of clones and analyzes the ORFs in the sequences. Newly developed or improved programs are used in each step. A new program, ESTiMateFull is used to evaluate and to **predict** the sequence-fullness based on comparisons with mRNA and **EST** sequences, respectively. The ATGpr program is used to **predict** sequence-fullness based on statistical information. The combination of full-length enriched cDNA clones and ATGpr fullness **prediction** resulted in 70% accuracy in the specificity and the sensitivity of the fullness **predictions**. For the ORFs **predicted** by the ATGpr, the signal peptides are **predicted** and a motif search is performed by our new system. We also developed a program that assembles our sequences with dbEST sequences and developed a system to retrieve clones by the characteristics of the ORFs. As keywords, combination of various results of the analyses can be used for retrieval. And various results such as ORF features and database search results can be shown on the same screen by multiple displays. Full-length clones having interesting functions can thus be retrieved efficiently by using this system.

L35 ANSWER 4 OF 13 MEDLINE DUPLICATE 4

ACCESSION NUMBER: 2002188338 MEDLINE
DOCUMENT NUMBER: 21919610 PubMed ID: 11922602
TITLE: Establishment of a root proteome reference map for the model legume Medicago truncatula using the expressed

sequence tag **database** for peptide mass fingerprinting.

AUTHOR: Mathesius U; Keijzers G; Natera S H; Weinman J J; Djordjevic M A; Rolfe B G

CORPORATE SOURCE: Genomic Interactions Group, Research School of Biological Sciences, Australian National University, Canberra, ACT.

SOURCE: Proteomics, (2001 Nov) 1 (11) 1424-40.
Journal code: 101092707. ISSN: 1615-9853.

PUB. COUNTRY: Germany; Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200206

ENTRY DATE: Entered STN: 20020403
Last Updated on STN: 20020614
Entered Medline: 20020610

AB We have established a proteome reference map for *Medicago truncatula* root proteins using two-dimensional gel electrophoresis combined with peptide mass fingerprinting to aid the dissection of nodulation and root developmental pathways by proteome analysis. *M. truncatula* has been chosen

as a model legume for the study of nodulation-related genes and proteins. Over 2,500 root proteins could be displayed reproducibly across an isoelectric focussing range of 4-7. We analysed 485 proteins by peptide mass fingerprinting, and 179 of those were identified by matching against the current *M. truncatula* expressed **sequence tag** (**EST**) database containing DNA sequences of approximately 105,000 **ESTs**. Matching the **EST** sequences to available plant DNA sequences by BLAST searches enabled us to **predict** protein function. The use of the **EST** database for peptide identification is discussed. The majority of identified proteins were metabolic enzymes and stress response proteins, and 44% of proteins occurred as isoforms, a result that could not have been **predicted** from sequencing data alone. We identified two nodulins in uninoculated root tissue, supporting evidence for a role of nodulins in normal plant development. This

proteome map will be updated continuously (<http://semele.anu.edu.au/2d/2d.html>) and will be a powerful tool for investigating the molecular mechanisms of root symbioses in legumes.

L35 ANSWER 5 OF 13 MEDLINE DUPLICATE 5

ACCESSION NUMBER: 2001543308 MEDLINE

DOCUMENT NUMBER: 21475973 PubMed ID: 11591886

TITLE: MRP8, a new member of ABC transporter superfamily, identified by **EST database** mining and gene **prediction** program, is highly expressed in breast cancer.

AUTHOR: Bera T K; Lee S; Salvatore G; Lee B; Pastan I

CORPORATE SOURCE: Laboratory of Molecular Biology, Division of Basic Sciences, National Cancer Institute, National Institutes of Health, Bethesda, Maryland 20892-4255, USA.

SOURCE: MOLECULAR MEDICINE, (2001 Aug) 7 (8) 509-16.
Journal code: 9501023. ISSN: 1076-1551.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200202

ENTRY DATE: Entered STN: 20011010

Last Updated on STN: 20020215

Entered Medline: 20020214

AB BACKGROUND: With the completion of the human draft genome sequence, efforts are now devoted to identifying new genes. We have developed a computer-based strategy that utilizes the **EST** database to identify new genes that could be targets for the immunotherapy of cancer or could be involved in the multistep process of cancer. MATERIALS AND METHODS: Utilizing our computer-based screening strategy, we identified a cluster of expressed **sequence tags (ESTs)** that are highly expressed in breast cancer. Northern blot and reverse transcriptase polymerase chain reaction (RT-PCR) analyses demonstrated

the

tissue specificity of the computer-generated cluster and comparison with the human genome sequence assisted in isolating a full-length cDNA clone. RESULTS: We identified a new gene that is highly expressed in breast cancer. This gene is expressed at moderate levels in normal breast and testis and at very low levels in liver, brain, and placenta. The gene has two major transcripts of 4.5 kb and 4.1 kb. The 4.5-kb transcript is very abundant in breast cancer, and has an open reading frame of 1382 amino acids. The **predicted** protein sequence of the 4.5-kb transcript reveals that it has high homology with MRP5, a member of multidrug resistant-associated protein family (MRP). There are seven reported members in the MRP family; we designate this gene as MRP8 (ABCC11). The 4.5-kb MRP8 transcript consists of 31 exons and is located in a genomic region of over 80.4 kb on chromosome 16q12.1. The smaller 4.1-kb transcript of MRP8 is found in testis and may initiate within intron 6 of the gene. CONCLUSION: The selective expression of MRP8 (ABCC11), a new member of ATP-binding cassette transporter superfamily could be a molecular target for the treatment of breast cancer.

L35 ANSWER 6 OF 13

MEDLINE

DUPLICATE 6

ACCESSION NUMBER: 2001233544 MEDLINE

DOCUMENT NUMBER: 21109940 PubMed ID: 11157793

TITLE: A cSNP map and **database** for human chromosome 21.

AUTHOR: Deutsch S; Iseli C; Bucher P; Antonarakis S E; Scott H S

CORPORATE SOURCE: Division of Medical Genetics, University of Geneva Medical School, Geneva, Switzerland.

SOURCE: GENOME RESEARCH, (2001 Feb) 11 (2) 300-7.

Journal code: 9518021. ISSN: 1088-9051.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200105

ENTRY DATE: Entered STN: 20010517

Last Updated on STN: 20010517

Entered Medline: 20010503

AB Single nucleotide polymorphisms (SNPs) are likely to contribute to the study of complex genetic diseases. The genomic sequence of human chromosome 21q was recently completed with 225 annotated genes, thus permitting efficient identification and precise mapping of potential

cSNPs

by bioinformatics approaches. Here we present a human chromosome 21 (HC21)

cSNP database and the first chromosome-specific cSNP map. Potential cSNPs were generated using three approaches: (1) Alignment of the complete HC21 genomic sequence to cognate **ESTs** and mRNAs. Candidate cSNPs were automatically extracted using a novel program for context-dependent SNP identification that efficiently discriminates between true variation,

poor

alignment quality sequencing, and paralogous gene alignments. (2) Multiple alignment

of all known HC21 genes to all other human database entries. (3) Gene-targeted cSNP discovery. To date we have identified 377 cSNPs averaging 1 SNP per 1.5 kb of transcribed sequence, covering 65% of known genes in the chromosome. Validation of our bioinformatics approach was demonstrated by a confirmation rate of 78% for the **predicted** cSNPs, and in total 32% of the cSNPs in our database have been confirmed. The database is publicly available at <http://csnp.unige.ch> or <http://csnp.isb-sib.ch>. These SNPs provide a tool to study the contribution of HC21 loci to complex diseases such as bipolar affective disorder and allele-specific contributions to Down syndrome phenotypes.

L35 ANSWER 7 OF 13 MEDLINE DUPLICATE 7
 ACCESSION NUMBER: 2001106597 MEDLINE
 DOCUMENT NUMBER: 20574807 PubMed ID: 11125105
 TITLE: SpliceDB: **database** of canonical and non-canonical mammalian splice sites.
 AUTHOR: Burset M; Seledtsov I A; Solovyev V V
 CORPORATE SOURCE: The Sanger Centre, Hinxton, Cambridge CB10 1SA, UK and Softberry Inc., 108 Corporate Park Drive, Suite 120, White Plains, NY 10604, USA.
 SOURCE: NUCLEIC ACIDS RESEARCH, (2001 Jan 1) 29 (1) 255-9. Journal code: 0411011. ISSN: 1362-4962.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200102
 ENTRY DATE: Entered STN: 20010322
 Last Updated on STN: 20010521
 Entered Medline: 20010208
 AB A database (SpliceDB) of known mammalian splice site sequences has been developed. We extracted 43 337 splice pairs from mammalian divisions of the gene-centered Infogene database, including sites from incomplete or alternatively spliced genes. Known **EST** sequences supported 22 815 of them. After discarding sequences with putative errors and ambiguous location of splice junctions the verified dataset includes 22 489 entries.
 Of these, 98.71% contain canonical GT-AG junctions (22 199 entries) and 0.56% have non-canonical GC-AG splice site pairs. The remainder (0.73%) occurs in a lot of small groups (with a maximum size of 0.05%). We especially studied non-canonical splice sites, which comprise 3.73% of GenBank annotated splice pairs. **EST** alignments allowed us to verify only the exonic part of splice sites. To check the conservative dinucleotides we compared sequences of human non-canonical splice sites with sequences from the high throughput genome sequencing project (HTG). Out of 171 human non-canonical and **EST**-supported splice pairs, 156 (91.23%) had a clear match in the human HTG. They can be classified after sequence analysis as: 79 GC-AG pairs (of which one was an error that corrected to GC-AG), 61 errors corrected to GT-AG canonical pairs, six AT-AC pairs (of which two were errors corrected to AT-AC), one case was produced from a non-existent intron, seven cases were found in HTG that were deposited to GenBank and finally there were only two other cases left of supported non-canonical splice pairs. The information about verified splice site sequences for canonical and non-canonical sites is presented in SpliceDB with the supporting evidence. We also built weight matrices for the major splice groups, which can be incorporated into gene **prediction** programs. SpliceDB is available at the computational genomic Web server of the Sanger Centre: <http://genomic.sanger.ac>.

uk/spldb/SpliceDB.html and at <http://www.softberry.com/spldb/SpliceDB.html>.

L35 ANSWER 8 OF 13 MEDLINE DUPLICATE 8
ACCESSION NUMBER: 2001106564 MEDLINE
DOCUMENT NUMBER: 20574776 PubMed ID: 11125074
TITLE: trEST, trGEN and Hits: access to **databases** of
predicted protein sequences.
AUTHOR: Pagni M; Iseli C; Junier T; Falquet L; Jongeneel V; Bucher
P
CORPORATE SOURCE: Swiss Institute of Bioinformatics, Ludwig Institute for
Cancer Research, Chemin des Boveresses 155, CH-1066,
Epalinges s/Lausanne, Switzerland.
SOURCE: NUCLEIC ACIDS RESEARCH, (2001 Jan 1) 29 (1) 148-51.
Journal code: 0411011. ISSN: 1362-4962.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200102
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010521
Entered Medline: 20010208

AB High throughput genome (HTG) and expressed **sequence tag**
(**EST**) sequences are currently the most abundant nucleotide
sequence classes in the public database. The large volume, high degree of
fragmentation and lack of gene structure annotations prevent efficient
and

effective searches of HTG and **EST** data for protein sequence
homologies by standard search methods. Here, we briefly describe three
newly developed resources that should make discovery of interesting genes
in these sequence classes easier in the future, especially to biologists
not having access to a powerful local bioinformatics environment. trEST
and trGEN are regularly regenerated databases of hypothetical protein
sequences **predicted** from **EST** and HTG sequences,
respectively. Hits is a web-based data retrieval and analysis system
providing access to precomputed matches between protein sequences
(including sequences from trEST and trGEN) and patterns and profiles from
Prosite and Pfam. The three resources can be accessed via the Hits home
page (<http://hits.isb-sib.ch>).

L35 ANSWER 9 OF 13 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:350913 BIOSIS
DOCUMENT NUMBER: PREV200200350913
TITLE: Molecular chaperone genes in the sugarcane expressed
sequence **database** (SUCEST).
AUTHOR(S): Borges, Julio C.; Peroto, Maria C.; Ramos, Carlos H. I.
(1)
CORPORATE SOURCE: (1) Centro de Biologia Molecular Estrutural, Laboratorio
Nacional de Luz Sincrotron, 13084-971, Campinas, SP:
cramos@lnls.br Brazil
SOURCE: Genetics and Molecular Biology, (March, 2001) Vol. 24, No.
1-4, pp. 85-92. print.
ISSN: 1415-4757.
DOCUMENT TYPE: Article
LANGUAGE: English

AB Some newly synthesized proteins require the assistance of molecular
chaperones for their correct folding. Chaperones are also involved in the
dissolution of protein aggregates making their study significant for both
biotechnology and medicine and the identification of chaperones and
stress-related protein sequences in different organisms is an important

task. We used bioinformatic tools to investigate the information generated by the Sugarcane Expressed **Sequence Tag** (SUCEST) genome project in order to identify and annotate molecular chaperones. We considered that the SUCEST sequences belonged to this category of proteins when their E-values were lower than 1.0e-05. Our annotation shows that 4,164 of the 5' expressed **sequence tag** (**EST**) sequences were homologous to molecular chaperones, nearly 1.8% of all the 5' **ESTs** sequenced during the SUCEST project. About 43% of the chaperones which we found were Hsp70 chaperones and its co-chaperones, 10% were Hsp90 chaperones and 13% were peptidyl-prolyl cis, trans isomerase. Based on the annotation results we **predicted** 156 different chaperone gene subclasses in the sugarcane genome. Taken together, our results indicate that genes which encode chaperones were diverse and abundantly expressed in sugarcane cells, which emphasizes their biological importance.

L35 ANSWER 10 OF 13 MEDLINE DUPLICATE 9
 ACCESSION NUMBER: 2000243852 MEDLINE
 DOCUMENT NUMBER: 20243852 PubMed ID: 10779492
 TITLE: Using **database** matches with for HMMGene for automated gene detection in Drosophila.
 COMMENT: Comment in: Genome Res. 2000 Apr;10(4):391-7
 AUTHOR: Krogh A
 CORPORATE SOURCE: Center for Biological Sequence Analysis, Technical University of Denmark, 2800 Lyngby, Denmark..
 SOURCE: krogh@cbs.dtu.dk
 GENOME RESEARCH, (2000 Apr) 10 (4) 523-8.
 Journal code: 9518021. ISSN: 1088-9051.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200006
 ENTRY DATE: Entered STN: 20000622
 Last Updated on STN: 20000622
 Entered Medline: 20000609

AB The application of the gene finder HMMGene to the Adh region of the Drosophila melanogaster is described, and the **prediction** results are analyzed. HMMGene is based on a probabilistic model called a hidden Markov model, and the probabilistic framework facilitates the inclusion of database matches of varying degrees of certainty. It is shown that database matches clearly improve the performance of the gene finder. For instance, the sensitivity for coding exons **predicted** with both ends correct grows from 62% to 70% on a high-quality test set, when matches to proteins, cDNAs, repeats, and transposons are included. The specificity drops more than the sensitivity increases when **ESTs** are used. This is due to the high noise level in **EST** matches, and it is discussed in more detail why this is and how it might be improved.

L35 ANSWER 11 OF 13 MEDLINE
 ACCESSION NUMBER: 2000410546 MEDLINE
 DOCUMENT NUMBER: 20360648 PubMed ID: 10902191
 TITLE: **EST databases** as multi-conditional gene expression datasets.
 AUTHOR: Ewing R M; Claverie J M

CORPORATE SOURCE: Carnegie Institution of Washington, Department of Plant
Biology, Stanford, California 94305, USA..
ewing@genome.stanford.edu
SOURCE: PACIFIC SYMPOSIUM ON BIOCOMPUTING, (2000) 430-42.
Journal code: 9711271.
PUB. COUNTRY: Singapore
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200008
ENTRY DATE: Entered STN: 20000907
Last Updated on STN: 20000907
Entered Medline: 20000829

AB Large-scale expression data, such as that generated by hybridization to
microarrays, is potentially a rich source of information on gene function
and regulation. By clustering genes according to their expression
profiles, groups of genes involved in the same pathways or sharing common
regulatory mechanisms may be identified. Publicly-available **EST**
collections are a largely unexplored source of expression data. We
previously used a sample of rice **ESTs** to generate 'digital
expression profiles' by counting the frequency of tags for different
genes

sequenced from different cDNA libraries. A simple statistical test was
used to associate genes or cDNA libraries having similar expression
profiles. Here we further validate this approach using larger samples of
ESTs from the UniGene projects (clustered human, mouse and rat
ESTs). Our results show that genes clustered on the basis of
expression profile may represent genes implicated in similar pathways or
coding for different subunits of multi-component enzyme complexes. In
addition we suggest that comparison of clusters from different species,
may be useful for confirmation or **prediction** of orthologs.

L35 ANSWER 12 OF 13 MEDLINE
ACCESSION NUMBER: 1999332695 MEDLINE
DOCUMENT NUMBER: 99332695 PubMed ID: 10404616
TITLE: Protein-coding region discovery in organisms
underrepresented in **databases**.
AUTHOR: Quentin Y; Voiblet C; Martin F; Fichant G
CORPORATE SOURCE: LCB-IBSM CNRS, Marseille, France.
SOURCE: COMPUTERS AND CHEMISTRY, (1999 Jun 15) 23 (3-4) 209-17.
Journal code: 7607706. ISSN: 0097-8485.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199907
ENTRY DATE: Entered STN: 19990806
Last Updated on STN: 19990806
Entered Medline: 19990728

AB The **prediction** of coding sequences has received a lot of
attention during the last decade. We can distinguish two kinds of
methods,
those that rely on training with sets of example and counter-example
sequences, and those that exploit the intrinsic properties of the DNA
sequences to be analyzed. The former are generally more powerful but
their
domains of application are limited by the availability of a training set.
The latter avoid this drawback but can only be applied to sequences that
are long enough to allow computation of the statistics. Here, we present
a
method that fills the gap between the two approaches. A learning step is

applied using a set of sequences that are assumed to contain coding and non-coding regions, but with the boundaries of these regions unknown. A test step then uses the discriminant function obtained during the learning to **predict** coding regions in sequences from the same organism. The learning relies upon a correspondence analysis and **prediction** is presented on a graphical display. The method has been evaluated on a sample of yeast sequences, and the analysis of a set of expressed **sequence tags** from the *Eucalyptus globulus*-*Pisolithus tinctorius* ectomycorrhiza illustrates the relevance of the approach in its biological context.

L35 ANSWER 13 OF 13 MEDLINE
ACCESSION NUMBER: 97336902 MEDLINE
DOCUMENT NUMBER: 97336902 PubMed ID: 9193649
TITLE: Use of the EST **database** resource to identify and clone novel mono(ADP-ribosyl)transferase gene family members.
AUTHOR: Braren R; Firner K; Balasubramanian S; Bazan F; Thiele H G;
Haag F; Koch-Nolte F
CORPORATE SOURCE: Department of Immunology, University Hospital, Hamburg, Germany.
SOURCE: ADVANCES IN EXPERIMENTAL MEDICINE AND BIOLOGY, (1997) 419 163-8. Ref: 19
Journal code: 0121103. ISSN: 0065-2598.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-C03716; GENBANK-H12146; GENBANK-L49677;
GENBANK-N20756; GENBANK-N70349; GENBANK-N76036;
GENBANK-R07880; GENBANK-R35364; GENBANK-T19112;
GENBANK-T70606; GENBANK-T70872; GENBANK-W04280;
GENBANK-W04281; GENBANK-W08722; GENBANK-W12489;
GENBANK-W12573; GENBANK-W18805; GENBANK-W20908;
GENBANK-W34749; GENBANK-W36909; GENBANK-W40714;
GENBANK-W41414; GENBANK-W41430; GENBANK-W42131;
GENBANK-Z24839
ENTRY MONTH: 199709
ENTRY DATE: Entered STN: 19970916
Last Updated on STN: 19970916
Entered Medline: 19970904

AB We searched the database of expressed **sequence tags** (dbEST) for relatives of the known human and murine mono(ADP-ribosyl)transferases (mADPRT), poly(ADP-ribosyl)polymerases (PARP), ADP-ribosyl cyclases, and ADP-ribosylarginine hydrolases (ARH). By May 31, 1996, all of the known enzymes except for RT6 were represented in dbEST by exact sequence matches from mouse and/or human tissues. Several **ESTs** show significant sequence similarity but not identity to known mADPRTs. We isolated, cloned, and sequenced the corresponding genes. Our results show that seven human **ESTs** stem from a novel gene, provisionally designated LART, which is specifically expressed in lymphatic tissues. Five human **ESTs** stem from a novel gene, here designated TART1, which is specifically expressed in testis. This gene is

also represented by a single mouse **EST**. One other mouse **EST** stems from a distinct gene, here designated TART2, which is also expressed in testis. These genes have similar exon/intron structures.

The **predicted** LART and TART1 gene products contain hydrophobic N- and C-terminal signal peptides characteristic for GPI-anchored surface proteins, TART2 lacks the GPI-anchor signal peptide. The **predicted** native proteins show 28-42% sequence identity to one another. They each contain four cysteine residues that probably form conserved disulfide bonds. They each also contain a conserved glutamic acid residue within the proposed active site motif LART and TART1 show interesting deviations from the surrounding consensus sequence.

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
19:04:09
ON 08 JUL 2002

L1 13496 S EST
L2 34 S L1(S) (NO#(W) CORRELAT?)
L3 21 DUP REM L2 (13 DUPLICATES REMOVED)
L4 3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5 1972 S L4(S) (PROTEIN OR PEPTIDE)
L6 1748 S L5(S) (EXPRESS?)
L7 775 S L6(S) DATABASE#
L8 355 DUP REM L7 (420 DUPLICATES REMOVED)
L9 96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN)
L10 47 S L8(S) GENBANK
L11 87 S L8(S) (HEART OR BONE OR BRAIN)
L12 137 S L11 OR L9
L13 1 S L12 AND (NO#(W) EXPRESS?)
L14 67 S L12(S) (TRANSCRI?)
L15 86 S L8(S) NORTHERN
L16 50 S L1(S) (NO#(2W) CORRELAT?)
L17 16 S L16 NOT L2
L18 12 DUP REM L17 (4 DUPLICATES REMOVED)
L19 54 S L1(S) (NO#(3W) CORRELAT?)
L20 0 S L19 NOT L1
L21 20 S L19 NOT L2
L22 4 S L21 NOT L16

FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002

L23 13496 S EST OR (SEQUENCE(W) TAG#)
L24 234 S L23 AND DATABASE#/TI
L25 0 S L24 AND (NO(3W) CORRELAT?)
L26 234 S L24(S) DATABASE#
L27 2221 S L23(S) DATABASE#
L28 4 S L27(S) (NO#(3W) CORRELAT?)
L29 1174 S L23(S) (BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVA)
L30 310 S L29(S) NORTHERN
L31 133 S L30 AND DATABASE#
L32 78 DUP REM L31 (55 DUPLICATES REMOVED)
L33 1072 S L23(S) (PREDICT? OR ANTICIPAT?)
L34 22 S L33 AND DATABASE#/TI
L35 13 DUP REM L34 (9 DUPLICATES REMOVED)

=> s l34(s)database#
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L169(S)DATABASE#'
PROXIMITY OPERATOR LEVEL NOT CONSISTENT WITH
FIELD CODE - 'AND' OPERATOR ASSUMED 'L170(S)DATABASE#'
L36 22 L34(S) DATABASE#

=> s l23(s)database#
L37 2221 L23(S) DATABASE#

=> s l37(s)tissue
L38 612 L37(S) TISSUE

=> s l38(s)prostate
L39 58 L38(S) PROSTATE

=> s l39 and predict?
L40 10 L39 AND PREDICT?

=> dup rem l40
PROCESSING COMPLETED FOR L40
L41 6 DUP REM L40 (4 DUPLICATES REMOVED)

=> d ibib abs tot

L41 ANSWER 1 OF 6 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2002296408 IN-PROCESS
DOCUMENT NUMBER: 22032796 PubMed ID: 12036949
TITLE: Identification of differentially expressed genes in normal
 and malignant prostate by electronic profiling of
expressed
 sequence tags.
AUTHOR: Asmann Yan W; Kosari Farhad; Wang Kai; Cheville John C;
 Vasmatazis George
CORPORATE SOURCE: Division of Experimental Pathology, Department of
 Laboratory Medicine and Pathology, and Mayo Cancer Center,
 Mayo Clinic and Foundation, Rochester, Minnesota, 55905.
SOURCE: CANCER RESEARCH, (2002 Jun 1) 62 (11) 3308-14.
 Journal code: 2984705R. ISSN: 0008-5472.
PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020531
 Last Updated on STN: 20020531
AB Differentially expressed genes between corresponding normal and
 cancertissue can advance our understanding of the molecular basis of
 malignancy and potentially serve as biomarkers or prognostic markers of
 malignancy. To identify differentially expressed genes in **prostate**
 cancer, we used a procedure combining electronic expression profiling of
 the **prostate** expressed **sequence tag** (**EST**) **database** and molecular biology techniques. A novel
 electronic expression-profiling algorithm was developed to search
publicly
 available **EST** sequences for genes that show significant
 differential expression in **prostate** cancer compared with normal
 prostate tissue. Approximately 600 genes expressed in
 prostate were identified through adequate **EST** counts of
 ESTs for electronic profiling. Of these 600 genes, 9 showed
 statistically significant differences in their **EST** counts
 between cancer and normal **prostate** and were further analyzed.

The **predictions** associated with electronic profiling were experimentally verified for two genes, cysteine-rich secretory protein 3 (CRISP-3) and deadenylating nuclease (DAN), using real-time reverse transcription-PCR with total RNA extracted from cells isolated by laser capture microdissection. In five of five Gleason score 6 cancer cases, CRISP-3 expression was increased >50 fold, whereas the expression of DAN was reduced by >80%.

L41 ANSWER 2 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:199005 BIOSIS
DOCUMENT NUMBER: PREV200200199005
TITLE: The transcriptome of bone marrow cells in chronic leukemias.
AUTHOR(S): Silva, Wilson A., Jr. (1); Alberto, Fernando L.; Uliana, Ronie M. (1); Simpson, Andrew J.; Costa, Fernando F.; Zago, Marco A. (1)
CORPORATE SOURCE: (1) Center for Cell Therapy, Regional Blood Center, Ribeirao Preto Brazil
SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 1, pp. 550a-551a. <http://www.bloodjournal.org/>. print.
Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 1 Orlando, Florida, USA December 07-11, 2001
ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English
AB The complete collection of transcripts generated from the human genome cannot be **predicted** from the genome sequence, but should be directly determined for each **tissue**, due to variations of gene expression in different **tissues** and disease states, and because genes can encode multiple transcripts derived from alternate splicing and polyadenylation sites. As part of larger project that produced over 1.2 million expressed **sequence tags (EST)** from different cancer **tissues**, we constructed a set of cDNAs obtained from bone marrow cells of patients with CML and CLL, that represent partial expressed gene sequences that are biased toward the central coding regions of the resulting transcripts (Dias-Neto E et al, Proc Nat Acad Sci USA 97:3491, 2000). The 51,102 **ESTs** were assembled into 5,002 contigs containing 2 to 1,008 **ESTs** (leaving 24,679 isolated sequences), of which 1,160 were classified on the basis of the annotation of the matched sequences into 8 functional categories (cell cycle 5.0%, cell motility and structure 9.3%, signaling and communication 31.0%, DNA metabolism 3.8%, RNA metabolism 10.3%, defense and homeostasis 7.9%, metabolism 24.7%, protein metabolism 7.9%). Of the remaining 3,842 contigs, 2,990 matched human **ESTs** (dbEST), putative proteins with unknown functions, DNA clones orthologs and paralogs, whereas 852 were classified as no hits. The abundance of **ESTs** that matched the contigs formed by the larger number of **EST** in bone marrow cells was compared with other normal and neoplastic **tissues** from breast, **prostate**, colon, and brain. Of the 10 larger contigs, 5 genes were commonly expressed in most of the other **tissues**, one was exclusively found in bone marrow (beta-globin), and 4 were classified as no hits. Among the 50 larger contigs, the following genes were found exclusively or predominantly in bone marrow: lactoferrin, myeloperoxidase, defensin, epithelin, autocrine motility factor receptor, bactericidal permeability increasing protein, beta-globin and Xg antigen. Among 852

contigs that did not match annotated regions of the genome (no hits), the **predicted** protein sequence of 77 contigs matched known protein domains when evaluated by pfam (protein family **database** of alignment and HMMs), representing candidate unannotated genes. To search for single nucleotide polymorphisms (SNP) in the coding region of genes, the **EST** were anchored on approximately 13,000 genes for which the complete coding sequences (CDS) are known. After exclusion of paralogs, the clusters were analyzed by PolyBayes, an algorithm that identifies SMPs by multiple alignments followed by Bayesian inference to calculate the probability associated with each candidate site (Marth GT et al, Nat Genet 23:452, 1999). A total of 278 candidate SNPs were detected in the coding region 163 genes (average 1.7 SNP/gene), of which 176 are expected to change the amino acid sequence (non synonymous). The wealthy of information provided by this approach demonstrates its usefulness for the analysis of gene expression in specific hematopoietic **tissues** and diseases.

L41 ANSWER 3 OF 6 MEDLINE DUPLICATE 2
 ACCESSION NUMBER: 2001155138 MEDLINE
 DOCUMENT NUMBER: 21092618 PubMed ID: 11162530
 TITLE: Molecular cloning of a novel human gene on chromosome 4p11 by immunoscreening of an ovarian carcinoma cDNA library.
 AUTHOR: Luo L Y; Soosaipillai A; Diamandis E P
 CORPORATE SOURCE: Department of Pathology and Laboratory Medicine, Mount Sinai Hospital, Toronto, Ontario, M5G 1X5, Canada.
 SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2001 Jan 12) 280 (1) 401-6.
 Journal code: 0372516. ISSN: 0006-291X.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200103
 ENTRY DATE: Entered STN: 20010404
 Last Updated on STN: 20010404
 Entered Medline: 20010322

AB In our efforts to identify immunoreactive antigens in ovarian cancer, we used the method of immunoscreening of an ovarian carcinoma cDNA expression library with ascites fluid from ovarian cancer patients. Among many positive clones, one was found to contain partial sequence of a novel gene. By searching expressed **sequence tags** (**ESTs**) and human genome project **databases** as well as by screening other cDNA libraries and by RT-PCR strategies, we were able to obtain the full-length cDNA sequence (1.4 kb) and establish the genomic organization of this new gene. We also identified two alternatively spliced forms, encoding for slightly different proteins. The longer form (1.4 kb) is **predicted** to encode for a 27.6 kDa protein of 245 amino acids. The shorter form (1.3 kb) encodes for a truncated protein of 20.7 kDa and 208 amino acids. These proteins are not significantly homologous to any known protein in the GenBank **database**. This gene is composed of nine exons and eight introns. By fluorescence in situ hybridization (FISH), it was mapped to chromosome 4p11. This gene is highly expressed in many **tissues**, including testis, brain, placenta, ovary, **prostate**, and mammary gland. The high level expression of the shorter form is restricted to the central nervous system, including brain, cerebellum, and spinal cord, suggesting that this

form may have a unique function in the central nervous system.
Copyright 2001 Academic Press.

L41 ANSWER 4 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:151895 BIOSIS
DOCUMENT NUMBER: PREV200200151895
TITLE: The transcriptome of bone marrow cells in chronic leukemia.
AUTHOR(S): Silva-Junior, Wilson A. (1); Alberto, Fernando L.; Uliana, Ronie M. (1); Simpson, Andrew J.; Costa, Fernando F.; Zago, Marco A.
CORPORATE SOURCE: (1) Center for Cell Therapy, Regional Blood Center, Ribeirao Preto Brazil
SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 2, pp. 131b. <http://www.bloodjournal.org/>. print.
Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 2 Orlando, Florida, USA December 07-11, 2001
ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English
AB The complete collection of transcripts generated from the human genome cannot be **predicted** from the genome sequence, but should be directly determined for each **tissue**, due to variations of gene expression in different **tissues** and disease states, and because genes can encode multiple transcripts derived from alternate splicing and polyadenylation sites. As part of larger project that produced over 1.2 million expressed **sequence tags (EST)** from different cancer **tissues**, we constructed a set of cDNAs obtained from bone marrow cells of patients with CML and CLL, that represent partial expressed gene sequences that are biased toward the central coding regions of the resulting transcripts (Dias-Neto E et al, Proc Nat Acad Sci USA 97:3491, 2000), The 51,102 **ESTs** were assembled into 5,002 contigs containing 2 to 1,008 **ESTs** (leaving 24,679 isolated sequences), of which 1,160 were classified on the basis of the annotation of the matched sequences into 8 functional categories (cell cycle 5.0%, cell motility and structure 9.3%, signaling and communication 31.0%, DNA metabolism 3.8%, RNA metabolism 10.3%, defense and homeostasis 7.9%, metabolism 24.7%, protein metabolism 7.9%). Of the remaining 3,842 contigs, 2,990 matched human **ESTs** (dbEST), putative proteins with unknown functions, DNA clones, orthologs and paralogs, whereas 852 were classified as no hits. The abundance of **ESTs** that matched the contigs formed by the larger number of **EST** in bone marrow cells was compared with other normal and neoplastic **tissues** from breast, **prostate**, colon, and brain. Of the 10 larger contigs, 5 genes were commonly expressed in most of the other **tissues**, one was exclusively found in bone marrow (beta-globin), and 4 were classified as no hits. Among the 50 larger contigs, the following genes were found exclusively or predominantly in bone marrow: lactoferrin, myeloperoxidase, defensin, epithelin, autocrine motility factor receptor, bactericidal permeability increasing protein, beta-globin and Xg antigen. Among 852 contigs that did not match annotated regions of the genome (no hits), the **predicted** protein sequence of 77 contigs matched known protein domains when evaluated by pfam (protein family **database** of alignment and HMMs), representing candidate unannoted genes. To search for

single nucleotide polymorphisms (SNP) in the coding region of genes, the **EST** were anchored on approximately 13,000 genes for which the complete coding sequences (CDS) are known. After exclusion of paralogs, the clusters were analyzed by PolyBayes, an algorithm that identifies

SNPs

by multiple alignments followed by Bayesian inference to calculate the probability associated with each candidate site (Marth GT et al, Nat

Genet

23:452, 1999). A total of 278 candidate SNPs were detected in the coding region 163 genes (average 1.7 SNP/gene), of which 176 are expected to change the amino acid sequence (non synonymous). The wealth of information provided by this approach demonstrates its usefulness for the analysis of gene expression in specific hematopoietic **tissues** and diseases.

L41 ANSWER 5 OF 6 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 2001070001 MEDLINE
DOCUMENT NUMBER: 20510030 PubMed ID: 11054574
TITLE: Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.
AUTHOR: Gan L; Lee I; Smith R; Argonza-Barrett R; Lei H; McCuaig J;
Moss P; Paeper B; Wang K
CORPORATE SOURCE: Chiroscience R and D Inc. 1631 220th St. SE. Bothell, WA 98021, USA.
SOURCE: GENE, (2000 Oct 17) 257 (1) 119-30.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF243527
ENTRY MONTH: 200101
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010104

AB The human kallikrein gene cluster, located in the chromosome band 19q13, contains several **tissue**-specific serine protease genes including the **prostate**-specific KLK2, KLK3 and prostase genes. To further characterize the gene cluster, we have mapped, sequenced, and analyzed the genomic sequence from the region. The results of **EST** database searches and GENSCAN gene **prediction** analysis reveal 13 serine protease genes and several pseudogenes in the region. Expression analysis by RT-PCR indicates that most of these protease genes are expressed only in a subset of the 35 different normal **tissues** that have been examined. Several protease genes expressed in skin show higher expression levels in psoriatic lesion samples than in non-lesional skin samples from the same patient. This suggests that the imbalance of a complex protease cascade in skin may contribute to the pathology of disease. The proteases, excluding the kallikrein genes, share approximately 40% of their sequences suggesting that the serine protease gene cluster on chromosome 19q13 arose from ancient gene duplications.

L41 ANSWER 6 OF 6 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 97079209 MEDLINE
DOCUMENT NUMBER: 97079209 PubMed ID: 8920941
TITLE: Identification of MMP-18, a putative novel human matrix metalloproteinase.
AUTHOR: Cossins J; Dudgeon T J; Catlin G; Gearing A J; Clements J
M

CORPORATE SOURCE: British Biotech Pharmaceuticals, Oxford, United Kingdom..
 cossins@britbio.co.uk
 SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1996
 Nov 12) 228 (2) 494-8.
 Journal code: 0372516. ISSN: 0006-291X.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-Y08622
 ENTRY MONTH: 199612
 ENTRY DATE: Entered STN: 19970128
 Last Updated on STN: 20000303
 Entered Medline: 19961230

AB A partial cDNA encoding the 3' end of a putative novel human matrix
 metalloproteinase (MMP) was identified by sequence similarity searching
 of
databases containing expressed **sequence tags**.
 The remaining 5' end of the MMP cDNA was amplified by PCR from human
 mammary gland cDNA. The **predicted** protein product displays all
 the structural features characteristic of the MMP family and has closest
 identity with MMP-1, -3, -10, and 11. We have provisionally designated
 this novel MMP as MMP-18. MMP-18 mRNA is expressed in a wide variety of
 normal human **tissues**, including mammary gland, placenta, lung,
 pancreas, ovary, small intestine, spleen, thymus, **prostate**,
 testis, colon, and heart, but is not detected in brain, skeletal muscle,
 kidney, liver, or peripheral blood leucocytes.

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
 19:04:09
 ON 08 JUL 2002

L1 13496 S EST
 L2 34 S L1(S) (NO#(W) CORRELAT?)
 L3 21 DUP REM L2 (13 DUPLICATES REMOVED)
 L4 3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
 L5 1972 S L4(S) (PROTEIN OR PEPTIDE)
 L6 1748 S L5(S) (EXPRESS?)
 L7 775 S L6(S) DATABASE#
 L8 355 DUP REM L7 (420 DUPLICATES REMOVED)
 L9 96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
 L10 47 S L8(S) GENBANK
 L11 87 S L8(S) (HEART OR BONE OR BRAIN)
 L12 137 S L11 OR L9
 L13 1 S L12 AND (NO#(W) EXPRESS?)
 L14 67 S L12(S) (TRANSCRI?)
 L15 86 S L8(S) NORTHERN
 L16 50 S L1(S) (NO#(2W) CORRELAT?)
 L17 16 S L16 NOT L2
 L18 12 DUP REM L17 (4 DUPLICATES REMOVED)
 L19 54 S L1(S) (NO#(3W) CORRELAT?)
 L20 0 S L19 NOT L1
 L21 20 S L19 NOT L2
 L22 4 S L21 NOT L16

FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002
 L23 13496 S EST OR (SEQUENCE(W) TAG#)

L24 234 S L23 AND DATABASE#/TI
 L25 0 S L24 AND (NO(3W)CORRELAT?)
 L26 234 S L24(S)DATABASE#
 L27 2221 S L23(S)DATABASE#
 L28 4 S L27(S) (NO#(3W)CORRELAT?)
 L29 1174 S L23(S) (BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVA
 L30 310 S L29(S)NORTHERN
 L31 133 S L30 AND DATABASE#
 L32 78 DUP REM L31 (55 DUPLICATES REMOVED)
 L33 1072 S L23(S) (PREDICT? OR ANTICIPAT?)
 L34 22 S L33 AND DATABASE#/TI
 L35 13 DUP REM L34 (9 DUPLICATES REMOVED)
 L36 22 S L34(S)DATABASE#
 L37 2221 S L23(S)DATABASE#
 L38 612 S L37(S)TISSUE
 L39 58 S L38(S)PROSTATE
 L40 10 S L39 AND PREDICT?
 L41 6 DUP REM L40 (4 DUPLICATES REMOVED)

=> s l23(s) (cannot(3w)predict)
 L42 1 L23(S) (CANNOT(3W) PREDICT)

=> d ibib abs tot

L42 ANSWER 1 OF 1 MEDLINE
 ACCESSION NUMBER: 2002172902 IN-PROCESS
 DOCUMENT NUMBER: 21859662 PubMed ID: 11870237
 TITLE: High frequency of DAZ1/DAZ2 gene deletions in patients
 with severe oligozoospermia.
 AUTHOR: Fernandes S; Huellen K; Goncalves J; Dukal H; Zeisler J;
 Rajpert De Meyts E; Skakkebaek N E; Habermann B; Krause W;
 Sousa M; Barros A; Vogt P H
 CORPORATE SOURCE: Reproduction Genetics, Institute of Human Genetics,
 University of Heidelberg, Heidelberg, Germany.
 SOURCE: MOLECULAR HUMAN REPRODUCTION, (2002 Mar) 8 (3) 286-98.
 Journal code: 9513710. ISSN: 1360-9947.
 PUB. COUNTRY: England: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
 ENTRY DATE: Entered STN: 20020322
 Last Updated on STN: 20020322
 AB Deletions of the DAZ gene family in distal Yq11 are always associated
 with deletions of the azoospermia factor c (AZFc) region, which we now
 estimate extends to 4.94 Mb. Because more Y gene families are located in this
 chromosomal region, and are expressed like the DAZ gene family only in
 the male germ line, the testicular pathology associated with complete AZFc
 deletions **cannot predict** the functional contribution
 of the DAZ gene family to human spermatogenesis. We therefore established
 a DAZ gene copy specific deletion analysis based on the DAZ-BAC sequences
 in GenBank. It includes the deletion analysis of eight DAZ-DNA PCR
 markers [six DAZ-single nucleotide variants (SNVs) and two DAZ-sequence
 tag sites (STS)] selected from the 5' to the 3' end of each DAZ
 gene and a deletion analysis of the gene copy specific EcoRV and TaqI
 restriction fragments identified in the internal repetitive DAZ gene
 regions (DYS1 locus). With these diagnostic tools, 63 DNA samples from
 men

with idiopathic oligozoospermia and 107 DNA samples from men with proven fertility were analysed for the presence of the complete DAZ gene locus, encompassing the four DAZ gene copies. In five oligozoospermic patients, we found a DAZ-SNV/STS and DYS1/EcoRV and TaqI fragment deletion pattern indicative for deletion of the DAZ1 and DAZ2 gene copies; one of these deletions could be identified as a 'de-novo' deletion because it was absent in the DAZ locus of the patient's father. The same DAZ deletions were not found in any of the 107 fertile control samples. We therefore conclude that the deletion of the DAZ1/DAZ2 gene doublet in five out of our 63 oligozoospermic patients (8%) is responsible for the patients' reduced sperm numbers. It is most likely caused by intrachromosomal recombination events between two long repetitive sequence blocks (AZFc-Repl) flanking the DAZ gene structures.

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
19:04:09
ON 08 JUL 2002

```
L1      13496 S EST
L2      34 S L1(S) (NO#(W) CORRELAT?)
L3      21 DUP REM L2 (13 DUPLICATES REMOVED)
L4      3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5      1972 S L4(S) (PROTEIN OR PEPTIDE)
L6      1748 S L5(S) (EXPRESS?)
L7      775 S L6(S) DATABASE#
L8      355 DUP REM L7 (420 DUPLICATES REMOVED)
L9      96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
L10     47 S L8(S) GENBANK
L11     87 S L8(S) (HEART OR BONE OR BRAIN)
L12     137 S L11 OR L9
L13      1 S L12 AND (NO#(W) EXPRESS?)
L14     67 S L12(S) (TRANSCRI?)
L15     86 S L8(S) NORTHERN
L16     50 S L1(S) (NO#(2W) CORRELAT?)
L17     16 S L16 NOT L2
L18     12 DUP REM L17 (4 DUPLICATES REMOVED)
L19     54 S L1(S) (NO#(3W) CORRELAT?)
L20      0 S L19 NOT L1
L21     20 S L19 NOT L2
L22      4 S L21 NOT L16
```

FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002

```
L23     13496 S EST OR (SEQUENCE(W) TAG#)
L24     234 S L23 AND DATABASE#/TI
L25      0 S L24 AND (NO(3W) CORRELAT?)
L26     234 S L24(S) DATABASE#
L27     2221 S L23(S) DATABASE#
L28      4 S L27(S) (NO#(3W) CORRELAT?)
L29     1174 S L23(S) (BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVA
L30     310 S L29(S) NORTHERN
L31     133 S L30 AND DATABASE#
L32      78 DUP REM L31 (55 DUPLICATES REMOVED)
L33     1072 S L23(S) (PREDICT? OR ANTICIPAT?)
L34      22 S L33 AND DATABASE#/TI
L35      13 DUP REM L34 (9 DUPLICATES REMOVED)
L36      22 S L34(S) DATABASE#
L37     2221 S L23(S) DATABASE#
```

L38 612 S L37(S)TISSUE
 L39 58 S L38(S)PROSTATE
 L40 10 S L39 AND PREDICT?
 L41 6 DUP REM L40 (4 DUPLICATES REMOVED)
 L42 1 S L23(S) (CANNOT(3W)PREDICT)

=> log h

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	84.29	401.00

SESSION WILL BE HELD FOR 60 MINUTES
 STN INTERNATIONAL SESSION SUSPENDED AT 21:17:07 ON 08 JUL 2002

Welcome to STN International! Enter x:x

LOGINID:ssspta1600kxc

PASSWORD:

* * * * * RECONNECTED TO STN INTERNATIONAL * * * * *
 SESSION RESUMED IN FILE 'MEDLINE, BIOSIS' AT 21:24:26 ON 08 JUL 2002
 FILE 'MEDLINE' ENTERED AT 21:24:26 ON 08 JUL 2002
 FILE 'BIOSIS' ENTERED AT 21:24:26 ON 08 JUL 2002
 COPYRIGHT (C) 2002 BIOLOGICAL ABSTRACTS INC.(R)

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	84.29	401.00

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
 19:04:09
 ON 08 JUL 2002

L1 13496 S EST
 L2 34 S L1(S) (NO#(W)CORRELAT?)
 L3 21 DUP REM L2 (13 DUPLICATES REMOVED)
 L4 3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
 L5 1972 S L4(S) (PROTEIN OR PEPTIDE)
 L6 1748 S L5(S) (EXPRESS?)
 L7 775 S L6(S)DATABASE#
 L8 355 DUP REM L7 (420 DUPLICATES REMOVED)
 L9 96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
 L10 47 S L8(S)GENBANK
 L11 87 S L8(S) (HEART OR BONE OR BRAIN)
 L12 137 S L11 OR L9
 L13 1 S L12 AND (NO#(W)EXPRESS?)
 L14 67 S L12(S) (TRANSCRI?)
 L15 86 S L8(S)NORTHERN
 L16 50 S L1(S) (NO#(2W)CORRELAT?)
 L17 16 S L16 NOT L2
 L18 12 DUP REM L17 (4 DUPLICATES REMOVED)
 L19 54 S L1(S) (NO#(3W)CORRELAT?)
 L20 0 S L19 NOT L1
 L21 20 S L19 NOT L2
 L22 4 S L21 NOT L16

FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002

L23 13496 S EST OR (SEQUENCE(W)TAG#)
 L24 234 S L23 AND DATABASE#/TI
 L25 0 S L24 AND (NO(3W)CORRELAT?)
 L26 234 S L24(S)DATABASE#
 L27 2221 S L23(S)DATABASE#
 L28 4 S L27(S) (NO#(3W)CORRELAT?)
 L29 1174 S L23(S) (BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVA
 L30 310 S L29(S)NORTHERN
 L31 133 S L30 AND DATABASE#
 L32 78 DUP REM L31 (55 DUPLICATES REMOVED)
 L33 1072 S L23(S) (PREDICT? OR ANTICIPAT?)
 L34 22 S L33 AND DATABASE#/TI
 L35 13 DUP REM L34 (9 DUPLICATES REMOVED)
 L36 22 S L34(S)DATABASE#
 L37 2221 S L23(S)DATABASE#
 L38 612 S L37(S)TISSUE
 L39 58 S L38(S)PROSTATE
 L40 10 S L39 AND PREDICT?
 L41 6 DUP REM L40 (4 DUPLICATES REMOVED)
 L42 1 S L23(S) (CANNOT(3W)PREDICT)

=> s l23 or dbEST
 L43 13596 L23 OR DBEST

=> s l43(s)express?
 L44 6719 L43(S) EXPRESS?

=> s l44(s)blast
 L45 192 L44(S) BLAST

=> s l45(s)predict?
 L46 47 L45(S) PREDICT?

=> dup rem l46
 PROCESSING COMPLETED FOR L46
 L47 27 DUP REM L46 (20 DUPLICATES REMOVED)

=> d ibib abs tot

L47 ANSWER 1 OF 27 MEDLINE DUPLICATE 1
 ACCESSION NUMBER: 2002174733 MEDLINE
 DOCUMENT NUMBER: 21904442 PubMed ID: 11907331
 TITLE: Linkage on chromosome 10 of several murine retroviral
 integration loci associated with leukaemia.
 AUTHOR: Haviernik Peter; Festin Stephen M; Opavsky Rene; Koller
 Richard P; Barr Nighean I; Neil James C; Wolff Linda
 CORPORATE SOURCE: Leukemogenesis Section, Laboratory of Cellular Oncology,
 National Cancer Institute, NIH, Bethesda, MD 20892-4255,
 USA.
 SOURCE: JOURNAL OF GENERAL VIROLOGY, (2002 Apr) 83 (Pt 4) 819-27.

 Journal code: 0077340. ISSN: 0022-1317.
 PUB. COUNTRY: England: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200205
 ENTRY DATE: Entered STN: 20020322
 Last Updated on STN: 20020503
 Entered Medline: 20020502

AB Mml loci have been identified as provirus integration sites among a
 subset

of monocytic tumours induced by murine leukaemia virus (MuLV) infection of BALB/c and DBA/2 mice. These myeloid leukaemias contain a retrovirus integrated on chromosome 10 in proximity to the c-myb locus; however, c-myb **expression** was not altered. Detailed physical mapping enabled placement of the retroviral integration sites approximately 25 kb (Mml1), approximately 51 kb (Mml2), and approximately 70 kb (Mml3) upstream of the c-myb locus. Furthermore, the Ftl1 (fit-1) locus, a common integration site in feline leukaemia virus-induced T cell lymphomas, was mapped upstream of Mml3. Sequence analysis of Mml1, Mml2 and Mml3 loci (39.6, 16.4 and 5.9 kb, respectively) in conjunction with the **BLAST** (basic local alignment search tool) homology searches against the **expressed sequence tag** (**EST**) database and the use of gene/exon **prediction** programs revealed potential coding sequences that were not confirmed by Northern analysis or RT-PCR. The sequences between c-myb and Ftl1, which were shown to include two potential scaffold/matrix attachment regions (S/MARs), are most likely regulatory in nature. An extended search for transcribed sequences far upstream of Mml3 revealed five genes, four of which were **expressed** in multiple tissues in mice. These genes could not be linked to tumour formation by the virus but their homologous sequences were found on human chromosome 6, thus allowing extension of the syntenic region on mouse chromosome 10 to approximately 250 kb.

L47 ANSWER 2 OF 27 MEDLINE DUPLICATE 2
 ACCESSION NUMBER: 2002211494 IN-PROCESS
 DOCUMENT NUMBER: 21945267 PubMed ID: 11944991
 TITLE: The Identification of the Inhibitory gamma-Subunits of the Type 6 Retinal Cyclic Guanosine Monophosphate Phosphodiesterase in Non-retinal Tissues: Differential Processing of mRNA Transcripts.
 AUTHOR: Tate Rothwelle J; Arshavsky Vadim Y; Pyne Nigel J
 CORPORATE SOURCE: Department of Physiology and Pharmacology, Strathclyde Institute for Biomedical Sciences, University of Strathclyde, 27 Taylor Street, Glasgow, G4 0NR, Scotland.
 SOURCE: GENOMICS, (2002 Apr) 79 (4) 582-6.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
 ENTRY DATE: Entered STN: 20020412
 Last Updated on STN: 20020412

AB Here, we report that mouse lung **expresses** gamma-subunit (PDEgamma) transcripts of the rod and cone photoreceptor cGMP phosphodiesterase genes (Pde6g and Pde6h, respectively). Moreover, a major 14-kDa protein (p14) in lung membranes was immunostained with antibodies that react with both rod and cone PDEgamma. We show that p14 is, in fact, a mixture of rod and cone PDEgamma, based on three additional lines of evidence. First, p14 was also immunostained with antibodies specific for the cone PDEgamma isoform. Second, the **expression** of p14 immunostained with antibodies recognizing both rod and cone PDEgamma was substantially reduced in lung membranes from Pde6g(-/-) mice. In contrast, the fraction of p14 stained with cone PDEgamma-specific antibodies was not altered in the Pde6g(-/-) mice. Third, the absence of the Pde6g transcript

was correlated with reduced levels of p14 in Pde6g(-/-) mice. We have also found that mouse lung contains a small Pde6h transcript that has a 41-bp deletion resulting in a frame change, derived by differential mRNA processing of exon 3 of Pde6h. **BLAST** searches also revealed a rat ovary **EST** that has the same 41-bp deletion causing the same frame change. However, the premature in-frame stop codon seen in the short Pde6h transcript is absent and the regular stop codon is out of frame leading to a **predicted** ORF extension into the 3' UTR. These findings show that rod and cone PDEgamma isoforms are **expressed** in lung and seem to have a critical role in regulating p42/p44 mitogen-activated protein kinase signaling. (c)2002 Elsevier Science (USA).

L47 ANSWER 3 OF 27 MEDLINE DUPLICATE 3
 ACCESSION NUMBER: 2001544620 MEDLINE
 DOCUMENT NUMBER: 21475670 PubMed ID: 11591643
 TITLE: Abundance, distribution, and transcriptional activity of repetitive elements in the maize genome.
 AUTHOR: Meyers B C; Tingey S V; Morgante M
 CORPORATE SOURCE: E.I. duPont de Nemours and Company, DuPont Crop Genetics-Genomics, Newark, Delaware 19714-6104, USA.
 SOURCE: GENOME RESEARCH, (2001 Oct) 11 (10) 1660-76.
 Journal code: 9518021. ISSN: 1088-9051.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200112
 ENTRY DATE: Entered STN: 20011010
 Last Updated on STN: 20020122
 Entered Medline: 20011204

AB Long terminal repeat (LTR) retrotransposons have been shown to make up much of the maize genome. Although these elements are known to be prevalent in plant genomes of a middle-to-large size, little information is available on the relative proportions composed by specific families of elements in a single genome. We sequenced a library of randomly sheared genomic DNA from maize to characterize this genome. **BLAST** analysis of these sequences demonstrated that the maize genome is

composed of diverse sequences that represent numerous families of retrotransposons.

The largest families contain the previously described elements Huck, Ji, and Opie. Approximately 5% of the sequences are **predicted** to encode proteins. The genomic abundance of 16 families of elements was estimated by hybridization to an array of 10,752 maize bacterial artificial chromosome (BAC) clones. Comparisons of the number of elements present on individual BACs indicated that retrotransposons are in general randomly distributed across the maize genome. A second library was constructed that was selected to contain sequences hypomethylated in the maize genome. Sequence analysis of this library indicated that retroelements abundant in the genome are poorly represented in hypomethylated regions. Fifty-six retroelement sequences corresponding to the integrase and reverse transcriptase domains were isolated from approximately 407,000 maize **expressed sequence tags (ESTs)**. Phylogenetic analysis of these and the genomic retroelement sequences indicated that elements most abundant in the genome are less abundant at the transcript level than are more rare retrotransposons. Additional phylogenies also demonstrated that rice and maize retrotransposon families are frequently more closely related to

each

other than to families within the same species. An analysis of the GC content of the maize genomic library and that of maize **ESTs** did not support recently published data that the gene space in maize is found within a narrow GC range, but does indicate that genic sequences have a higher GC content than intergenic sequences (52% vs. 47% GC).

L47 ANSWER 4 OF 27 MEDLINE DUPLICATE 4

ACCESSION NUMBER: 2002188338 MEDLINE

DOCUMENT NUMBER: 21919610 PubMed ID: 11922602

TITLE: Establishment of a root proteome reference map for the model legume *Medicago truncatula* using the expressed sequence tag database for peptide mass fingerprinting.

AUTHOR: Mathesius U; Keijzers G; Natera S H; Weinman J J; Djordjevic M A; Rolfe B G

CORPORATE SOURCE: Genomic Interactions Group, Research School of Biological Sciences, Australian National University, Canberra, ACT.

SOURCE: Proteomics, (2001 Nov) 1 (11) 1424-40.
Journal code: 101092707. ISSN: 1615-9853.

PUB. COUNTRY: Germany; Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200206

ENTRY DATE: Entered STN: 20020403
Last Updated on STN: 20020614
Entered Medline: 20020610

AB We have established a proteome reference map for *Medicago truncatula* root proteins using two-dimensional gel electrophoresis combined with peptide mass fingerprinting to aid the dissection of nodulation and root developmental pathways by proteome analysis. *M. truncatula* has been chosen as a model legume for the study of nodulation-related genes and proteins. Over 2,500 root proteins could be displayed reproducibly across an isoelectric focussing range of 4-7. We analysed 485 proteins by peptide mass fingerprinting, and 179 of those were identified by matching against the current *M. truncatula* **expressed sequence tag (EST)** database containing DNA sequences of approximately 105,000 **ESTs**. Matching the **EST** sequences to available plant DNA sequences by **BLAST** searches enabled us to **predict** protein function. The use of the **EST** database for peptide identification is discussed. The majority of identified proteins were metabolic enzymes and stress response proteins, and 44% of proteins occurred as isoforms, a result that could not have been **predicted** from sequencing data alone. We identified two nodulins in uninoculated root tissue, supporting evidence for a role of nodulins in normal plant development. This proteome map will be updated continuously (<http://semele.anu.edu.au/2d/2d.html>) and will be a powerful tool for investigating the molecular mechanisms of root symbioses in legumes.

L47 ANSWER 5 OF 27 MEDLINE DUPLICATE 5

ACCESSION NUMBER: 2002249856 IN-PROCESS

DOCUMENT NUMBER: 21985902 PubMed ID: 11990509

TITLE: Characterisation of rice anther proteins expressed at the young microspore stage.

AUTHOR: Imin N; Kerim T; Weinman J J; Rolfe B G

CORPORATE SOURCE: Genomic Interactions Group, Research School of Biological Sciences, Australian National University, Canberra City, ACT.

SOURCE: Proteomics, (2001 Sep) 1 (9) 1149-61.
Journal code: 101092707. ISSN: 1615-9853.

PUB. COUNTRY: Germany: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020507
Last Updated on STN: 20020507

AB In combination with two-dimensional polyacrylamide gel electrophoresis
(2-DE) protein mapping and mass spectrometry analysis, the pattern of
gene **expression** in specific tissues at a specific stage can be
displayed and characterised. We used this approach for rice (*Oryza sativa*
L. cultivar Doongara) to display and assign identity to proteins in the
anthers at the young microspore stage. Over 4000 anther proteins in the
pI range of 4-11 and molecular mass range of 6-122 kDa were reproducibly
resolved after silver staining, representing about 10% of the estimated
total genomic output of rice. Two hundred and seventy-three protein spots
have been extracted either from polyninylidene difluoride membrane blots
or from colloidal Coomassie blue stained 2-DE gels and analysed by
N-terminal sequencing, Matrix-assisted laser desorption/ionization-time
of flight mass spectrometry (MS) analysis or tandem MS sequencing. This
enabled identification of 53 anther protein spots representing 43
different proteins. Using the publicly available rice **expressed**
sequence tag (EST) database at the National
Centre for Biotechnology Information, a further 37 protein spots were
matched to **ESTs**. After **BLAST** searching with these
ESTs, we were able to **predict** the identity of 22 of
these protein spots. Proteome reference maps of rice anthers have been
constructed according to the SWISS-2DPAGE standards and are available for
public access at <http://semele.anu.edu.au/2d/2d.html>.

L47 ANSWER 6 OF 27 MEDLINE DUPLICATE 6

ACCESSION NUMBER: 2001692422 MEDLINE
DOCUMENT NUMBER: 21602807 PubMed ID: 11738710
TITLE: Profiling the malaria genome: a gene survey of three
species of malaria parasite with comparison to other
apicomplexan species.
AUTHOR: Carlton J M; Muller R; Yowell C A; Fluegge M R; Sturrock K
A; Pritt J R; Vargas-Serrato E; Galinski M R; Barnwell J
W;
CORPORATE SOURCE: Mulder N; Kanapin A; Cawley S E; Hide W A; Dame J B
Computational Biology Branch, National Center for
Biotechnology Information, National Library of Medicine,
National Institutes of Health, Bethesda, MD 20892, USA..
carlton@tigr.org
CONTRACT NUMBER: N01-A1-65315
SOURCE: MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (2001 Dec) 118 (2)
201-10.
Journal code: 8006324. ISSN: 0166-6851.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AZ521913; GENBANK-AZ521914; GENBANK-AZ521915;
GENBANK-AZ521916; GENBANK-AZ521917; GENBANK-AZ521918;
GENBANK-AZ521919; GENBANK-AZ521920; GENBANK-AZ521921;
GENBANK-AZ521922; GENBANK-AZ521923; GENBANK-AZ521924;
GENBANK-AZ521925; GENBANK-AZ521926; GENBANK-AZ521927;
GENBANK-AZ521928; GENBANK-AZ521929; GENBANK-AZ521930;
GENBANK-AZ521931; GENBANK-AZ521932; GENBANK-AZ521933;

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

GENBANK-AZ522849; GENBANK-AZ522850; GENBANK-AZ522851;
 GENBANK-AZ522852; GENBANK-AZ522853; GENBANK-AZ522854;
 GENBANK-AZ522855; GENBANK-AZ522856; GENBANK-AZ522857;
 GENBANK-AZ522858; GENBANK-AZ522859; GENBANK-AZ522860;
 GENBANK-AZ522861; GENBANK-AZ522862; GENBANK-AZ522863;
 GENBANK-AZ522864; GENBANK-AZ522865; GENBANK-AZ522866;
 GENBANK-AZ522867; GENBANK-AZ522868; GENBANK-AZ522869;
 GENBANK-AZ522870; GENBANK-AZ522871; GENBANK-AZ522872;
 GENBANK-AZ522873; GENBANK-AZ522874; GENBANK-AZ522875;
 GENBANK-AZ522876; GENBANK-AZ522877; GENBANK-AZ522878;
 GENBANK-AZ522879; GENBANK-AZ522880; GENBANK-AZ522881;
 GENBANK-AZ522882; GENBANK-AZ522883; GENBANK-AZ522884;
 GENBANK-AZ522885; GENBANK-AZ522886; GENBANK-AZ522887;
 GENBANK-AZ522888; GENBANK-AZ522889; GENBANK-AZ522890;
 GENBANK-AZ522891; GENBANK-AZ522892; GENBANK-AZ522893;
 GENBANK-AZ522894; GENBANK-AZ522895; GENBANK-AZ522896;
 GENBANK-AZ522897; GENBANK-AZ522898; GENBANK-AZ522899;
 GENBANK-AZ522900; GENBANK-AZ522901; GENBANK-AZ522902;
 GENBANK-AZ522903; GENBANK-AZ522904; GENBANK-AZ522905;
 GENBANK-AZ522906; GENBANK-AZ522907; GENBANK-AZ522908;
 GENBANK-AZ522909; GENBANK-AZ522910; GENBANK-AZ522911;
 GENBANK-AZ522912

ENTRY MONTH:

200202

ENTRY DATE:

Entered STN: 20011213

Last Updated on STN: 20020228

Entered Medline: 20020227

AB We have undertaken the first comparative pilot gene discovery analysis of approximately 25,000 random genomic and **expressed sequence tags (ESTs)** from three species of *Plasmodium*, the infectious agent that causes malaria. A total of 5482 genome survey sequences (GSSs) and 5582 **ESTs** were generated from mung bean nuclease (MBN) and cDNA libraries, respectively, of the ANKA line of the rodent malaria parasite *Plasmodium berghei*, and 10,874 GSSs generated from MBN libraries of the Salvador I and Belem lines of *Plasmodium vivax*, the most geographically wide-spread human malaria pathogen. These tags, together with 2438 *Plasmodium falciparum* sequences present in GenBank, were used to perform first-pass assembly and transcript reconstruction, and non-redundant consensus sequence datasets created. The datasets were compared against public protein databases and more than 1000 putative new *Plasmodium* proteins identified based on sequence similarity. Homologs of previously characterized *Plasmodium* genes

were also identified, increasing the number of *P. vivax* and *P. berghei* sequences in public databases at least 10-fold. Comparative studies with other species of Apicomplexa identified interesting homologs of possible therapeutic or diagnostic value. A gene **prediction** program, Phat, was used to **predict** probable open reading frames for proteins in all three datasets. **Predicted** and non-redundant **BLAST**-matched proteins were submitted to InterPro, an integrated database of protein domains, signatures and families, for functional classification. Thus a partial **predicted** proteome was created for each species. This first comparative analysis of *Plasmodium* protein coding sequences represents a valuable resource for further studies on the biology of this important pathogen.

L47 ANSWER 7 OF 27 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2002:350932 BIOSIS

DOCUMENT NUMBER: PREV200200350932

TITLE: Mitochondrial and chloroplast localization of FtsH-like proteins in sugarcane based on their phylogenetic profile.

AUTHOR(S): Marbach, Phellippe A. Santos; Coelho, Alexandre S. Guedes; Silva-Filho, Marcio C. (1)
CORPORATE SOURCE: (1) Departamento de Genetica, Escola Superior de Agricultura 'Luiz de Queiroz', Universidade de Sao Paulo, 13400-970, Piracicaba, SP: mdcsilva@esalq.usp.br Brazil
SOURCE: Genetics and Molecular Biology, (March, 2001) Vol. 24, No. 1-4, pp. 183-190. print.
ISSN: 1415-4757.

DOCUMENT TYPE: Article

LANGUAGE: English

AB A phylogenetic analysis of plant FtsH-like proteins was performed using protein sequences from the GENE BANK database and five groups of plant FtsH-like proteins were identified by neighbor-joining analysis. **Prediction** of the subcellular location of the proteins suggested that two (FtsH-m1 & FtsH-m2) were mitochondrial and three (FtsH-p1, FtsH-p2, FtsH-p3) were plastid targeting. The phylogenetic profile of plant FtsH-like proteins was used to search sugarcane **expressed sequence tag (EST)** clusters in the SUCEST database. Initially, 153 clusters presenting homology with FtsH-like proteins were recovered, of which 23 were confirmed by a **BLAST** search in the GENE BANK database and by comparison of their hidropathy index with that of previously described FtsH-like proteins. Sugarcane presented **EST** clusters in all phylogenetic groups. In silico **expression** analysis showed that the groups are differentially **expressed** in sugarcane tissues, with FtsH-p2 and FtsH-m1 presenting increased levels of **expression**.

L47 ANSWER 8 OF 27 MEDLINE DUPLICATE 7
ACCESSION NUMBER: 2001240166 MEDLINE
DOCUMENT NUMBER: 21233589 PubMed ID: 11334717
TITLE: Cloning and characterization of a human lysyl oxidase-like 3 gene (hLOXL3).
AUTHOR: Huang Y; Dai J; Tang R; Zhao W; Zhou Z; Wang W; Ying K; Xie Y; Mao Y
CORPORATE SOURCE: Institute of Genetics, School of Life Sciences, Fudan University, Shanghai 200433, PR China.
SOURCE: MATRIX BIOLOGY, (2001 Apr) 20 (2) 153-7.
Journal code: 9432592. ISSN: 0945-053X.
PUB. COUNTRY: Germany: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF284815
ENTRY MONTH: 200110
ENTRY DATE: Entered STN: 20011008
Last Updated on STN: 20011008
Entered Medline: 20011004

AB Using the PCR primers generated from human **expressed sequence tag (EST)**, the cDNA of lysyl oxidase-like gene 3 (LOXL3), a new member of human lysyl oxidases gene family, was cloned from the human fetal brain mRNA. The **predicted** amino acid sequence of the hLOXL3 gene was highly homologous to mLOR2. Bioinformatics analysis shows that hLOXL3 protein is also a member of the scavenger receptor cysteine-rich family, which contains a 25 amino acids signal peptide. The hLOXL3 gene was mapped to human 2p13 locus by **BLAST** search and at least 14 exons were found. **Expression** of the hLOXL3 gene was detected in several human tissues and especially high in spleen and testis.

L47 ANSWER 9 OF 27 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2002:129805 BIOSIS
DOCUMENT NUMBER: PREV200200129805
TITLE: Notch signaling pathway modifier Lunatic Fringe gene is upregulated by retinoic acid during granulocytic differentiation in APL.
AUTHOR(S): Park, Dorothy J. (1); Vuong, Peter T. (1); Koeffler, H. Phillip (1)
CORPORATE SOURCE: (1) Hematology/Oncology, Cedars-Sinai Medical Center, Los Angeles, CA USA
SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 1, pp. 89a.
<http://www.bloodjournal.org/>. print.
Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 1 Orlando, Florida, USA December

07-11,

2001
ISSN: 0006-4971.

DOCUMENT TYPE: Conference
LANGUAGE: English

AB Retinoids and their nuclear receptors play an important role in the regulation of cellular differentiation. In acute promyelocytic leukemia (APL), chromosomal translocations involving retinoic acid receptor alpha (RARalpha) and its various aberrant fusion partners, such as PML and

PLZF, play a causative role in pathogenesis of the disease, presumably by repressing downstream target genes. PML/RARalpha is also responsible for the in vitro and in vivo sensitivity to cell differentiation mediated by retinoic acid (RA). Using a PCR-based cDNA subtractive hybridization method, we have cloned a RA-regulated transcript 11.20. 11.20 was

strongly upregulated by retinoic acid in a time-dependent manner in the APL cell line NB4 find the retinoid-responsive AML cell line HL60.

Retinoid-dependent induction of 11.20 mRNA **expression** occurred independently of new protein synthesis. Similar pattern of **expression** was observed in normal CD34+ cells that were induced to differentiate into the granulocytic lineage by cytokines. DNA sequences from the partial cDNA encoding the 3' untranslated region of our clone

and

corresponding **ESTs** in the **dbEST** database at NCBI were used in the homology search using GenBank **Blast** search. **Blast** search identified a genomic clone CTD-231213 (GenBank Accession number AC012351) from human chromosome 7, and the genomic sequence (136,000 to 147,000) of this clone was used to **predict** a gene utilizing GraileXP v3.0 via internet. GraileXP **predicted** a putative gene encompassing a 7 kb genomic fragment. This gene was **predicted** to have 8 exons (1077 base pair, 358 amino acids), and it matched with a partial coding sequence of a human Drosophila Lunatic Fringe gene homologue and complete coding sequence of murine Lunatic Fringe gene. Members of the notch signaling pathway play critical roles

in

the determination of cell fate and maintenance of progenitors in many developmental systems including myeloid differentiation. Lunatic Fringe belongs to the family of notch signaling modifiers along with Radical and Manic Fringe genes. Therefore, retinoid-dependent induction of Lunatic Fringe gene **expression** in APL may play an important role in the granulocytic differentiation process.

L47 ANSWER 10 OF 27

MEDLINE

DUPLICATE 8

ACCESSION NUMBER: 2001076340 MEDLINE

DOCUMENT NUMBER: 20524101 PubMed ID: 11050182

TITLE: Purification, molecular cloning, and sequence analysis of

sucrose-6F-phosphate phosphohydrolase from plants.
 AUTHOR: Lunn J E; Ashton A R; Hatch M D; Heldt H W
 CORPORATE SOURCE: Commonwealth Scientific and Industrial Research
 Organization Plant Industry, GPO Box 1600, Canberra, ACT
 2601, Australia.. john.lunn@pi.csiro.au
 SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE
 UNITED STATES OF AMERICA, (2000 Nov 7) 97 (23) 12914-9.
 Journal code: 7505876. ISSN: 0027-8424.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF283564; GENBANK-AF283565; GENBANK-AF283566;
 GENBANK-AF300455
 ENTRY MONTH: 200101
 ENTRY DATE: Entered STN: 20010322
 Last Updated on STN: 20010322
 Entered Medline: 20010111

AB Sucrose-6(F)-phosphate phosphohydrolase (SPP; EC) catalyzes the final
 step in the pathway of sucrose biosynthesis and is the only enzyme of
 photosynthetic carbon assimilation for which the gene has not been
 identified. The enzyme was purified to homogeneity from rice (*Oryza*
sativa
 L.) leaves and partially sequenced. The rice leaf enzyme is a dimer with
 a
 native molecular mass of 100 kDa and a subunit molecular mass of 50 kDa.
 The enzyme is highly specific for sucrose 6(F)-phosphate with a K(m) of
 65
 microM and a specific activity of 1250 micromol min⁻¹ mg⁻¹ protein.
 The activity is dependent on Mg(2+) with a remarkably low K(a) of 8-9
 microM and is weakly inhibited by sucrose. Three peptides from cleavage
 of
 the purified rice SPP with endoproteinase Lys-C showed similarity to the
 deduced amino acid sequences of three **predicted** open reading
 frames (ORF) in the Arabidopsis thaliana genome and one in the genome of
 the cyanobacterium *Synechocystis* sp. PCC6803, as well as cDNA clones from
 Arabidopsis, maize, and other species in the GenBank database of
expressed sequence tags. The putative maize
 SPP cDNA clone contained an ORF encoding a 420-amino acid polypeptide.
 Heterologous **expression** in *Escherichia coli* showed that this
 cDNA clone encoded a functional SPP enzyme. The 260-amino acid N-terminal
 catalytic domain of the maize SPP is homologous to the C-terminal region
 of sucrose-phosphate synthase. A PSI-BLAST search of the GenBank
 database indicated that the maize SPP is a member of the haloacid
 dehalogenase hydrolase/phosphatase superfamily.

L47 ANSWER 11 OF 27 MEDLINE DUPLICATE 9
 ACCESSION NUMBER: 2000167136 MEDLINE
 DOCUMENT NUMBER: 20167136 PubMed ID: 10702226
 TITLE: Molecular cloning and expression of mouse
 GD1alpha/GT1alpha/GQ1balpha synthase (ST6GalNAc VI)
 gene.
 AUTHOR: Okajima T; Chen H H; Ito H; Kiso M; Tai T; Furukawa K;
 Urano T; Furukawa K
 CORPORATE SOURCE: Department of Biochemistry II, Nagoya University School of
 Medicine, Tsurumai, Nagoya 466-0065, Bunkyo-ku, Tokyo
 113-8613, Japan.
 SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2000 Mar 10) 275 (10)
 6717-23.
 Journal code: 2985121R. ISSN: 0021-9258.
 PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200004
ENTRY DATE: Entered STN: 20000413
Last Updated on STN: 20000413
Entered Medline: 20000403

AB A novel member of the mouse CMP-NeuAc:beta-N-acetylgalactosaminide
VI, alpha2,6-sialyltransferase (ST6GalNAc) subfamily, designated ST6GalNAc

was identified by **BLAST** analysis of **expressed sequence tags**. The sequence of the cDNA clone of ST6GalNAc VI encoded a type II membrane protein with 43 amino acids composing the cytoplasmic domain, 21 amino acids composing the transmembrane region, and 269 amino acids composing the catalytic domain. The **predicted** amino acid sequence showed homology to the previously cloned ST6GalNAc III, IV, and V, with common amino acid sequences in sialyl motif L and S among these four enzymes. A fusion protein with protein A and extracts from L cells transfected with ST6GalNAc VI in an **expression** vector showed enzyme activity of alpha2,6-sialyltransferase for GM1b, GT1b, and GD1a but not toward glycoproteins. Thin layer chromatography-immunostaining revealed that the products were GD1alpha, GQ1balpha, and GT1aalpha. Northern blotting revealed that this gene was **expressed** in a wide range of mouse tissues such as colon, liver, heart, spleen, and brain. It is concluded that this enzyme is a novel sialyltransferase involved in the synthesis of alpha-series gangliosides in the nervous tissues and many other tissues.

L47 ANSWER 12 OF 27 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:324417 BIOSIS
DOCUMENT NUMBER: PREV200100324417
TITLE: Identification of MLA1 a member of a novel family of adaptor and scaffold genes expressed in myeloma and leukemias.

AUTHOR(S): Claudio, Jaime (1); Falcioni, Nathan (1); Zhu, Yuan Xiao (1); Stewart, A. Keith (1)
CORPORATE SOURCE: (1) Experimental Therapeutics, University Health Network, Toronto, ON Canada
SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 1, pp. 472a. print.
Meeting Info.: 42nd Annual Meeting of the American Society of Hematology San Francisco, California, USA December 01-05, 2000 American Society of Hematology
. ISSN: 0006-4971.

DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

AB In our transcriptional study of genes **expressed** in myeloma, we identified a clone that by **Blast** analysis in **dbEST** appeared to have restricted **expression** in hematopoietic cells such macrophages, hematopoietic progenitors, T cells and germinal center

B cells. Northern analysis demonstrated that this gene is **expressed** as a 2.2 kb transcript in hematopoietic malignancies including myeloid and

T cell leukemias, myeloma and in bone marrow, heart, brain, placenta and lung on a multiple tissue blot. Full length sequencing of cDNA clones revealed a novel gene which we called Myeloma and Leukemia Adaptor 1 (MLA1). MLA1 encodes a 441 amino acid protein containing two domains frequently associated with signaling molecules. An SH3 motif is

predicted in the middle half of the protein and a SAM domain is located toward the carboxy-terminal end. The presence of SAM and SH3, or SAM and SH2 domains in a protein is often indicative of adaptor or scaffolding functions. The SH3 domain of MLA1 is homologous to the SH3 in CRK and its SAM domain is identical to those in a family of uncharacterized putative scaffold and adaptor proteins. There are three **predicted** consensus nuclear localization signals and tyrosine kinase phosphorylation motif. MLA1 is a member of a novel gene family of putative adaptors and scaffold proteins. This family includes 2 uncharacterized hypothetical proteins dJ753P9.2 (MLA2) and KIAA0790.

These

proteins show strong similarity throughout but highest homology is observed in both the SH3 and SAM domain regions. Genomic sequence analysis

of BAC clones from chromosome 21 suggests that MLA1 spans 50 kb and consists of at least 9 exons. MLA1 maps to human chromosome 21q11.2 in a region that is frequently disrupted by translocation events in hematopoietic malignancies. A polyclonal antibody detected a protein of approximately 49.5 kDa in myeloma cell lines. Western analysis of lysates from myeloma cell lines detected a doublet protein band in some cell lines. Immunocytochemistry staining localizes MLA1 protein **expression** to the nucleus. In order to identify potential interacting proteins, we used immunoprecipitation in combination with western analysis of lysates from Jurkat T cells and OCIMy4 myeloma cells. Our result indicates that MLA1 does not interact with HPK1, a hematopoietic **expressed** Crk interacting serine-threonine protein kinase. Although binding partners and function are as yet unknown we hypothesize that MLA1 may be analogous to adaptors that function by mediating interactions between proteins involved in signal transduction cascades.

L47 ANSWER 13 OF 27 MEDLINE DUPLICATE 10
 ACCESSION NUMBER: 2000221370 MEDLINE
 DOCUMENT NUMBER: 20221370 PubMed ID: 10756093
 TITLE: A new gene family including DSCR1 (Down Syndrome Candidate Region 1) and ZAKI-4: characterization from yeast to human and identification of DSCR1-like 2, a novel human member (DSCR1L2).
 AUTHOR: Strippoli P; Lenzi L; Petrini M; Carinci P; Zannotti M
 CORPORATE SOURCE: Istituto di Istologia ed Embriologia Generale, Universita di Bologna, Bologna, Italy.
 SOURCE: GENOMICS, (2000 Mar 15) 64 (3) 252-63.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF174139; GENBANK-AF176115; GENBANK-AF176116;
 GENBANK-AF176117
 ENTRY MONTH: 200005
 ENTRY DATE: Entered STN: 20000613
 Last Updated on STN: 20000613
 Entered Medline: 20000531

AB A new gene family has been identified on the basis of in-depth bioinformatics analysis of the Down syndrome candidate region 1 (DSCR1) gene, located on 21q22.1. We have determined the complete coding sequences of similar genes in *Saccharomyces cerevisiae* and *Caenorhabditis elegans*, as well as that of a novel human gene, named DSCR1L2 (DSCR1-like 2). Peripheral blood leukocyte cDNA sequencing **predicts** as its product a 241-amino-acid protein highly similar to products of the human

genes DSCR1 and ZAKI-4 (HGMW-approved symbol DSCR1L1). The highest level of **expression** of DSCR1L2 mRNA was found by Northern blot analysis in heart and skeletal muscles, liver, kidney, and peripheral blood leukocytes (three transcripts of 3.2, 5.2, and 7.5 kb). The gene consists of four exons and spans about 22 kb on chromosome 1 (1p33-p35.3) (Human Chromosome 1, Sanger Centre). Exon/intron organization is highly conserved between DSCR1 and DSCR1L2. Two alternative DSCR1L2 mRNA

splicing

forms have been recognized, with one lacking 10 amino acids in the middle of the protein. Analysis of **expressed sequence tags (ESTs)** shows DSCR1L2 **expression** in fetal tissues (heart, liver, and spleen) and in adenocarcinomas. **ESTs** related to the murine DSCR1L2 orthologue are found in the 2-cell stage mouse embryo, in developing brain stem and spinal cord, and in thymus and T cells. The most prominent feature identified in the protein family is a central short, unique serine-proline motif (including an ISPPXSPP box), which is strongly conserved from yeast to human but is absent in

bacteria.

Moreover, homology with the RNA-binding domain was weakly but consistently

detected in a stretch of 80 amino acids at the amino-terminus by fine sequence analysis based on tools utilizing both hidden Markov models and **BLAST**. The identification of this new gene family should allow a better understanding of the functions of the genes belonging to it.
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L47 ANSWER 14 OF 27 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2000:387606 BIOSIS

DOCUMENT NUMBER: PREV200000387606

TITLE: Criteria for gene identification and features of genome organization: Analysis of 6.5 Mb of DNA sequence from human

chromosome 21.

AUTHOR(S): Slavov, Dobromir; Hattori, Masahira; Sakaki, Yoshiyuki; Rosenthal, Andre; Shimizu, Nobuyoshi; Minoshima, Shinsei; Kudoh, Jun; Yaspo, Marie-Laure; Ramser, Julianne;

Reinhardt,

Richard; Reimer, Candy; Clancy, Kevin; Rynditch, Alla; Gardiner, Katherine (1)

CORPORATE SOURCE: (1) Eleanor Roosevelt Institute, 1899 Gaylord Street, Denver, CO, 80206 USA

SOURCE: Gene (Amsterdam), (April 18, 2000) Vol. 247, No. 1-2, pp. 215-232. print.
ISSN: 0378-1119.

DOCUMENT TYPE: Article

LANGUAGE: English

SUMMARY LANGUAGE: English

AB To establish criteria for and the limitations of novel gene identification, to identify novel genes of potential relevance to Down Syndrome and to investigate features of genome organization, 6.5 Mb of

DNA

sequence, dispersed throughout the long arm of human chromosome 21, have been annotated computationally and experimentally. Exon **prediction** with four programs, protein and **EST** database searches, two-sequence **BLAST** searches and CpG island characterization identified 41 genes with known or new protein homologies. Features of these genes suggested criteria for **prediction** of novel genes (those lacking any protein homology) with the following characteristics: (1) exon + **EST** genes: genes with excellent patterns of **predicted** exons and one or more matches in **dbEST**; (2) exon-**EST** genes: genes with good patterns of **predicted**

exons and no matches in **dbEST**; (3) **EST**-exon genes: genes without any patterns of reliable exon **prediction** but with matches in **dbEST**; and (4) isolated CpG island genes: genes consisting of strong CpG islands that are apparently unique sequences and found in regions lacking any consistent exon **predictions** within > 50 kb. In total, 41 novel gene models were **predicted**, and for a subset of these, RT-PCR experiments helped to verify and refine the models, and were used to assess **expression** in early development and in adult brain regions of potential relevance to Down syndrome. Results suggest generally low and/or restricted patterns of **expression**, and also reveal examples of complex alternative processing, especially in brain, that may have important implications for regulation of protein function. Analysis of complete gene structures of the known genes identified a number of very large introns, a number of very short intergenic distances, and at least one potentially bi-directional promoter. At least 3/4 of known genes and 1/2 of **predicted** genes are associated with CpG islands. For novel genes, three cases of overlapping genes are **predicted**. Results of these analyses illustrate some of the complexities inherent in mammalian genome organization and some of the limitations of current sequence analysis technologies. They also doubled the number of potential genes within the region.

L47 ANSWER 15 OF 27 MEDLINE DUPLICATE 11
 ACCESSION NUMBER: 2001136373 MEDLINE
 DOCUMENT NUMBER: 20538011 PubMed ID: 11087176
 TITLE: Analysis of the expressed genome of the lone star tick, *Amblyomma americanum* (Acari: Ixodidae) using an expressed sequence tag approach.
 AUTHOR: Hill C A; Gutierrez J A
 CORPORATE SOURCE: Elanco Animal Health, A Division of Eli Lilly and Company, Greenfield, Indiana 46140, USA..
 hill_catherine_a@lilly.com
 SOURCE: MICROBIAL AND COMPARATIVE GENOMICS, (2000) 5 (2) 89-101.
 Journal code: 9616596. ISSN: 1090-6592.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200103
 ENTRY DATE: Entered STN: 20010404
 Last Updated on STN: 20010404
 Entered Medline: 20010301

AB An **expressed sequence tag (EST)** approach was used to study the genome of two developmental stages of the lone star tick, *Amblyomma americanum*. cDNA libraries were constructed from the larval and adult stages of *A. americanum*. In total, 1942 **ESTs** were sequenced (1462 adult **ESTs** and 480 larval **ESTs**) and analyzed using bioinformatic programs. Contig assembly using the CAP11 program revealed 11% and 15% redundancy of sequences in the larval and adult **ESTs**, respectively. Of the 1942 **ESTs**, 1738 sequences were considered quality sequences and of these, 771 or approximately 44.4% of the sequences were putatively identified based on amino acid identity using the protein Basic Local Alignment Search Tool (**BLAST**) algorithm. Putatively identified sequences were classified according to their **predicted** gene function. In total, 967 sequences, or 55.6% of the quality sequences, had limited or no protein similarity to previously identified gene products. Sequences lacking protein homology were analyzed using an automated sequence annotation

system for **predicted** protein characteristics such as open reading frames, signal peptides, protein motifs, and transmembrane regions. In this paper we describe the sequencing of the largest number of

ESTs obtained from an arachnid species to date and the subsequent detailed analysis of these sequences.

L47 ANSWER 16 OF 27 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:60942 BIOSIS
DOCUMENT NUMBER: PREV200100060942
TITLE: Analysis of grape ESTs: Global gene expression patterns in leaf and berry.
AUTHOR(S): Ablett, Effie (1); Seaton, George; Scott, Kirsten; Shelton, Dale; Graham, Michael W.; Baverstock, Peter; Lee, L. Slade;
CORPORATE SOURCE: Henry, Robert
(1) Centre for Plant Conservation Genetics, Southern Cross University, Lismore, NSW, 2480: eablett@scu.edu.au Australia
SOURCE: Plant Science (Shannon), (October 8th, 2000) Vol. 159, No. 1, pp. 87-95. print.
ISSN: 0168-9452.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Analysis of 2479 **ESTs** from *Vitis vinifera* berry tissue and 2438 from leaf revealed that 1% of the **ESTs** match to known *Vitis* proteins, 72% to plant proteins, 11% to non-plant, and 16% had no match ($P(N) > 0.5$). The levels of redundancy were similar in the leaf and berry libraries. Only 12% of the genes matched by the **ESTs** were common to both libraries indicating marked differences in the genes **expressed** in the two tissues. The abundance of transcripts with **predicted** cellular roles in leaf and berry were estimated by classifying the primary **BLAST** matches to known proteins (score > 80) into functional categories. Thirty-six percent of the leaf transcripts were involved in photosynthesis, compared to 3% in the berry. This is a much higher proportion of transcripts involved with a function limited to specialized cells, than was found when transcripts of 33 human tissues were compared using a similar approach, suggesting plant cells may involve their cellular machinery to a greater extent in specialized activities than animal cells. Relatively enhanced **expression** of specific transcription factors, and genes involved in defense, detoxification, stress response, proteolysis, trafficking, and signal transduction, suggests berry tissue is actively engaged in responding to environmental stimuli.

L47 ANSWER 17 OF 27 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:514713 BIOSIS
DOCUMENT NUMBER: PREV200100514713
TITLE: Analysis of the filarial parasite *Brugia malayi* adult male stage EST clusters for novel gene identification.
AUTHOR(S): Kamal, Ibrahim H. (1); Ganatra, Mehul B. (1); Foster, Jeremy M. (1); Moran, Laurie S. (1); Ware, Jennifer L. (1);
Guiliano, David; Blaxter, Mark L.; Helmy, Hanan; Slatk, Barton E. (1); Ramzy, Reda M.
CORPORATE SOURCE: (1) New England Biolabs, Inc., Beverly, MA USA
SOURCE: International Genome Sequencing and Analysis Conference,

(2000) Vol. 12, pp. 70-71. print.

Meeting Info.: 12th International Genome Sequencing and
Analysis Conference Miami Beach, Florida, USA September
12-15, 2000

DOCUMENT TYPE: Conference

LANGUAGE: English

SUMMARY LANGUAGE: English

AB The current database of *Brugia malayi* (a filarial nematode responsible
for

lymphatic elephantiasis) contains DNA sequences of more than 22,000
expressed sequence tags (ESTs)
providing a resource for identifying new genes and determining their
functions. The *B. malayi* adult male cDNA library was selected for
detailed

analysis. A total of 1611 **ESTs** from *B. malayi* adult male stage
were identified, clustered by a sequence similarity algorithm and
assembled into 1356 separate clusters. All the sequences have been
submitted to **dbEST/GenBank**. These clusters of the Filarial
database version 2.0 (FilDB v. 2.0) were analyzed using **BLAST**
search for the identification of novel genes. Comparison of these

clusters
with GenBank database identified 151 clusters hitting the free living
nematode *Caenorhabditis elegans*, 90 clusters hitting other organisms and
704 as novel genes which have no significant similarities in the
database.

The remaining 411 clusters, (30%) are not included in these analyses
since

they are shorter than 200 bp in length and contain more than 10% Ns
(aNybase). Members of many gene families, including cytoskeletal house
keeping proteins, GTB-binding proteins, and house keeping enzymes were
identified. Other identified genes include RAS-related signaling protein,
calcium activated potassium channel protein, aspartyl and cysteine
proteases, sex determining gene (*her-1*) and major sperm protein. About

50%
of the clusters that hit the *C. elegans* database have similarity to
hypothetical or **predicted** proteins. Among those novel genes
(52%) there is a set of potentially *Brugia* specific targets for
immunotherapy and drug development. The variety and redundancy of
ESTs in this study suggest that the cDNA library reflects in vivo
gene **expression**. A large scale **EST** effort should
uncover many new genes and provide information about genes involved in

the
biochemical pathways of the nematode. As this approach is expanded to the
analysis of **ESTs** from other *B. malayi* stages, other genes
involved in development and/or pathogenicity are likely to be revealed.

L47 ANSWER 18 OF 27

MEDLINE

DUPLICATE 12

ACCESSION NUMBER: 2000183851 MEDLINE

DOCUMENT NUMBER: 20183851 PubMed ID: 10717299

TITLE: Preliminary profile of the *Cryptosporidium parvum* genome:
an expressed sequence tag and genome survey sequence
analysis.

AUTHOR: Strong W B; Nelson R G

CORPORATE SOURCE: Division of Infectious Diseases, San Francisco General
Hospital, San Francisco, CA, USA.

CONTRACT NUMBER: R0-1 AI42565 (NIAID)

U0-1 AI40319 (NIAID)

SOURCE: MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (2000 Mar 15) 107
(1) 1-32.

Journal code: 8006324. ISSN: 0166-6851.

PUB. COUNTRY: Netherlands

Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AA167850; GENBANK-AA167851; GENBANK-AA167852;
 GENBANK-AA167853; GENBANK-AA167854; GENBANK-AA167855;
 GENBANK-AA167856; GENBANK-AA167857; GENBANK-AA167858;
 GENBANK-AA167859; GENBANK-AA167860; GENBANK-AA167861;
 GENBANK-AA167862; GENBANK-AA167863; GENBANK-AA167864;
 GENBANK-AA167865; GENBANK-AA167866; GENBANK-AA167867;
 GENBANK-AA167868; GENBANK-AA167869; GENBANK-AA167870;
 GENBANK-AA167871; GENBANK-AA167872; GENBANK-AA167873;
 GENBANK-AA167874; GENBANK-AA167875; GENBANK-AA167876;
 GENBANK-AA167877; GENBANK-AA167878; GENBANK-AA167879; +
 ENTRY MONTH: 200006
 ENTRY DATE: Entered STN: 20000616
 Last Updated on STN: 20000616
 Entered Medline: 20000606

AB *Cryptosporidium parvum* is a protozoan enteropathogen that infects humans and animals and causes a pronounced diarrheal disease that can be life-threatening in immunocompromised hosts. No specific chemo- or immunotherapies exist to treat cryptosporidiosis and little molecular information is available to guide development of such therapies. To accelerate gene discovery and identify genes encoding potential drug and vaccine targets we constructed sporozoite cDNA and genomic DNA sequencing libraries from the Iowa isolate of *C. parvum* and determined approximately 2000 **sequence tags** by single-pass sequencing of random clones. Together, the 567 **expressed sequence tags (ESTs)** and 1507 genome survey sequences (GSSs) totaled one megabase (1 mb) of unique genomic sequence indicating that approximately 10% of the 10.4 mb *C. parvum* genome has been sequence tagged in this gene discovery expedition. The tags were used to search the public nucleic acid and protein databases via **BLAST** analyses, and 180 **ESTs** (32%) and 277 GSSs (18%) exhibited similarity with database sequences at smallest sum probabilities $P(N) < \text{or} = 10^{-8}$. Some tags encoded proteins with clear therapeutic potential including S-adenosylhomocysteine hydrolase, histone deacetylase, polyketide/fatty-acid synthases, various cyclophilins, thrombospondin-related cysteine-rich protein and ATP-binding-cassette transporters. Several anonymous **ESTs** encoded proteins **predicted** to contain signal peptides or multiple transmembrane spanning segments suggesting they were destined for membrane-bound compartments, the cell surface or extracellular secretion. One-hundred four simple sequence repeats were identified within the nonredundant **sequence tag** collection with (TAA) (> or = 6) / (TTA) (> or = 6) and (TA) (> or = 10) / (AT) (> or = 10) being the most prevalent, occurring 40 and 15 times, respectively. Various cellular RNAs and their genes were also identified including the small and large ribosomal RNAs, five tRNAs, the U2 small nuclear RNA, and the small and large virus-like, double-stranded RNAs. This investigation has demonstrated that survey sequencing is an efficient procedure for gene discovery and genome characterization and has identified and sequence tagged many *C. parvum* genes encoding potential therapeutic targets.

L47 ANSWER 19 OF 27 MEDLINE DUPLICATE 13
 ACCESSION NUMBER: 1999452943 MEDLINE
 DOCUMENT NUMBER: 99452943 PubMed ID: 10521438
 TITLE: Molecular cloning of brain-specific GD1alpha synthase (ST6GalNAc V) containing CAG/Glutamine repeats.
 COMMENT: Erratum in: J Biol Chem 2000 Jan 14;275(2):1520

AUTHOR: Okajima T; Fukumoto S; Ito H; Kiso M; Hirabayashi Y; Urano T; Furukawa K
 CORPORATE SOURCE: Department of Biochemistry II, Nagoya University School of Medicine, Tsurumai, Nagoya 466-0065, Japan.
 SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1999 Oct 22) 274 (43) 30557-62.
 Journal code: 2985121R. ISSN: 0021-9258.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AB030836
 ENTRY MONTH: 199911
 ENTRY DATE: Entered STN: 20000111
 Last Updated on STN: 20000330
 Entered Medline: 19991123

AB A novel member of the mouse CMP-NeuAc: beta-N-acetylgalactosaminide alpha2,6-sialyltransferase (ST6GalNAc) subfamily, designated ST6GalNAc V, was identified by **BLAST** analysis of **expressed sequence tags**. The sequence of the longest cDNA clone of ST6GalNAc V encoded a type II membrane protein with 8 amino acids comprising the cytoplasmic domain, 21 amino acids comprising the transmembrane region, and 306 amino acids comprising the catalytic domain.

The **predicted** amino acid sequence showed homology to the previously cloned ST6GalNAc III and IV, with common amino acid sequences in sialyl motifs L and S among these three enzymes. Eleven CAG repeats were found in the stem region. A fusion protein with protein A and extracts from L cells transfected with ST6GalNAc V in a **expression** vector showed enzyme activity of alpha2,6-sialyltransferase almost exclusively for GM1b, but not toward glycoproteins. Sialidase treatment and thin layer chromatography immunostaining revealed that the product was

GD1alpha. Northern blotting revealed that three transcripts of the gene were **expressed** specifically in brain tissues. It is concluded that this enzyme is involved in the synthesis of GD1alpha in the nervous tissues, and the CAG repeats may have implications in neurodegenerative diseases.

L47 ANSWER 20 OF 27 MEDLINE DUPLICATE 14
 ACCESSION NUMBER: 1999377055 MEDLINE
 DOCUMENT NUMBER: 99377055 PubMed ID: 10446192
 TITLE: Molecular cloning of the human gene, PNKP, encoding a polynucleotide kinase 3'-phosphatase and evidence for its role in repair of DNA strand breaks caused by oxidative damage.
 AUTHOR: Jilani A; Ramotar D; Slack C; Ong C; Yang X M; Scherer S W;
 Lasko D D
 CORPORATE SOURCE: Molecular Oncology Group, Lady Davis Institute for Medical Research, Sir Mortimer B. Davis-Jewish General Hospital, Montreal, Quebec H3T 1E2.
 SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1999 Aug 20) 274 (34) 24176-86.
 Journal code: 2985121R. ISSN: 0021-9258.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF126486
 ENTRY MONTH: 199909

ENTRY DATE: Entered STN: 19990921
Last Updated on STN: 19990921
Entered Medline: 19990909

AB Mammalian polynucleotide kinases catalyze the 5'-phosphorylation of nucleic acids and can have associated 3'-phosphatase activity, **predictive** of an important function in DNA repair following ionizing radiation or oxidative damage. The sequences of three tryptic peptides from a bovine 60-kDa polypeptide that correlated with 5'-DNA kinase and 3'-phosphatase activities identified human and murine **dbEST** clones. The 57.1-kDa conceptual translation product of this gene, polynucleotide kinase 3'-phosphatase (PNKP), contained a putative ATP binding site and a potential 3'-phosphatase domain with similarity to L-2-haloacid dehalogenases. **BLAST** searches identified possible homologs in *Caenorhabditis elegans*, *Schizosaccharomyces pombe*, and *Drosophila melanogaster*. The gene was localized to chromosome 19q13.3-13.4. Northern analysis indicated a 2-kilobase mRNA in eight human tissues. A glutathione S-transferase-PNKP fusion protein displayed 5'-DNA kinase and 3'-phosphatase activities. PNKP is the first gene for a DNA-specific kinase from any organism. PNKP **expression** partially rescued the sensitivity to oxidative damaging agents of the *Escherichia coli* DNA repair-deficient xth nfo double mutant. PNKP gene function restored termini suitable for DNA polymerase, consistent with in vivo removal of 3'-phosphate groups, facilitating DNA repair.

L47 ANSWER 21 OF 27 MEDLINE DUPLICATE 15
ACCESSION NUMBER: 99143102 MEDLINE
DOCUMENT NUMBER: 99143102 PubMed ID: 9988682
TITLE: Control of O-glycan branch formation. Molecular cloning of human cDNA encoding a novel beta1,6-N-acetylglucosaminyltransferase forming core 2 and core 4.
AUTHOR: Schwientek T; Nomoto M; Lavery S B; Merkx G; van Kessel A G; Bennett E P; Hollingsworth M A; Clausen H
CORPORATE SOURCE: School of Dentistry, University of Copenhagen, Norre Alle 20, 2200 Copenhagen N, Denmark.
CONTRACT NUMBER: 1 RO1 CA66234 (NCI)
1RO1 CA66234 (NCI)
5 P41 RR05351 (NCRR)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1999 Feb 19) 274 (8) 4504-12.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF038650
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990326
Last Updated on STN: 20000303
Entered Medline: 19990318

AB A novel human UDP-GlcNAc:Gal/GlcNAc-beta1-3GalNAc-alpha-beta1,6GlcNAc-transferase, designated C2/4GnT, was identified by **BLAST** analysis of **expressed sequence tags**. The sequence of C2/4GnT encoded a putative type II transmembrane protein with significant sequence similarity to human C2GnT and IGnT. **Expression** of the secreted form of C2/4GnT in insect cells showed that the gene product had UDP-N-acetyl-alpha-D-glucosamine:acceptor beta1,6-N-acetylglucosaminyltransferase (beta1,6GlcNAc-transferase) activity. Analysis of substrate specificity revealed that the enzyme catalyzed O-glycan branch formation of the core 2 and core 4 type. NMR analyses of

the product formed with core 3-para-nitrophenyl confirmed the product core 4-para-nitrophenyl. The coding region of C2/4GnT was contained in a single exon and located to chromosome 15q21.3. Northern analysis revealed a restricted **expression** pattern of C2/4GnT mainly in colon, kidney, pancreas, and small intestine. No **expression** of C2/4GnT was detected in brain, heart, liver, ovary, placenta, spleen, thymus, and peripheral blood leukocytes. The **expression** of core 2 O-glycans has been correlated with cell differentiation processes and cancer. The results confirm the **predicted** existence of a beta1,6GlcNAc-transferase that functions in both core 2 and core 4 O-glycan branch formation. The redundancy in beta1,6GlcNAc-transferases capable of forming core 2 O-glycans is important for understanding the mechanisms leading to specific changes in core 2 branching during cell development and malignant transformation.

L47 ANSWER 22 OF 27 MEDLINE DUPLICATE 16
 ACCESSION NUMBER: 1999263508 MEDLINE
 DOCUMENT NUMBER: 99263508 PubMed ID: 10329012
 TITLE: LHFP, a novel translocation partner gene of HMGIC in a lipoma, is a member of a new family of LHFP-like genes.
 AUTHOR: Petit M M; Schoenmakers E F; Huysmans C; Geurts J M; Mandahl N; Van de Ven W J
 CORPORATE SOURCE: Laboratory for Molecular Oncology, Center for Human Genetics, University of Leuven and Flanders Interuniversity
 SOURCE: Institute of Biotechnology, Herestraat 49, Leuven, B-3000, Belgium.
 GENOMICS, (1999 May 1) 57 (3) 438-41.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF098807
 ENTRY MONTH: 199908
 ENTRY DATE: Entered STN: 19990816
 Last Updated on STN: 19990816
 Entered Medline: 19990802
 AB A major cytogenetic subgroup among human lipomas is characterized by translocations involving the HMGIC gene at 12q15. In the context of an ongoing research program aiming at the elucidation of the functional consequences of HMGIC translocations in the etiology of lipomas, we have isolated a novel human gene, LHFP (lipoma HMGIC fusion partner), that acts as a translocation partner of HMGIC in a lipoma with t(12;13). The LHFP gene was mapped to the long arm of chromosome 13, a region recurrently targeted by chromosomal aberrations in lipomas. By Northern blot analysis, a transcript of 2.4 kb was detected in a variety of human tissues. We assembled a cDNA contig containing the entire coding region of LHFP. Nucleotide sequence analysis of the composite LHFP cDNA revealed an open reading frame encoding a protein of 200 amino acids. The **predicted** human LHFP protein is almost identical to a translated mouse **EST** that covers almost the entire LHFP coding region. In addition, **BLAST** searches revealed that the LHFP protein belongs to a new protein family consisting of at least four or five members. In the lipoma studied, the **expressed** HMGIC/LHFP fusion transcript encodes the three DNA binding domains of HMGIC followed by 69 amino acids encoded by frame-shifted LHFP sequences. LHFP is the second translocation partner of

HMGIC identified in lipomas and represents a candidate target gene for lipomas with 13q aberrations.
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L47 ANSWER 23 OF 27 MEDLINE
ACCESSION NUMBER: 1999246055 MEDLINE
DOCUMENT NUMBER: 99246055 PubMed ID: 10231024
TITLE: Expressed sequence tags from immature female sexual organ of a liverwort, Marchantia polymorpha.
AUTHOR: Nagai J; Yamato K T; Sakaida M; Yoda H; Fukuzawa H; Ohyama K
CORPORATE SOURCE: Laboratory of Plant Molecular Biology, Division of Applied Life Sciences, Graduate School of Agriculture, Kyoto University, Japan.
SOURCE: DNA RESEARCH, (1999 Feb 26) 6 (1) 1-11.
Journal code: 9423827. ISSN: 1340-2838.
PUB. COUNTRY: Japan
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-C95643; GENBANK-C95644; GENBANK-C95645;
GENBANK-C95646; GENBANK-C95647; GENBANK-C95648;
GENBANK-C95649; GENBANK-C95650; GENBANK-C95651;
GENBANK-C95652; GENBANK-C95653; GENBANK-C95654;
GENBANK-C95655; GENBANK-C95656; GENBANK-C95657;
GENBANK-C95658; GENBANK-C95659; GENBANK-C95660;
GENBANK-C95661; GENBANK-C95662; GENBANK-C95663;
GENBANK-C95664; GENBANK-C95665; GENBANK-C95666;
GENBANK-C95667; GENBANK-C95668; GENBANK-C95669;
GENBANK-C95670; GENBANK-C95671; GENBANK-C95672
ENTRY MONTH: 199907
ENTRY DATE: Entered STN: 19990730
Last Updated on STN: 19990730
Entered Medline: 19990720
AB A total of 970 **expressed sequence tag** (**EST**) clones were generated from immature female sexual organ of a liverwort, Marchantia polymorpha. The 376 **ESTs** resulted in 123 redundant groups, thus the total number of unique sequences in the **EST** set was 717. Database search by **BLAST** algorithm showed that 302 of the unique sequences shared significant similarities to known nucleotide or amino acid sequences. Six unique sequences showed significant similarities to genes that are involved in flower development and sexual reproduction, such as cynarase, fimbriata-associated protein and S-receptor kinase genes. The remaining unique 415 sequences have no significant similarity with any database-registered genes or proteins.
The redundant 123 **ESTs** implied the presence of gene families and abundant transcripts of unknown identity. Analyses of the coding sequences of 61 unique sequences, which contained no ambiguous bases in the **predicted** coding regions, highly homologous to known sequences at the amino acid level with a similarity score greater than 400, and with stop codons at similar positions as their possible orthologues, indicated the presence of biased codon usage and higher GC content within the coding sequences (50.4%) than that within 3' flanking sequences (41.9%).

L47 ANSWER 24 OF 27 MEDLINE
ACCESSION NUMBER: 1998217377 MEDLINE
DOCUMENT NUMBER: 98217377 PubMed ID: 9548972

DUPLICATE 17

TITLE: Analysis of EST-driven gene annotation in human genomic sequence.

AUTHOR: Bailey L C Jr; Searls D B; Overton G C

CORPORATE SOURCE: Computational Biology and Informatics Laboratory,
Department of Genetics, University of Pennsylvania School
of Medicine, Philadelphia, Pennsylvania 19104, USA..
bailey@www.cbil.upenn.edu

CONTRACT NUMBER: R01-HG-01450-01 (NHGRI)
R011-HG-01539-01 (NHGRI)

SOURCE: GENOME RESEARCH, (1998 Apr) 8 (4) 362-76.
Journal code: 9518021. ISSN: 1088-9051.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199806

ENTRY DATE: Entered STN: 19980618
Last Updated on STN: 19990129
Entered Medline: 19980609

AB We have performed a systematic analysis of gene identification in genomic sequence by similarity search against **expressed sequence tags (ESTs)** to assess the suitability of this method for automated annotation of the human genome. A **BLAST**-based strategy was constructed to examine the potential of this approach, and was applied to test sets containing all human genomic sequences longer than 5 kb in public databases, plus 300 kb of exhaustively characterized benchmark sequence. At high stringency, 70%-90% of all annotated genes are detected by near-identity to **EST** sequence; >95% of **ESTs** aligning with well-annotated sequences overlap a gene. These **ESTs** provide immediate access to the corresponding cDNA clones for follow-up laboratory verification and subsequent biologic analysis. At lower stringency, up to 97% of annotated genes were identified by similarity to **ESTs**. The apparent false-positive rate rose to 55% of **ESTs** among all sequences and 20% among benchmark sequences at the lowest stringency, indicating that many genes in public database entries are unannotated. Approximately half of the alignments span multiple exons, and thus aid in the construction of gene **predictions** and elucidation of alternative splicing. In addition, **ESTs** from multiple cDNA libraries frequently cluster over genes, providing a starting point for crude **expression** profiles. Clone IDs may be used to form **EST** pairs, and particularly to extend models by associating alignments of lower stringency with high-quality alignments. These results demonstrate that **EST** similarity search is a practical general-purpose annotation technique that complements pattern recognition methods as a tool for gene characterization.

L47 ANSWER 25 OF 27 MEDLINE DUPLICATE 18

ACCESSION NUMBER: 1998324892 MEDLINE

DOCUMENT NUMBER: 98324892 PubMed ID: 9657971

TITLE: Sequence, catalytic properties and expression of chicken glutathione-dependent prostaglandin D2 synthase, a novel class Sigma glutathione S-transferase.

AUTHOR: Thomson A M; Meyer D J; Hayes J D

CORPORATE SOURCE: Biomedical Research Centre, Ninewells Hospital and Medical School, University of Dundee, Dundee DD1 9SY, Scotland, U.K.

SOURCE: BIOCHEMICAL JOURNAL, (1998 Jul 15) 333 (Pt 2) 317-25.
Journal code: 2984726R. ISSN: 0264-6021.

PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AJ006405
ENTRY MONTH: 199809
ENTRY DATE: Entered STN: 19980917
Last Updated on STN: 19980917
Entered Medline: 19980910

AB The **Expressed Sequence Tag** database has been screened for cDNA clones encoding prostaglandin D2 synthases (PGDSs) by using a **BLAST** search with the N-terminal amino acid sequence of rat GSH-dependent PGDS, a class Sigma glutathione S-transferase (GST). This resulted in the identification of a cDNA from chicken spleen containing an insert of approx. 950 bp that encodes a protein of 199 amino acid residues with a **predicted** molecular mass of 22732 Da. The deduced primary structure of the chicken protein was not only found to possess 70% sequence identity with rat PGDS but it also demonstrated more than 35% identity with class Sigma GSTs from a range of invertebrates. The open reading frame of the chicken cDNA was **expressed** in Escherichia coli and the purified protein was found to display high PGDS activity. It also catalysed the conjugation of glutathione with a wide range of aryl halides, organic isothiocyanates and alpha,beta-unsaturated carbonyls, and exhibited glutathione peroxidase activity towards cumene hydroperoxide. Like other GSTs, chicken PGDS was found to be inhibited by non-substrate ligands such as Cibacron Blue, haematin and organotin compounds. Western blotting experiments showed that among the organs studied, the **expression** of PGDS in the female chicken is highest in liver, kidney and intestine, with only small amounts of the enzyme being found in chicken spleen; in contrast, the rat has highest levels of PGDS in the spleen. Collectively, these results show that the structure and function, but not the **expression**, of the GSH-requiring PGDS is conserved between chicken and rat.

L47 ANSWER 26 OF 27 MEDLINE DUPLICATE 19
ACCESSION NUMBER: 1998070356 MEDLINE
DOCUMENT NUMBER: 98070356 PubMed ID: 9405390
TITLE: A family of human beta4-galactosyltransferases. Cloning and expression of two novel UDP-galactose:beta-n-acetylglucosamine beta1, 4-galactosyltransferases, beta4Gal-T2 and beta4Gal-T3.
COMMENT: Erratum in: J Biol Chem 1998 Jul 17;273(29):18674
AUTHOR: Almeida R; Amado M; David L; Levery S B; Holmes E H; Merckx G; van Kessel A G; Rygaard E; Hassan H; Bennett E; Clausen H
CORPORATE SOURCE: School of Dentistry, University of Copenhagen, Norre Alle 20, DK-2200 Copenhagen N, Denmark.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1997 Dec 19) 272 (51) 31979-91.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-Y12509; GENBANK-Y12510
ENTRY MONTH: 199801
ENTRY DATE: Entered STN: 19980130
Last Updated on STN: 19990129

Entered Medline: 19980122

AB **BLAST** analysis of **expressed sequence tags (ESTs)** using the coding sequence of the human UDP-galactose:beta-N-acetylglucosamine beta1, 4-galactosyltransferase, designated beta4Gal-T1, revealed a large number of **ESTs** with identical as well as similar sequences. **ESTs** with sequences similar to that of beta4Gal-T1 could be grouped into at least two non-identical sequence sets. Analysis of the **predicted** amino acid sequence of the novel **ESTs** with beta4Gal-T1 revealed conservation of short sequence motifs as well as cysteine residues previously shown to be important for the function of beta4Gal-T1. The likelihood that the identified **ESTs** represented novel galactosyltransferase genes was tested by cloning and sequencing of the full coding region of two distinct genes, followed by **expression**. **Expression** of soluble secreted constructs in the baculovirus system showed that these genes represented genuine UDP-galactose:beta-N-acetylglucosamine beta1, 4-galactosyltransferases, thus designated beta4Gal-T2 and beta4Gal-T3. Genomic cloning of the genes revealed that they have identical genomic organizations compared with beta4Gal-T1. The two novel genes were located on 1p32-33 and 1q23. The results demonstrate the existence of a family of homologous galactosyltransferases with related functions. The existence of multiple beta4-galactosyltransferases with the same or overlapping functions may be relevant for interpretation of biological functions previously assigned to beta4Gal-T1.

L47 ANSWER 27 OF 27 MEDLINE DUPLICATE 20
ACCESSION NUMBER: 97217792 MEDLINE
DOCUMENT NUMBER: 97217792 PubMed ID: 9063753
TITLE: A transcript map of the newly defined 165 kb
Wolf-Hirschhorn syndrome critical region.
AUTHOR: Wright T J; Ricke D O; Denison K; Abmayr S; Cotter P D;
Hirschhorn K; Keinanen M; McDonald-McGinn D; Somer M;
Spinner N; Yang-Feng T; Zackai E; Altherr M R
CORPORATE SOURCE: Life Sciences Division, Los Alamos National Laboratory, NM
87545, USA.
SOURCE: HUMAN MOLECULAR GENETICS, (1997 Feb) 6 (2) 317-24.
Journal code: 9208958. ISSN: 0964-6906.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF101434; GENBANK-AF101435
ENTRY MONTH: 199708
ENTRY DATE: Entered STN: 19970908
Last Updated on STN: 20000303
Entered Medline: 19970827

AB Wolf-Hirschhorn syndrome (WHS) is a multiple malformation syndrome characterised by mental and developmental defects resulting from the absence of a segment of one chromosome 4 short arm (4p16.3). Due to the complex and variable **expression** of this disorder, it is thought that the WHS is a contiguous gene syndrome with an undefined number of genes contributing to the phenotype. In an effort to identify genes that contribute to human development and whose absence results in this syndrome, we have utilised a series of landmark cosmid to characterise a collection of WHS patient derived cell lines. Fluorescence in situ hybridisation with these cosmid was used to refine the WHS critical region (WHSCR) to 260 kb. The genomic sequence of this region is available and analysis of this sequence through **BLAST** detected several cDNA clones in the **dbEST** data base. A total of nine independent cDNAs, and their **predicted** translation products, from this

analysis show no significant similarity to members of DNA or protein databases. Furthermore, these genes have been localised within the WHS critical region and reveal an interesting pattern of transcriptional organisation. A previously published report of a patient with proximal

4p- syndrome further refines the WHSCR to 165 kb defined by the loci D4S166 and D4S3327. This work provides the starting point to understand how multiple genes or other mechanisms can contribute to the complex phenotype associated with the Wolf-Hirschhorn syndrome.

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
19:04:09
ON 08 JUL 2002

L1 13496 S EST
L2 34 S L1(S) (NO#(W) CORRELAT?)
L3 21 DUP REM L2 (13 DUPLICATES REMOVED)
L4 3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5 1972 S L4(S) (PROTEIN OR PEPTIDE)
L6 1748 S L5(S) (EXPRESS?)
L7 775 S L6(S) DATABASE#
L8 355 DUP REM L7 (420 DUPLICATES REMOVED)
L9 96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
L10 47 S L8(S) GENBANK
L11 87 S L8(S) (HEART OR BONE OR BRAIN)
L12 137 S L11 OR L9
L13 1 S L12 AND (NO#(W) EXPRESS?)
L14 67 S L12(S) (TRANSCRI?)
L15 86 S L8(S) NORTHERN
L16 50 S L1(S) (NO#(2W) CORRELAT?)
L17 16 S L16 NOT L2
L18 12 DUP REM L17 (4 DUPLICATES REMOVED)
L19 54 S L1(S) (NO#(3W) CORRELAT?)
L20 0 S L19 NOT L1
L21 20 S L19 NOT L2
L22 4 S L21 NOT L16

FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002

L23 13496 S EST OR (SEQUENCE(W) TAG#)
L24 234 S L23 AND DATABASE#/TI
L25 0 S L24 AND (NO(3W) CORRELAT?)
L26 234 S L24(S) DATABASE#
L27 2221 S L23(S) DATABASE#
L28 4 S L27(S) (NO#(3W) CORRELAT?)
L29 1174 S L23(S) (BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVA
L30 310 S L29(S) NORTHERN
L31 133 S L30 AND DATABASE#
L32 78 DUP REM L31 (55 DUPLICATES REMOVED)
L33 1072 S L23(S) (PREDICT? OR ANTICIPAT?)
L34 22 S L33 AND DATABASE#/TI
L35 13 DUP REM L34 (9 DUPLICATES REMOVED)
L36 22 S L34(S) DATABASE#
L37 2221 S L23(S) DATABASE#
L38 612 S L37(S) TISSUE
L39 58 S L38(S) PROSTATE
L40 10 S L39 AND PREDICT?

L41 6 DUP REM L40 (4 DUPLICATES REMOVED)
 L42 1 S L23 (S) (CANNOT (3W) PREDICT)
 L43 13596 S L23 OR DBEST
 L44 6719 S L43 (S) EXPRESS?
 L45 192 S L44 (S) BLAST
 L46 47 S L45 (S) PREDICT?
 L47 27 DUP REM L46 (20 DUPLICATES REMOVED)

=> s l43(s)relied

L48 2 L43 (S) RELIED

=> d ibib abs tot

L48 ANSWER 1 OF 2 MEDLINE
 ACCESSION NUMBER: 1998324444 MEDLINE
 DOCUMENT NUMBER: 98324444 PubMed ID: 9662067
 TITLE: Digital cloning: identification of human cDNAs homologous to novel kinases through expressed sequence tag database searching.
 AUTHOR: Chen H C; Kung H J; Robinson D
 CORPORATE SOURCE: Molecular and Genomic Medicine Division, National Health Research Institutes, Taipei, Taiwan, ROC.
 CONTRACT NUMBER: CA 57179 (NCI)
 CA39207 (NCI)
 DK52659 (NIDDK)
 SOURCE: JOURNAL OF BIOMEDICAL SCIENCE, (1998) 5 (2) 86-92.
 Journal code: 9421567. ISSN: 1021-7770.
 PUB. COUNTRY: Switzerland
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199809
 ENTRY DATE: Entered STN: 19980925
 Last Updated on STN: 19980925
 Entered Medline: 19980916

AB Identification of novel kinases based on their sequence conservation within kinase catalytic domain has **relied** so far on two major approaches, low-stringency hybridization of cDNA libraries, and PCR method

using degenerate primers. Both of these approaches at times are technically difficult and time-consuming. We have developed a procedure that can significantly reduce the time and effort involved in searching for novel kinases and increase the sensitivity of the analysis. This procedure exploits the computer analysis of a vast resource of human cDNA sequences represented in the expressed **sequence tag** (**EST**) database. Seventeen novel human cDNA clones showing significant homology to serine/threonine kinases, including STE-20, CDK- and YAK-related family kinases, were identified by searching **EST** database. Further sequence analysis of these novel kinases obtained either

directly from **EST** clones or from PCR-RACE products confirmed their identity as protein kinases. Given the rapid accumulation of the **EST** database and the advent of powerful computer analysis software, this approach provides a fast, sensitive, and economical way to identify novel kinases as well as other genes from **EST** database.

L48 ANSWER 2 OF 2 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 1998:345679 BIOSIS
 DOCUMENT NUMBER: PREV199800345679
 TITLE: Digital cloning: Identification of human cDNAs homologous to novel kinases through expressed sequence tag database

searching.
AUTHOR(S): Chen, Hua-Chien (1); Kung, Hsing-Jien; Robinson, Dan
CORPORATE SOURCE: (1) Mol. Genomic Med. Div., Natl. Health Res. Inst., 128
Yen-Chiu-Yuan Rd., Sec. 2, Taipei 115 Taiwan
SOURCE: Journal of Biomedical Science, (March-April, 1998) Vol. 5,
No. 2, pp. 86-92.
ISSN: 1021-7770.

DOCUMENT TYPE: Article
LANGUAGE: English

AB Identification of novel kinases based on their sequence conservation
within kinase catalytic domain has **relied** so far on two major
approaches, low-stringency hybridization of cDNA libraries, and PCR
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using degenerate primers. Both of these approaches at times are
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sequences represented in the expressed **sequence tag** (**EST**) database. Seventeen novel human cDNA clones showing
significant homology to serine/threonine kinases, including STE-20, CDK-
and YAK-related family kinases, were identified by searching **EST**
database. Further sequence analysis of these novel kinases obtained

either
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their identity as protein kinases. Given the rapid accumulation of the
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software, this approach provides a fast, sensitive, and economical way to
identify novel kinases as well as other genes from **EST** database.

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FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
19:04:09
ON 08 JUL 2002

L1 13496 S EST
L2 34 S L1(S) (NO#(W) CORRELAT?)
L3 21 DUP REM L2 (13 DUPLICATES REMOVED)
L4 3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5 1972 S L4(S) (PROTEIN OR PEPTIDE)
L6 1748 S L5(S) (EXPRESS?)
L7 775 S L6(S) DATABASE#
L8 355 DUP REM L7 (420 DUPLICATES REMOVED)
L9 96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
L10 47 S L8(S) GENBANK
L11 87 S L8(S) (HEART OR BONE OR BRAIN)
L12 137 S L11 OR L9
L13 1 S L12 AND (NO#(W) EXPRESS?)
L14 67 S L12(S) (TRANSCRI?)
L15 86 S L8(S) NORTHERN
L16 50 S L1(S) (NO#(2W) CORRELAT?)
L17 16 S L16 NOT L2
L18 12 DUP REM L17 (4 DUPLICATES REMOVED)
L19 54 S L1(S) (NO#(3W) CORRELAT?)
L20 0 S L19 NOT L1
L21 20 S L19 NOT L2
L22 4 S L21 NOT L16

FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002

L23 13496 S EST OR (SEQUENCE(W)TAG#)
L24 234 S L23 AND DATABASE#/TI
L25 0 S L24 AND (NO(3W)CORRELAT?)
L26 234 S L24(S)DATABASE#
L27 2221 S L23(S)DATABASE#
L28 4 S L27(S) (NO#(3W)CORRELAT?)
L29 1174 S L23(S) (BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVA
L30 310 S L29(S)NORTHERN
L31 133 S L30 AND DATABASE#
L32 78 DUP REM L31 (55 DUPLICATES REMOVED)
L33 1072 S L23(S) (PREDICT? OR ANTICIPAT?)
L34 22 S L33 AND DATABASE#/TI
L35 13 DUP REM L34 (9 DUPLICATES REMOVED)
L36 22 S L34(S)DATABASE#
L37 2221 S L23(S)DATABASE#
L38 612 S L37(S)TISSUE
L39 58 S L38(S)PROSTATE
L40 10 S L39 AND PREDICT?
L41 6 DUP REM L40 (4 DUPLICATES REMOVED)
L42 1 S L23(S) (CANNOT(3W)PREDICT?)
L43 13596 S L23 OR DBEST
L44 6719 S L43(S)EXPRESS?
L45 192 S L44(S)BLAST
L46 47 S L45(S)PREDICT?
L47 27 DUP REM L46 (20 DUPLICATES REMOVED)
L48 2 S L43(S)RELIED

=> s l43(s)((not or cannot)(w)predict?)
MISSING TERM '((NOT'
The search profile entered contains a left parenthesis,
'(' followed by an operator.

=> s l43(s)(("not" or cannot)(w)predict?)
L49 1 L43(S)(("NOT" OR CANNOT)(W) PREDICT?)

=> d ibib abs

L49 ANSWER 1 OF 1 MEDLINE
ACCESSION NUMBER: 2002172902 IN-PROCESS
DOCUMENT NUMBER: 21859662 PubMed ID: 11870237
TITLE: High frequency of DAZ1/DAZ2 gene deletions in patients
with
severe oligozoospermia.
AUTHOR: Fernandes S; Huellen K; Goncalves J; Dukal H; Zeisler J;
Rajpert De Meyts E; Skakkebaek N E; Habermann B; Krause W;
Sousa M; Barros A; Vogt P H
CORPORATE SOURCE: Reproduction Genetics, Institute of Human Genetics,
University of Heidelberg, Heidelberg, Germany.
SOURCE: MOLECULAR HUMAN REPRODUCTION, (2002 Mar) 8 (3) 286-98.
Journal code: 9513710. ISSN: 1360-9947.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020322
Last Updated on STN: 20020322
AB Deletions of the DAZ gene family in distal Yq11 are always associated
with
deletions of the azoospermia factor c (AZFc) region, which we now
estimate

extends to 4.94 Mb. Because more Y gene families are located in this chromosomal region, and are expressed like the DAZ gene family only in the male germ line, the testicular pathology associated with complete AZFc deletions **cannot predict** the functional contribution of the DAZ gene family to human spermatogenesis. We therefore established a DAZ gene copy specific deletion analysis based on the DAZ-BAC sequences in GenBank. It includes the deletion analysis of eight DAZ-DNA PCR markers [six DAZ-single nucleotide variants (SNVs) and two DAZ-**sequence tag** sites (STS)] selected from the 5' to the 3' end of each DAZ gene and a deletion analysis of the gene copy specific EcoRV and TaqI restriction fragments identified in the internal repetitive DAZ gene regions (DYS1 locus). With these diagnostic tools, 63 DNA samples from men with idiopathic oligozoospermia and 107 DNA samples from men with proven fertility were analysed for the presence of the complete DAZ gene locus, encompassing the four DAZ gene copies. In five oligozoospermic patients, we found a DAZ-SNV/STS and DYS1/EcoRV and TaqI fragment deletion pattern indicative for deletion of the DAZ1 and DAZ2 gene copies; one of these deletions could be identified as a 'de-novo' deletion because it was absent in the DAZ locus of the patient's father. The same DAZ deletions were not found in any of the 107 fertile control samples. We therefore conclude that the deletion of the DAZ1/DAZ2 gene doublet in five out of our 63 oligozoospermic patients (8%) is responsible for the patients' reduced sperm numbers. It is most likely caused by intrachromosomal recombination events between two long repetitive sequence blocks (AZFc-Rep1) flanking the DAZ gene structures.

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT 19:04:09
ON 08 JUL 2002

```

L1      13496 S EST
L2      34 S L1(S) (NO#(W)CORRELAT?)
L3      21 DUP REM L2 (13 DUPLICATES REMOVED)
L4      3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5      1972 S L4(S) (PROTEIN OR PEPTIDE)
L6      1748 S L5(S) (EXPRESS?)
L7      775 S L6(S)DATABASE#
L8      355 DUP REM L7 (420 DUPLICATES REMOVED)
L9      96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN)
L10     47 S L8(S)GENBANK
L11     87 S L8(S) (HEART OR BONE OR BRAIN)
L12     137 S L11 OR L9
L13     1 S L12 AND (NO#(W)EXPRESS?)
L14     67 S L12(S) (TRANSCRI?)
L15     86 S L8(S)NORTHERN
L16     50 S L1(S) (NO#(2W)CORRELAT?)
L17     16 S L16 NOT L2
L18     12 DUP REM L17 (4 DUPLICATES REMOVED)
L19     54 S L1(S) (NO#(3W)CORRELAT?)
L20     0 S L19 NOT L1
L21     20 S L19 NOT L2
L22     4 S L21 NOT L16

```

FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002

```

L23      13496 S EST OR (SEQUENCE(W)TAG#)
L24      234 S L23 AND DATABASE#/TI
L25      0 S L24 AND (NO(3W)CORRELAT?)
L26      234 S L24(S)DATABASE#
L27      2221 S L23(S)DATABASE#
L28      4 S L27(S) (NO#(3W)CORRELAT?)
L29      1174 S L23(S) (BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVA
L30      310 S L29(S)NORTHERN
L31      133 S L30 AND DATABASE#
L32      78 DUP REM L31 (55 DUPLICATES REMOVED)
L33      1072 S L23(S) (PREDICT? OR ANTICIPAT?)
L34      22 S L33 AND DATABASE#/TI
L35      13 DUP REM L34 (9 DUPLICATES REMOVED)
L36      22 S L34(S)DATABASE#
L37      2221 S L23(S)DATABASE#
L38      612 S L37(S)TISSUE
L39      58 S L38(S)PROSTATE
L40      10 S L39 AND PREDICT?
L41      6 DUP REM L40 (4 DUPLICATES REMOVED)
L42      1 S L23(S) (CANNOT(3W)PREDICT)
L43      13596 S L23 OR DBEST
L44      6719 S L43(S)EXPRESS?
L45      192 S L44(S)BLAST
L46      47 S L45(S)PREDICT?
L47      27 DUP REM L46 (20 DUPLICATES REMOVED)
L48      2 S L43(S)RELIED
L49      1 S L43(S) (("NOT" OR CANNOT) (W) PREDICT?)

```

```

=> l43(s) (cannot(w)anticipate)
L43(S) (CANNOT(W)ANTICIPATE) IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

```

```

=> s l43(s) (cannot(w)anticipate)
L50      0 L43(S) (CANNOT(W) ANTICIPATE)

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```

=> s l43(s)transcripts
L51      797 L43(S) TRANSCRIPTS

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```

=> d history

```

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(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

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FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
19:04:09
ON 08 JUL 2002

```

```

L1      13496 S EST
L2      34 S L1(S) (NO#(W)CORRELAT?)
L3      21 DUP REM L2 (13 DUPLICATES REMOVED)
L4      3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5      1972 S L4(S) (PROTEIN OR PEPTIDE)
L6      1748 S L5(S) (EXPRESS?)
L7      775 S L6(S)DATABASE#
L8      355 DUP REM L7 (420 DUPLICATES REMOVED)
L9      96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
L10     47 S L8(S)GENBANK
L11     87 S L8(S) (HEART OR BONE OR BRAIN)
L12     137 S L11 OR L9
L13     1 S L12 AND (NO#(W)EXPRESS?)
L14     67 S L12(S) (TRANSCRI?)

```

L15 86 S L8(S)NORTHERN
 L16 50 S L1(S) (NO#(2W)CORRELAT?)
 L17 16 S L16 NOT L2
 L18 12 DUP REM L17 (4 DUPLICATES REMOVED)
 L19 54 S L1(S) (NO#(3W)CORRELAT?)
 L20 0 S L19 NOT L1
 L21 20 S L19 NOT L2
 L22 4 S L21 NOT L16

FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002

L23 13496 S EST OR (SEQUENCE(W)TAG#)
 L24 234 S L23 AND DATABASE#/TI
 L25 0 S L24 AND (NO(3W)CORRELAT?)
 L26 234 S L24(S)DATABASE#
 L27 2221 S L23(S)DATABASE#
 L28 4 S L27(S) (NO#(3W)CORRELAT?)
 L29 1174 S L23(S) (BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVA
 L30 310 S L29(S)NORTHERN
 L31 133 S L30 AND DATABASE#
 L32 78 DUP REM L31 (55 DUPLICATES REMOVED)
 L33 1072 S L23(S) (PREDICT? OR ANTICIPAT?)
 L34 22 S L33 AND DATABASE#/TI
 L35 13 DUP REM L34 (9 DUPLICATES REMOVED)
 L36 22 S L34(S)DATABASE#
 L37 2221 S L23(S)DATABASE#
 L38 612 S L37(S)TISSUE
 L39 58 S L38(S)PROSTATE
 L40 10 S L39 AND PREDICT?
 L41 6 DUP REM L40 (4 DUPLICATES REMOVED)
 L42 1 S L23(S) (CANNOT(3W)PREDICT)
 L43 13596 S L23 OR DBEST
 L44 6719 S L43(S)EXPRESS?
 L45 192 S L44(S)BLAST
 L46 47 S L45(S)PREDICT?
 L47 27 DUP REM L46 (20 DUPLICATES REMOVED)
 L48 2 S L43(S)RELIED
 L49 1 S L43(S) (("NOT" OR CANNOT) (W)PREDICT?)
 L50 0 S L43(S) (CANNOT(W)ANTICIPATE)
 L51 797 S L43(S)TRANSCRIPTS

=> s l43(s) ((no(w)expression) or ("not"(w)expressed))
 L52 28 L43(S) ((NO(W) EXPRESSION) OR ("NOT"(W) EXPRESSED))

=> dup rem l52
 PROCESSING COMPLETED FOR L52
 L53 17 DUP REM L52 (11 DUPLICATES REMOVED)

=> d ibib abs tot

L53 ANSWER 1 OF 17 MEDLINE DUPLICATE 1
 ACCESSION NUMBER: 2002274201 MEDLINE
 DOCUMENT NUMBER: 22008789 PubMed ID: 12014646
 TITLE: Cloning, sequencing and expression analysis of a novel
 gene
 BR-1 that is expressed in normal human brain tissue but
 not
 in glioma tumor samples.
 AUTHOR: Wei Kuo Chen; Berger Mitchel S; Sehgal Anil
 CORPORATE SOURCE: Chang Gung Memorial Hospital, 1st Division of
 Neurosurgery,
 Taoyuan, Taiwan.

SOURCE: ANTICANCER RESEARCH, (2002 Mar-Apr) 22 (2A) 745-53.
Journal code: 8102988. ISSN: 0250-7005.
PUB. COUNTRY: Greece
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200206
ENTRY DATE: Entered STN: 20020517
Last Updated on STN: 20020628
Entered Medline: 20020627

AB Using the technique of differential hybridization of a human fetal brain library, we identified a novel gene, brain 1 (BR-1). This gene is expressed in normal brain but has low or **no expression** in human gliomas. We have cloned and sequenced the full-length cDNA corresponding to this gene. A data base search for the nucleotide sequence
homology was performed for BR-1. The BR-1 sequence showed strong homology to a human genomic clone from chromosome 2. Moderate sequence homology was
observed between BR-1 and an expressed **sequence tag** (**EST**) from a human placenta library. Three different regions of BR-1 also showed homology to a mouse **EST** that is similar to EL-10 gene. Sequence analysis indicated that the protein sequence for
BR-1 has one tyrosine kinase phosphorylation site and two N-myristoylation sites. Northern blot analysis indicated that the BR-1 gene is expressed
in heart, placenta, lung, liver, skeletal muscle, kidney and pancreas. A low level of expression of BR-1 is observed in the cerebellum, cerebral cortex, spinal cord, occipital lobe and putamen. The BR-1 gene is also expressed in fetal brain, liver and kidney. Low expression of BR-1 gene was observed in a number of non-brain tumor cell lines. RT-PCR analysis indicated that the BR-1 gene was expressed in non-neoplastic (epilepsy specimens) but not in six oligodendrogliomas and three oligoastrocytoma tumor samples analyzed. BR-1 was not expressed in either seven low grade gliomas or eight grade IV glioblastoma tumor tissue samples analyzed. Three glioblastoma cell lines did show low expression of the BR-1 gene.
On the basis of its expression properties, we conclude that BR-1 is a potential novel tumor suppressor gene.

L53 ANSWER 2 OF 17 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2002274188 MEDLINE
DOCUMENT NUMBER: 22008775 PubMed ID: 12014633
TITLE: Molecular characterization of a novel BR-2 gene that is down-regulated in human low grade glioma tumors.
AUTHOR: Wei Kuo Chen; Berger Mitchel S; Sehgal Anil
CORPORATE SOURCE: Chang Gung Memorial Hospital, 1st Division of Neurosurgery,
Taoyuan, Taiwan.

SOURCE: ANTICANCER RESEARCH, (2002 Mar-Apr) 22 (2A) 649-57.
Journal code: 8102988. ISSN: 0250-7005.
PUB. COUNTRY: Greece
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200206
ENTRY DATE: Entered STN: 20020517
Last Updated on STN: 20020628
Entered Medline: 20020627

AB Using the technique of differential hybridization of a human fetal brain

library, we have identified a novel gene, brain 2 (BR-2). This gene is expressed in normal brain but has low or **no expression** in human oligodendrogliomas and other brain tumor samples. We have cloned and sequenced the full-length cDNA corresponding to this gene. A data base search for the nucleotide sequence homology was performed for BR-2. BR-2 sequence showed strong homolog to a human genomic clone from chromosome 2.

Moderate sequence homology was observed between BR-2 and an **EST** from a human placenta library. Multiple tissue dot blot analysis indicated that the BR-2 gene is expressed in a number of tissues including brain, heart, lung, placenta, lymph node, trachea and kidney. The BR-2 gene is also expressed in fetal heart, spleen and lung tissue. An extremely high level of BR-2 expression is observed in the left atrium of the heart. Low or **no expression** of BR-2 expression is observed in sixteen human cancer cell lines. RT-PCR analysis indicated that the BR-2 gene is expressed at high levels in two of the five normal brain tissue samples analyzed. Except for low expression in one oligodendroglioma, **no expression** of BR-1 gene was observed in eight anaplastic astrocytomas and glioblastoma multiforme tissue samples. Four of nine glioblastoma tumor cell lines did show a low level of BR-2 expression. On the basis of its expression and sequence, we conclude that BR-2 is a novel gene with unique expression properties in human brain tumors.

L53 ANSWER 3 OF 17 MEDLINE
 ACCESSION NUMBER: 2002296564 IN-PROCESS
 DOCUMENT NUMBER: 22032968 PubMed ID: 12036595
 TITLE: Characterization and expression of the mouse tat interactive protein 60 kD (TIP60) gene.
 AUTHOR: McAllister Donna; Merlo Xanthi; Lough John
 CORPORATE SOURCE: Department of Cell Biology, Neurobiology and Anatomy and Cardiovascular Research Center, Medical College of Wisconsin, 8701 West Watertown Plank Road, Milwaukee, WI 53226, USA.
 SOURCE: GENE, (2002 May 1) 289 (1-2) 169-76.
 Journal code: 7706761. ISSN: 0378-1119.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
 ENTRY DATE: Entered STN: 20020531
 Last Updated on STN: 20020531

AB Tat interactive protein-60 (TIP60) is a novel histone acetyltransferase-containing protein that has been implicated in the regulation of transcription, DNA repair and apoptosis. In this report we describe the structure and expression of the mouse TIP60 gene, as well the localization of TIP60 protein at the cellular level. The gene contains 14 exons within a DNA sequence interval of 6611 bp. The assembled exons comprise a 1,539 bp DNA complementary to RNA (cDNA) having 91.7 and 78.7% homology with respective human and chick TIP60 cDNAs. Translation predicts a approximately 59 kD protein having 99.6 and 91.6% sequence homology with respective human and chick proteins. Alignment with mouse expressed **sequence tag** database entries indicates, similar to human and chick TIP60, the existence of an alternative splice created by removal of exon 5 that results in a 1383 bp cDNA with a predicted translation product of approximately 53 kD. Northern hybridization analysis reveals a peak of TIP60 expression during mouse embryogenesis at E11; in adult tissues TIP60 is expressed in the following order of

intensity: testis>heart>brain>kidney>liver>lung, with little to **no expression** in spleen and skeletal muscle. Cellular localization using green fluorescent protein-TIP fusion constructs and immunohistochemistry reveal that TIP53 and TIP60 are nuclear proteins.

L53 ANSWER 4 OF 17 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 2001228177 MEDLINE
DOCUMENT NUMBER: 21164809 PubMed ID: 11264177
TITLE: Nucleotide sequence, transcription map, and mutation analysis of the 13q14 chromosomal region deleted in B-cell chronic lymphocytic leukemia.
AUTHOR: Migliazza A; Bosch F; Komatsu H; Cayanis E; Martinotti S; Toniato E; Guccione E; Qu X; Chien M; Murty V V; Gaidano G;
Inghirami G; Zhang P; Fischer S; Kalachikov S M; Russo J; Edelman I; Efstratiadis A; Dalla-Favera R
CORPORATE SOURCE: Institute of Cancer Genetics, Columbia University, New York, New York 10032, USA.
SOURCE: BLOOD, (2001 Apr 1) 97 (7) 2098-104.
Journal code: 7603509. ISSN: 0006-4971.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
OTHER SOURCE: GENBANK-AF272953; GENBANK-AF279658; GENBANK-AF279659; GENBANK-AF279660
ENTRY MONTH: 200104
ENTRY DATE: Entered STN: 20010502
Last Updated on STN: 20010502
Entered Medline: 20010426
AB Deletions of the 13q14 chromosome region are associated with B-cell chronic lymphocytic leukemia (B-CLL) and several other types of cancer, suggesting the presence of a tumor suppressor gene. In previous studies the minimal region of deletion (MDR) was mapped to a less than 300-kilobase (kb) interval bordered by the markers 173a12-82 and 138G4/1.3R. For the identification of the putative tumor suppressor gene, the entire MDR (approximately 347 kb) has been sequenced, and transcribed regions have been identified by exon trapping, **EST**-based full-length complementary DNA cloning, database homology searches, and computer-assisted gene prediction analyses. The MDR contains 2 pseudogenes and 3 transcribed genes: CAR, encoding a putative RING-finger containing protein; 1B4/Leu2, generating noncoding transcripts; and EST70/Leu1, probably representing another noncoding gene (longest open reading frame of 78 codons). These genes have been sequenced in 20 B-CLL cases with 13q14 hemizygous deletion, and no mutations were found. Moreover, no somatic variants were found in the entire MDR analyzed for nucleotide substitutions by a combination of direct sequencing and fluorescence-assisted mismatch analysis in 5 B-CLL cases displaying 13q14-monoallelic deletion. The nondeleted allele of the CAR and EST70/Leu1 genes was expressed in B-CLL specimens, including those with monoallelic loss, whereas **no expression** of 1B4/Leu2 was detectable in B-CLL, regardless of the 13q14 status. These results indicate that allelic loss and mutation of a gene within the MDR is an unlikely pathogenetic mechanism for B-CLL. However, haplo-insufficiency of one of the identified genes may contribute to tumorigenesis. (Blood. 2001;97:2098-2104)

L53 ANSWER 5 OF 17 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 2001653629 MEDLINE

DOCUMENT NUMBER: 21560218 PubMed ID: 11703281
TITLE: Keratin K6irs is specific to the inner root sheath of hair
follicles in mice and humans.
AUTHOR: Porter R M; Corden L D; Lunny D P; Smith F J; Lane E B;
McLean W H
CORPORATE SOURCE: CRC Cell Structure Research Group, School of Life
Sciences,
University of Dundee, Dundee DD1 4HN, UK.
SOURCE: BRITISH JOURNAL OF DERMATOLOGY, (2001 Oct) 145 (4) 558-68.
Journal code: 0004041. ISSN: 0007-0963.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AA354256
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20011115
Last Updated on STN: 20020123
Entered Medline: 20011210

AB BACKGROUND: Keratins are a multigene family of intermediate filament
proteins that are differentially expressed in specific epithelial
tissues.

To date, no type II keratins specific for the inner root sheath of the
human hair follicle have been identified. OBJECTIVES: To characterize a
novel type II keratin in mice and humans. METHODS: Gene sequences were
aligned and compared by BLAST analysis. Genomic DNA and mRNA sequences
were amplified by polymerase chain reaction (PCR) and confirmed by direct
sequencing. Gene expression was analysed by reverse transcription

(RT)-PCR

in mouse and human tissues. A rabbit polyclonal antiserum was raised
against a C-terminal peptide derived from the mouse K6irs protein.

Protein

expression in murine tissues was examined by immunoblotting and
immunofluorescence. RESULTS: Analysis of human expressed **sequence**
tag (EST) data generated by the Human Genome Project
revealed a fragment of a novel cytokeratin mRNA with characteristic amino
acid substitutions in the 2B domain. No further human **ESTs** were
found in the database; however, the complete human gene was identified in
the draft genome sequence and several mouse **ESTs** were
identified, allowing assembly of the murine mRNA. Both species' mRNA
sequences and the human gene were confirmed experimentally by PCR and
direct sequencing. The human gene spans more than 16 kb of genomic DNA

and

is located in the type II keratin cluster on chromosome 12q. A
comprehensive immunohistochemical survey of expression in the adult mouse
by immunofluorescence revealed that this novel keratin is expressed only
in the inner root sheath of the hair follicle. Immunoblotting of murine
epidermal keratin extracts revealed that this protein is specific to the
anagen phase of the hair cycle, as one would expect of an inner root
sheath marker. In humans, expression of this keratin was confirmed by
RT-PCR using mRNA derived from plucked anagen hairs and epidermal biopsy
material. By this means, strong expression was detected in human hair
follicles from scalp and eyebrow. Expression was also readily detected in
human palmoplantar epidermis; however, **no expression**
was detected in face skin despite the presence of fine hairs
histologically. CONCLUSIONS: This new keratin, designated K6irs, is a
valuable histological marker for the inner root sheath of hair follicles
in mice and humans. In addition, this keratin represents a new candidate
gene for inherited structural hair defects such as loose anagen syndrome.

ACCESSION NUMBER: 2002:350917 BIOSIS
DOCUMENT NUMBER: PREV200200350917
TITLE: In silico differential display of defense-related
expressed
sequence tags from sugarcane tissues infected with
diazotrophic endophytes.
AUTHOR(S): Lambais, Marcio R. (1)
CORPORATE SOURCE: (1) Departamento de Solos e Nutricao de Plantas, ESALQ,
Universidade de Sao Paulo, Av. Padua Dias, 11, 13418-900,
Piracicaba, SP: mlambais@carpa.ciagri.usp.br Brazil
SOURCE: Genetics and Molecular Biology, (March, 2001) Vol. 24, No.
1-4, pp. 103-111. print.
ISSN: 1415-4757.
DOCUMENT TYPE: Article
LANGUAGE: English

AB The expression patterns of 277 sugarcane expressed **sequence tags (EST)**-contigs encoding putative defense-related (DR) proteins were evaluated using the Sugarcane **EST** database. The DR proteins evaluated included chitinases, beta-1,3-glucanases, phenylalanine ammonia-lyases, chalcone synthases, chalcone isomerases, isoflavone reductases, hydroxyproline-rich glycoproteins, proline-rich glycoproteins, peroxidases, catalases, superoxide dismutases, WRKY-like transcription factors and proteins involved in cell death control. Putative sugarcane WRKY proteins were compared and their phylogenetic relationships determined. A hierarchical clustering approach was used to identify DR **ESTs** with similar expression profiles in representative cDNA libraries. To identify DR **ESTs** differentially expressed in sugarcane tissues infected with *Gluconacetobacter diazotrophicus* or *Herbaspirillum rubrisubalbicans*, 179 putative DR **EST**-contigs expressed in non-infected tissues (leaves and roots) and/or infected tissues were selected and arrayed by similarity of their expression profiles. Changes in the expression levels of 124 putative DR **EST**-contigs, expressed in non-infected tissues, were evaluated in infected tissues. Approximately 42% of these **EST**-contigs showed **no expression** in infected tissues, whereas 15% and 3% showed more than 2-fold suppression in tissues infected with *G. diazotrophicus* or *H. rubrisubalbicans*, respectively. Approximately 14 and 8% of the DR **EST**-contigs evaluated showed more than 2-fold induction in tissues infected with *G. diazotrophicus* or *H. rubrisubalbicans*, respectively. The differential expression of clusters of DR genes may be important in the establishment of a compatible interaction between sugarcane and diazotrophic endophytes. It is suggested that the hierarchical clustering approach can be used on a genome-wide scale to identify genes likely involved in controlling plant-microorganism interactions.

L53 ANSWER 7 OF 17 MEDLINE DUPLICATE 5
ACCESSION NUMBER: 2000414334 MEDLINE
DOCUMENT NUMBER: 20405050 PubMed ID: 10950117
TITLE: Differentially expressed genes in two LNCaP prostate
cancer
cell lines reflecting changes during prostate cancer
progression.
AUTHOR: Vaarala M H; Porvari K; Kyllonen A; Vihko P
CORPORATE SOURCE: Biocenter Oulu, World Health Organization Collaborating
Centre for Research on Reproductive Health, Finland.
SOURCE: LABORATORY INVESTIGATION, (2000 Aug) 80 (8) 1259-68.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200008
ENTRY DATE: Entered STN: 20000907
Last Updated on STN: 20000907
Entered Medline: 20000831

AB Prostate cancer tends to become transformed to androgen-independent disease over time when treated by androgen-deprivation therapy. We used two variants of the human prostate cancer cell line LNCaP to study gene expression differences during prostate cancer progression to androgen-independent disease. Production of prostate-specific antigen was regarded as a marker of androgen-dependence and loss of prostate-specific antigen was regarded as a marker of androgen-independence. mRNA from both cell lines was used for cDNA microarray screening. Differential expression

of several genes was confirmed by Northern blotting. Monoamine oxidase A, an Expressed Sequence Tag (EST) similar to rat P044, and EST AA412049 were highly overexpressed in androgen-dependent LNCaP cells. Tissue-type plasminogen activator, interferon-inducible protein p78 (MxB), an EST similar to galectin-1, follistatin, fatty acid-binding protein 5, EST AA609749, annexin I, the interferon-inducible gene 1-8U, and phospholipase

D1 were highly overexpressed in androgen-independent LNCaP cells. All studied genes had low or no expression in PC-3 cells.

The EST similar to rat P044, the EST similar to galectin-1, follistatin, annexin I, and the interferon-inducible gene 1-8U

were also expressed in benign prostatic hyperplasia tissue. The Y-linked ribosomal protein S4, Mat-8, and EST AA307912 were highly expressed in benign prostatic hyperplasia tissue. Additionally, both hybridization of differential expression in Northern blots and in situ hybridization were carried out for monoamine oxidase A, the EST similar to rat P044, the EST similar to galectin-1, fatty acid-binding protein 5, and the interferon-inducible gene 1-8U. We identified several potential prostate cancer markers, indicating that the method used is a useful tool for the screening of cancer markers, but other methods, such as in situ hybridization, are needed to further investigate the observations.

L53 ANSWER 8 OF 17

MEDLINE

ACCESSION NUMBER: 2000189213 MEDLINE

DOCUMENT NUMBER: 20189213 PubMed ID: 10726679

TITLE: RNA differential display of scarless wound healing in fetal

subunit rabbit indicates downregulation of a CCT chaperonin

and upregulation of a glycophorin-like gene transcript.

AUTHOR: Darden D L; Hu F Z; Ehrlich M D; Gorry M C; Dressman D; Li H S; Whitcomb D C; Hebda P A; Dohar J E; Ehrlich G D

CORPORATE SOURCE: Department of Pathology, Center for Genomic Sciences, University of Pittsburgh School of Medicine, PA, USA.

CONTRACT NUMBER: DC02148 (NIDCD)
DC02398 (NIDCD)
DC02697 (NIDCD)

SOURCE: +
JOURNAL OF PEDIATRIC SURGERY, (2000 Mar) 35 (3) 406-19.
Ref: 47

JOURNAL code: 0052631. ISSN: 0022-3468.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF023467; GENBANK-AF023469; GENBANK-M12857
ENTRY MONTH: 200004
ENTRY DATE: Entered STN: 20000413
Last Updated on STN: 20000413
Entered Medline: 20000404

AB BACKGROUND/PURPOSE: Scars form as wounds heal in adult organisms. In addition to disrupting cosmetic appearance, scar tissue can cause significant morbidity, and even death if it blocks vital organ function. Previous work has established that fetal wounds, especially in early to midgestation, can heal without scarring. Because such inherent physiological mechanisms ultimately are under genetic control, a study was initiated to elucidate the differences in gene expression that produce scarless wound healing in the mammalian fetus but scarring in postnatal wounds. Reverse transcription polymerase chain reaction (RT-PCR) differential display (DD) was used to detect differentially expressed mRNA transcripts in a rabbit model of wound healing. METHODS: Adult and 21-day fetal full-thickness rabbit skin specimens from wounded and unwounded sites were harvested 12 hours postwounding. RNA extracted from the tissue was used as a template in DD reactions using anchoring and random primers to generate tissue-specific gene expression fingerprints. The over 2,000 resulting amplimers (gene transcripts) were screened for differential expression among the 4 types of specimens: fetal control (unwounded), fetal wound, adult control, and adult wound. Selected bands distinctly upregulated or downregulated in fetal wound lanes on the DD gels were excised, and the cDNA was extracted, reamplified, cloned into vectors, and sequenced. DD results were confirmed by limiting-dilution RT-PCR using sequence-specific primers. RESULTS: Differential display (DD) showed 22 amplimers that were significantly upregulated in all fetal wound samples as compared with little or **no expression** in fetal control, adult control, or adult wound tissues. Conversely, 5 transcripts were downregulated in the fetal wound specimens but highly expressed in the 3 comparison tissues. Reamplification of selected transcripts by PCR, followed by cloning and DNA sequencing, yielded 7 distinct sequences, each representing a gene expressed differently in fetal wound than in the other 3 tissues. A transcript that was downregulated in fetal wound showed very high sequence homology to part of the human gene for the eta subunit of the hetero-oligomeric particle CCT (the chaperonin containing T-complex polypeptide 1 or TCP-1). An upregulated amplimer showed significant DNA sequence homology to glycophorins A and B. One sequence was identified as 28S rRNA. The remaining 4 candidate sequences showed no significant homology to known genes, but 1 had high homology to expressed **sequence tags** of unknown function. CONCLUSIONS: With careful experimental design and proper controls and verifications, differential display of RNA expression is a potentially powerful method of finding genes that specifically regulate a particular physiological process such as fetal wound healing. No a priori knowledge of what genes might be involved, or why, is necessary. This study indicates that downregulation of a gene that codes for a chaperonin subunit and

upregulation of several other genes may be involved in the striking scarless character of wound healing in the mammalian fetus. Results suggest the hypothesis that downregulation of the CCT chaperonin in fetal wound may inhibit the formation of myofibroblasts, a cell type that correlates highly with scarring in postnatal wound healing, by preventing the folding of sufficient alpha-smooth muscle actin to form the stress fibers characteristic of these cells.

L53 ANSWER 9 OF 17 MEDLINE

ACCESSION NUMBER: 2000456215 MEDLINE

DOCUMENT NUMBER: 20392318 PubMed ID: 10932001

TITLE: Molecular cloning of a novel gene located on chromosome 3p25.3 and an analysis of its expression in nasopharyngeal carcinoma.

AUTHOR: Xie Y; Deng L; Jiang N; Zhan F; Cao L; Qiu Y; Tang X; Li G
CORPORATE SOURCE: Cancer Research Institute, Hunan Medical University, Changsha, Hunan, P. R. China.

SOURCE: CHUNG-HUA I HSUEH I CHUAN HSUEH TSA CHIH, (2000 Aug) 17
(4)

225-8.

Journal code: 9425197. ISSN: 1003-9406.

PUB. COUNTRY: China

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: Chinese

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200009

ENTRY DATE: Entered STN: 20001005

Last Updated on STN: 20001005

Entered Medline: 20000925

AB OBJECTIVE: To obtain the novel genes associated with human nasopharyngeal carcinoma (NPC) on chromosome 3p24-26. METHODS: Twenty epithelial-derived expressed **sequence tags (EST)** were selected from chromosome 3p24-26 where loss of heterozygosity (LOH) frequently occurs in NPC tissues. Primers were designed based on the sequences of these **ESTs**. RT-PCR was used to amplify their corresponding cDNA fragments from NPC cell line HNE1 and primary cultures of normal nasopharyngeal epithelial cells. The differential expression of two **ESTs**, T93093 and R41598, was confirmed by Northern blot. Then, expression of **EST** T93093 was further detected in 7 normal nasopharyngeal and 19 NPC biopsies. cDNA library screening was used to

get its full cDNA sequence and the sequence of this novel gene was analyzed by

bioinformatics. RESULTS: Thirteen **ESTs** (T62511, N39155, N68660, R61275, T95314, R06143, H52697, H66521, AA128685, AA284537, N52379, AA054180, and H98090) showed the similar expression level and 5 **ESTs** (R00732, R07573, R98052, H91759, H17566) showed **no expression** in both types of cells. **EST** T93093 was down-expressed, whereas **EST** R41598 up-expressed in NPC HNE1 cells. The **EST** T93093 was also found to be down-expressed in 26.3% (5/19) of NPC biopsies. The full length cDNA of this gene was obtained and named NAG-7, which is located at chromosome 3p25.3. Its 1677 bp full length cDNA has a potential open reading frame (ORF) predicting a 94 amino acid protein with a molecular weight of 11023.87 Dalton. Bioinformatics analysis of the NAG-7 gene shows that it is a

transmembrane

protein containing a protein kinase C (PKC) phosphorylation site and a myristyl site. It has no significant homology to any reported genes in database of GenBank (AF086709). CONCLUSION: NAG-7 is a novel gene down-expressed in NPC, which may be involved in the development of NPC.

L53 ANSWER 10 OF 17 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2000:478547 BIOSIS

DOCUMENT NUMBER: PREV200000478547

TITLE: Molecular cloning and characterization of a plant
homologue

AUTHOR(S): Kimura, Seisuke; Ishibashi, Toyotaka; Hatanaka, Masami;
Sakakibara, Yoshikiyo; Hashimoto, Junji; Sakaguchi, Kengo
(1)

CORPORATE SOURCE: (1) Department of Applied Biological Science, Faculty of
Science and Technology, Science University of Tokyo, 2641
Yamazaki, Noda-shi, Chiba-ken, 278-8510 Japan

SOURCE: Plant Science (Shannon), (September 8, 2000) Vol. 158, No.
1-2, pp. 33-39. print.
ISSN: 0168-9452.

DOCUMENT TYPE: Article

LANGUAGE: English

SUMMARY LANGUAGE: English

AB By using the rice **EST** database, we have isolated a 2.8 kb cDNA,
termed *Oryza sativa* ORC1 (OsORC1), from rice (*O. sativa*) encoding a
protein that shows homology with the eukaryotic ORC1 proteins. Alignment
of the OsORC1 protein sequence with the sequence of ORC1 from human and
yeasts *S. cerevisiae* and *S. pombe* showed a high degree of sequence
homology (38.7, 32.9 and 35.0% identity, respectively), particularly
around the C-terminal region containing the CDC-NTP domain.

Interestingly,
the OsORC1 protein had an A + T hook-like motif, which was not present in
the human or yeast genes. Genomic analysis indicated that OsORC1 existed
as a single copy per genome. OsORC1 transcripts were expressed strongly
in

root tips and weakly in young leaves containing root apical meristem and
marginal meristem, respectively. **No expression** was
detected in the mature leaves. The level of OsORC1 expression was
significantly reduced when cell proliferation was temporarily halted by
the removal of sucrose from the growth medium. When the growth-halted
cells began to re-grow following addition of sucrose to the medium,

OsORC1
was again expressed at high levels. These results suggested that OsORC1
is
required for cell proliferation. The role of OsORC1 in plant DNA
replication will be discussed.

L53 ANSWER 11 OF 17 MEDLINE

DUPLICATE 6

ACCESSION NUMBER: 2000090242 MEDLINE

DOCUMENT NUMBER: 20090242 PubMed ID: 10626816

TITLE: CTp11, a novel member of the family of human cancer/testis
antigens.

AUTHOR: Zendman A J; Cornelissen I M; Weidle U H; Ruiter D J; van
Muijen G N

CORPORATE SOURCE: Department of Pathology, University Hospital, Nijmegen,
The

Netherlands.. H.Zendman@pathol.azn.nl
SOURCE: CANCER RESEARCH, (1999 Dec 15) 59 (24) 6223-9.
Journal code: 2984705R. ISSN: 0008-5472.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AJ238277

ENTRY MONTH: 200001

ENTRY DATE: Entered STN: 20000204

Last Updated on STN: 20000204

Entered Medline: 20000124

AB To identify new genes that may contribute to the metastatic pathway of neoplastic cells, we compared mRNA expression of the parental human melanoma cell line 1F6 and its metastatic variant 1F6m using mRNA differential display. We isolated a cDNA clone that was exclusively expressed in 1F6m. Northern blot analysis on a broader panel of human melanoma cell lines with different metastatic capacity following s.c. inoculation into nude mice demonstrated that the gene was expressed only in the most aggressive, highly metastatic cell lines, giving a band of 0.5 kb. The isolated full length cDNA clone showed an open reading frame of 97 amino acids. To study the subcellular localization of the gene product, COS-1 cells were transfected with cDNA of the gene fused to eGFP. We found the fusion protein to be exclusively present in the nucleus. A computer search showed strong homology with human genomic clones all localized on chromosome X (Xq26.3-Xq27.1) and with several expressed **sequence tags**, all from testis. Localization of the gene on chromosome X was confirmed by genomic PCR on a panel of human chromosome-specific rodent/human hybrid cell lines. Northern blotting and reverse transcription-PCR on 17 different normal human tissue samples showed that the gene was only expressed in normal testis. Reverse transcription-PCR on a great number of different human tumor cell lines showed expression in 25-30% of the melanoma and bladder carcinoma cell lines. Only 2 of 29 other tumor cell lines were positive. Nested PCR analysis of a series of fresh human melanocytic tumors demonstrated expression in 7 of 10 melanomas tested. **No expression** was seen in benign melanocytic tumors. In addition to melanoma, some malignant tumors from other histological types were also found to be positive. Based on these data, we conclude that the described gene, CTP11 (cancer/testis-associated protein of 11 kDa), is a novel member of the family of cancer/testis antigens.

L53 ANSWER 12 OF 17 MEDLINE DUPLICATE 7
ACCESSION NUMBER: 1999143102 MEDLINE
DOCUMENT NUMBER: 99143102 PubMed ID: 9988682
TITLE: Control of O-glycan branch formation. Molecular cloning of human cDNA encoding a novel beta1,6-N-acetylglucosaminyltransferase forming core 2 and core 4.
AUTHOR: Schwientek T; Nomoto M; Lavery S B; Merx G; van Kessel A G; Bennett E P; Hollingsworth M A; Clausen H
CORPORATE SOURCE: School of Dentistry, University of Copenhagen, Norre Alle 20, 2200 Copenhagen N, Denmark.
CONTRACT NUMBER: 1 RO1 CA66234 (NCI)
1RO1 CA66234 (NCI)
5 P41 RR05351 (NCRR)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1999 Feb 19) 274 (8) 4504-12.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF038650
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990326
Last Updated on STN: 20000303

Entered Medline: 19990318

AB A novel human UDP-GlcNAc:Gal/GlcNAc β 1-3GalNAc α 1 β 1, 6GlcNAc-transferase, designated C2/4GnT, was identified by BLAST analysis of expressed **sequence tags**. The sequence of C2/4GnT encoded a putative type II transmembrane protein with significant sequence similarity to human C2GnT and IGnT. Expression of the secreted form of C2/4GnT in insect cells showed that the gene product had UDP-N-acetyl- α -D-glucosamine:acceptor β 1, 6-N-acetylglucosaminyltransferase (β 1,6GlcNAc-transferase) activity. Analysis of substrate specificity revealed that the enzyme catalyzed O-glycan branch formation of the core 2 and core 4 type. NMR analyses of the product formed with core 3-para-nitrophenyl confirmed the product core 4-para-nitrophenyl. The coding region of C2/4GnT was contained in a single exon and located to chromosome 15q21.3. Northern analysis revealed a restricted expression pattern of C2/4GnT mainly in colon, kidney, pancreas, and small intestine. **No expression** of C2/4GnT was detected in brain, heart, liver, ovary, placenta, spleen, thymus, and peripheral blood leukocytes. The expression of core 2 O-glycans has been correlated with cell differentiation processes and cancer. The results confirm the predicted existence of a β 1,6GlcNAc-transferase that functions in both core 2 and core 4 O-glycan branch formation. The redundancy in β 1,6GlcNAc-transferases capable of forming core 2 O-glycans is important for understanding the mechanisms leading to specific changes in core 2 branching during cell development and malignant transformation.

L53 ANSWER 13 OF 17 MEDLINE DUPLICATE 8
ACCESSION NUMBER: 1998440830 MEDLINE
DOCUMENT NUMBER: 98440830 PubMed ID: 9753662
TITLE: Carnitine biosynthesis: identification of the cDNA encoding human gamma-butyrobetaine hydroxylase.
AUTHOR: Vaz F M; van Gool S; Ofman R; Ijlst L; Wanders R J
CORPORATE SOURCE: Department of Clinical Chemistry and Pediatrics, Academic Medical Center, University of Amsterdam, The Netherlands.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1998 Sep 18) 250 (2) 506-10.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF082868
ENTRY MONTH: 199811
ENTRY DATE: Entered STN: 19990106
Last Updated on STN: 20000303
Entered Medline: 19981105
AB gamma-Butyrobetaine hydroxylase (EC 1.14.11.1) is the last enzyme in the biosynthetic pathway of L-carnitine and catalyzes the formation of L-carnitine from gamma-butyrobetaine, a reaction dependent on alpha-ketoglutarate, Fe²⁺, and oxygen. We report the purification of the protein from rat liver to apparent homogeneity, which allowed N-terminal sequencing using Edman degradation. The obtained amino acid sequence was used to screen the expressed **sequence tag** database and led to the identification of a human cDNA containing an open reading frame of 1161 base pairs encoding a polypeptide of 387 amino acids with a predicted molecular weight of 44.7 kDa. Heterologous expression of the

open reading frame in the yeast *Saccharomyces cerevisiae* confirmed that the cDNA encodes the human gamma-butyrobetaine hydroxylase. Northern blot analysis showed gamma-butyrobetaine hydroxylase expression in kidney (high), liver (moderate), and brain (very low), while **no expression** could be detected in the other investigated tissues.

L53 ANSWER 14 OF 17 MEDLINE DUPLICATE 9
ACCESSION NUMBER: 1998054123 MEDLINE
DOCUMENT NUMBER: 98054123 PubMed ID: 9393974
TITLE: Suppression of anchorage-independent growth and matrigel invasion and delayed tumor formation by elevated expression
expression
of fibulin-1D in human fibrosarcoma-derived cell lines.
AUTHOR: Qing J; Maher V M; Tran H; Argraves W S; Dunstan R W; McCormick J J
CORPORATE SOURCE: Department of Biochemistry, The Cancer Center, Michigan State University, East Lansing 48824, USA.
CONTRACT NUMBER: AG11026 (NIA)
CA60907 (NCI)
GM42912 (NIGMS)
SOURCE: ONCOGENE, (1997 Oct) 15 (18) 2159-68.
Journal code: 8711562. ISSN: 0950-9232.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199712
ENTRY DATE: Entered STN: 19980109
Last Updated on STN: 19980109
Entered Medline: 19971223
AB Using differential display, we identified an mRNA that is markedly down-regulated in cell line 6A/SB1, derived from a fibrosarcoma formed in an athymic mouse following injection of carcinogen-transformed MSU-1.1 cells. The nontumorigenic parental cell strain, MSU-1.1, expresses high levels of this mRNA. Sequencing of the corresponding cDNA fragment revealed that it corresponded to an expressed **sequence tag**, which ultimately led to its identification as the fibulin-1D gene. Fibulin-1 is a cysteine-rich, calcium-binding extracellular matrix and plasma protein, which has four isoforms, A-D, derived from alternative
splicing. Northern and Western blotting analysis of 16 cell lines established from tumors formed in athymic mice by MSU-1.1-derived cell strains independently transformed in culture showed that 44% exhibited low
level or lack of expression of fibulin-1D mRNA and protein. In a similar analysis of 15 malignant cell lines derived from patients, 80% showed low level or **no expression**. To study the role of fibulin-1D in transformation, we transfected 6A/SB1 cells and a human fibrosarcoma-derived cell line (SHAC) with a fibulin-1D cDNA expression construct. Transfectants displaying high levels of fibulin-1D were isolated and characterized. Elevated expression of fibulin-1D led to reduced ability to form colonies in soft agar and reduced invasive potential as tested in a matrigel in vitro invasion assay. Furthermore, expression of fibulin-1D resulted in a markedly extended latency in tumor formation in athymic mice. These results indicate that low expression of fibulin-1D plays a role in tumor formation and invasion.

L53 ANSWER 15 OF 17 MEDLINE DUPLICATE 10
ACCESSION NUMBER: 97288381 MEDLINE
DOCUMENT NUMBER: 97288381 PubMed ID: 9143359
TITLE: Expression of CYP71B7, a cytochrome P450 expressed sequence

Tag from *Arabidopsis thaliana*.
 AUTHOR: Maughan J A; Nugent J H; Hallahan D L
 CORPORATE SOURCE: Biology Department, University College London, United Kingdom.
 SOURCE: ARCHIVES OF BIOCHEMISTRY AND BIOPHYSICS, (1997 May 1) 341 (1) 104-11.
 Journal code: 0372430. ISSN: 0003-9861.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-X97864
 ENTRY MONTH: 199706
 ENTRY DATE: Entered STN: 19970612
 Last Updated on STN: 19970612
 Entered Medline: 19970603

AB The systematic sequencing of anonymous cDNA clones (expressed **sequence tags** or **ESTs**) from the plant *Arabidopsis thaliana* has identified a number of cDNAs with similarity to known cytochrome P450 sequences. The partial sequence of one of these cDNAs, 5G6, indicated that it was likely to encode a full-length cytochrome P450 monooxygenase (cyt P450) sequence. In this paper we describe the complete sequence of this clone, which has been designated CYP71B7 in accordance with the nomenclature for the cyt P450 gene superfamily. The cDNA was used to determine the pattern of expression of the corresponding gene in *A. thaliana*. Northern hybridization analysis indicated that maximal expression of CYP71B7 occurred in rosette leaves. Weaker hybridizing bands were also detected by Northern analysis of RNA from roots, leaves, flowers, and siliques. **No expression** could be detected in stem tissue. Southern analysis indicated that the CYP71B7 gene was likely to exist as a single copy in the genome of *A. thaliana*. CYP71B7 was expressed episomally in yeast, and microsomes prepared from transgenic yeast exhibited a carbon monoxide difference spectrum characteristic of cyt P450. Microsomes from yeast expressing CYP71B7 were assayed for enzymatic activity with synthetic model cyt P450 substrates. Microsomes from yeast cells expressing CYP71B7 or those from control cells exhibited no detectable NADPH-supported 7-ethoxycoumarin or 7-ethoxyresorufin deethylase activities. However, in the presence of cumene hydroperoxide, activity was observed with microsomes from cells expressing CYP71B7 with 7-ethoxycoumarin as substrate. Organic hydroperoxides are well known to support cyt P450 catalysis in the absence of electrons from NADPH. The yeast microsomes contained high levels of endogenous NADPH-ferricytochrome P450 reductase (CPR) activity. The data suggest that this *A. thaliana* cyt P450, although expressed in an active form, is incapable of accepting electrons from the endogenous yeast CPR protein.

L53 ANSWER 16 OF 17 MEDLINE DUPLICATE 11
 ACCESSION NUMBER: 96207310 MEDLINE
 DOCUMENT NUMBER: 96207310 PubMed ID: 8617497
 TITLE: Regional assignment and tissue expression of twenty-three expressed sequence tags (ESTs) from human chromosome 5.
 AUTHOR: Feldblyum T V; Maglott D R; McPherson J D; Adams M; Apostol
 CORPORATE SOURCE: B L; Durkin A S; Wasmuth J J; Nierman W C
 American Type Culture Collection, 12301 Parklawn Drive, Rockville, Maryland, 20852, USA.
 SOURCE: GENOMICS, (1996 Apr 1) 33 (1) 128-30.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199606
ENTRY DATE: Entered STN: 19960620
Last Updated on STN: 19960620
Entered Medline: 19960613

AB Regional localization and expression patterns are reported for 19 expressed **sequence tags (ESTs)** from human chromosome 5, two of which were derived from the same transcript. Two of the **ESTs** correspond to genes not previously characterized in humans: a stress-activated protein kinase and nicotinamide nucleotide transhydrogenase. Expression was determined by three methods: Northern blots, PCR from tissue-specific cDNA libraries, and sequence sampling from **EST** sequencing projects. Six of the **ESTs** show **no expression**, and EST01986 appears to be expressed predominantly in the brain by all methods tested.

L53 ANSWER 17 OF 17 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1980:175539 BIOSIS
DOCUMENT NUMBER: BA69:50535
TITLE: TISSUE DISTRIBUTION AND POPULATION VARIABILITY OF
ESTERASES

IN CAVIA-APEREA.
AUTHOR(S): MONJELO L A S; CORDEIRO A R
CORPORATE SOURCE: UNIV. AMAZONAS, MANAUS, AMAZONAS, BRAZ.
SOURCE: REV BRAS GENET, (1979 (RECD 1980)) 2 (3), 211-222.
CODEN: RBGED3. ISSN: 0100-8455.
FILE SEGMENT: BA; OLD
LANGUAGE: English

AB The electrophoretic patterns of 17 esterase bands observed in starch gel were submitted to inhibition and activation tests, and their distribution in different *C. aperea* tissues was studied. At least 13 loci, 5 of which are polymorphic, could account for these zymogram patterns. The allelic frequencies of the 5 polymorphic loci were established in a sample of 96 animals from 2 sites in Dois Irmãos County, State of Rio Grande do Sul, Brazil. Six animals showed little or **no expression** of the major kidney esterases and enhancement of other bands, suggesting a compensatory change in regulation. The high frequency of homozygotes for the **Est-70** and **Est-90** silent alleles, especially in adult animals, may be due to differential selection or to regulatory phenomena.

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
19:04:09
ON 08 JUL 2002

L1 13496 S EST
L2 34 S L1(S) (NO#(W) CORRELAT?)
L3 21 DUP REM L2 (13 DUPLICATES REMOVED)
L4 3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5 1972 S L4(S) (PROTEIN OR PEPTIDE)
L6 1748 S L5(S) (EXPRESS?)
L7 775 S L6(S) DATABASE#
L8 355 DUP REM L7 (420 DUPLICATES REMOVED)
L9 96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN

L10 47 S L8(S)GENBANK
 L11 87 S L8(S) (HEART OR BONE OR BRAIN)
 L12 137 S L11 OR L9
 L13 1 S L12 AND (NO#(W)EXPRESS?)
 L14 67 S L12(S) (TRANSCRI?)
 L15 86 S L8(S)NORTHERN
 L16 50 S L1(S) (NO#(2W)CORRELAT?)
 L17 16 S L16 NOT L2
 L18 12 DUP REM L17 (4 DUPLICATES REMOVED)
 L19 54 S L1(S) (NO#(3W)CORRELAT?)
 L20 0 S L19 NOT L1
 L21 20 S L19 NOT L2
 L22 4 S L21 NOT L16

FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002

L23 13496 S EST OR (SEQUENCE(W)TAG#)
 L24 234 S L23 AND DATABASE#/TI
 L25 0 S L24 AND (NO(3W)CORRELAT?)
 L26 234 S L24(S)DATABASE#
 L27 2221 S L23(S)DATABASE#
 L28 4 S L27(S) (NO#(3W)CORRELAT?)
 L29 1174 S L23(S) (BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVA
 L30 310 S L29(S)NORTHERN
 L31 133 S L30 AND DATABASE#
 L32 78 DUP REM L31 (55 DUPLICATES REMOVED)
 L33 1072 S L23(S) (PREDICT? OR ANTICIPAT?)
 L34 22 S L33 AND DATABASE#/TI
 L35 13 DUP REM L34 (9 DUPLICATES REMOVED)
 L36 22 S L34(S)DATABASE#
 L37 2221 S L23(S)DATABASE#
 L38 612 S L37(S)TISSUE
 L39 58 S L38(S)PROSTATE
 L40 10 S L39 AND PREDICT?
 L41 6 DUP REM L40 (4 DUPLICATES REMOVED)
 L42 1 S L23(S) (CANNOT(3W)PREDICT)
 L43 13596 S L23 OR DBEST
 L44 6719 S L43(S)EXPRESS?
 L45 192 S L44(S)BLAST
 L46 47 S L45(S)PREDICT?
 L47 27 DUP REM L46 (20 DUPLICATES REMOVED)
 L48 2 S L43(S)RELIED
 L49 1 S L43(S) (("NOT" OR CANNOT) (W)PREDICT?)
 L50 0 S L43(S) (CANNOT(W)ANTICIPATE)
 L51 797 S L43(S)TRANSCRIPTS
 L52 28 S L43(S) ((NO(W)EXPRESSION) OR ("NOT"(W)EXPRESSED))
 L53 17 DUP REM L52 (11 DUPLICATES REMOVED)

=> s l43 and (expression(a)pattern#)
 L54 546 L43 AND (EXPRESSION(A) PATTERN#)

=> s l54 and database#/ti
 L55 15 L54 AND DATABASE#/TI

=> dup rem l55
 PROCESSING COMPLETED FOR L55
 L56 9 DUP REM L55 (6 DUPLICATES REMOVED)

=> d ibib abs tot

L56 ANSWER 1 OF 9 MEDLINE
 ACCESSION NUMBER: 2002185034 MEDLINE

DUPLICATE 1

DOCUMENT NUMBER: 21917691 PubMed ID: 11920606
 TITLE: Identification of cancer/testis genes by **database** mining and mRNA expression analysis.
 AUTHOR: Scanlan Matthew J; Gordon Claudia M; Williamson Barbara; Lee Sang-Yull; Chen Yao-Tseng; Stockert Elisabeth; Jungbluth Achim; Ritter Gerd; Jager Dirk; Jager Elke; Knuth Alexander; Old Lloyd J
 CORPORATE SOURCE: Ludwig Institute for Cancer Research, New York Branch at Memorial Sloan-Kettering Cancer Center, New York, NY 10021, USA.. scanlanm@mskcc.org
 SOURCE: INTERNATIONAL JOURNAL OF CANCER, (2002 Apr 1) 98 (4) 485-92.
 Journal code: 0042124. ISSN: 0020-7136.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200205
 ENTRY DATE: Entered STN: 20020403
 Last Updated on STN: 20020511
 Entered Medline: 20020510

AB Cancer/testis (CT) antigens are immunogenic proteins expressed predominantly in gametogenic tissue and cancer; they are considered promising target molecules for cancer vaccines. The identification of new CT genes is essential to the development of polyvalent cancer vaccines designed to overcome tumor heterogeneity and antigen loss. In the current study, a search for new CT genes was conducted by mining the Unigene database for gene clusters that contain expressed **sequence tags** derived solely from both normal testis and tumor-derived cDNA libraries. This search identified 1,325 different cancer/testis-associated Unigene clusters. The mRNA **expression pattern** of 73 cancer/testis-associated Unigene clusters was assessed by reverse transcriptase polymerase chain reaction. Three gene products, CT15/Hs.177959, CT16/Hs.245431 and CT17/Hs.178062, were detected only in testis and in tumor tissue. CT15 is equivalent to ADAM2/fertilin-beta. CT16, an uncharacterized gene product, has homology (30-50%) to members of the GAGE gene family and is 89% identical to CT16.2/Hs.293317, indicating that CT16 and CT16.2 are members of a new GAGE gene family. The uncharacterized gene product, CT17, has homology (30%) to phospholipase A1. RT-PCR analysis showed that CT15 is expressed exclusively in renal cancer, whereas CT16 and CT17 are expressed in a range of human cancers. Real-time RT-PCR analysis of newly defined CT genes and the prototype CT antigens, MAGE-3 and NY-ESO-1, revealed low levels (less than 3% of the level detected in testis) of CT15, CT16 and NY-ESO-1 in a limited range of normal, non-gametogenic tissues. This study demonstrates the merits of database mining with respect to the identification of tissue-restricted gene products expressed in cancer.
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L56 ANSWER 2 OF 9 MEDLINE
 ACCESSION NUMBER: 2001268448 MEDLINE
 DOCUMENT NUMBER: 21108743 PubMed ID: 11165518
 TITLE: Use of mass spectrometry-derived data to annotate nucleotide and protein sequence **databases**.
 AUTHOR: Mann M; Pandey A
 CORPORATE SOURCE: Protein Interaction Laboratory (PIL), Center for

Experimental Bioinformatics, University of Southern
Denmark, Campusvej 55, DK-5230, and MDS-Protana,
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CONTRACT NUMBER: KO1 CA75447 (NCI)
SOURCE: TRENDS IN BIOCHEMICAL SCIENCES, (2001 Jan) 26 (1) 54-61.
Ref: 42
Journal code: 7610674. ISSN: 0968-0004.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010529
Last Updated on STN: 20010529
Entered Medline: 20010521

AB Mass spectrometry-based proteomic methodologies can be used to annotate both nucleotide and protein sequence databases. Because such data have to be derived from proteins, they can be used to identify coding regions of the genome as well as provide the complete primary sequence of proteins and their **expression patterns** and post-translational modifications.

L56 ANSWER 3 OF 9 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2001075345 MEDLINE
DOCUMENT NUMBER: 20566896 PubMed ID: 11114628
TITLE: Strategy for identification of novel glucose transporter family members by using internet-based genomic **databases**.
AUTHOR: Phay J E; Hussain H B; Moley J F
CORPORATE SOURCE: Washington University School of Medicine and the St Louis Veteran's Administration Medical Center, St Louis, MO, USA.
SOURCE: SURGERY, (2000 Dec) 128 (6) 946-51.
Journal code: 0417347. ISSN: 0039-6060.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 200101
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010103

AB BACKGROUND: We previously reported that medullary thyroid carcinomas and pheochromocytomas avidly take up the glucose analog fluoro-deoxyglucose on positron emission tomography but do not express any of the known human facilitative glucose transporters. We therefore hypothesized that a novel glucose transporter is responsible for glucose uptake in these tumors. METHODS: Internet-based Expressed **Sequence Tags** and high throughput genome sequence databases were screened for novel sequences homologous to the known glucose transporters. Derived clones were used to screen cDNA libraries. Sequence comparison and hydropathic analysis of the putative proteins were performed. RESULTS: We identified

2 novel genes (GLUT8 and GLUT9) that are members of the facilitative glucose transporter family. The putative GLUT8 and GLUT9 proteins have 44% and 31%

sequence identity to GLUT5 and GLUT3, respectively. Hydropathic analysis showed both have exofacial and transmembrane domains consistent with a hexose transporter. **CONCLUSIONS:** By using the Expressed **Sequence Tags** database, we identified novel members of the glucose transporter family. Further work will establish function and **expression patterns** in medullary thyroid carcinomas and pheochromocytomas. Internet-based genomic databases allow rapid screening and identification of candidate sequences of novel members of human gene families.

L56 ANSWER 4 OF 9 MEDLINE DUPLICATE 3
 ACCESSION NUMBER: 2000063237 MEDLINE
 DOCUMENT NUMBER: 20063237 PubMed ID: 10592203
 TITLE: BodyMap: a human and mouse gene expression **database**

AUTHOR: Hishiki T; Kawamoto S; Morishita S; Okubo K
 CORPORATE SOURCE: Institute for Molecular and Cellular Biology, Osaka University, 1-3 Yamadaoka, Suita, Osaka 565-0871, Japan.
 SOURCE: NUCLEIC ACIDS RESEARCH, (2000 Jan 1) 28 (1) 136-8.
 Journal code: 0411011. ISSN: 0305-1048.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200002
 ENTRY DATE: Entered STN: 20000314
 Last Updated on STN: 20000314
 Entered Medline: 20000225

AB BodyMap is a human and mouse gene expression database that has been maintained since 1993. It is based on site-directed 3'-**ESTs** collected from non-biased cDNA libraries constructed at Osaka University and contains >270 000 sequences from 60 human and 38 mouse tissues. The site-directed nature of the **sequence tags** allows unequivocal grouping of tags representing the same transcript and provides abundance information for each transcript in different parts of the body. Our collection of **ESTs** was compared periodically with other public databases for cross referencing. The histological resolution of source tissues and unique cloning strategy that minimized cloning bias enabled BodyMap to support three unique mRNA based experiments in silico. First, the recurrence information for clones in each library provides a rough estimate of the mRNA composition of each source tissue. Second, a user can search the entire data set with nucleotide sequences or keywords to assess **expression patterns** of particular genes. Third, and most important, BodyMap allows a user to select genes that have a desired **expression pattern** in humans and mice. BodyMap is accessible through the WWW at <http://bodymap.ims.u-tokyo.ac.jp>

L56 ANSWER 5 OF 9 MEDLINE
 ACCESSION NUMBER: 2000241926 MEDLINE
 DOCUMENT NUMBER: 20241926 PubMed ID: 10777660
 TITLE: Determination of X-chromosome inactivation status using X-linked expressed polymorphisms identified by **database** searching.
 AUTHOR: Kutsche R; Brown C J
 CORPORATE SOURCE: Department of Medical Genetics, University of British Columbia, Vancouver, British Columbia, V6T 1Z3, Canada.
 SOURCE: GENOMICS, (2000 Apr 1) 65 (1) 9-15.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200006
ENTRY DATE: Entered STN: 20000616
Last Updated on STN: 20000616
Entered Medline: 20000605

AB The large number of redundant sequences available in nucleotide databases provides a resource for the identification of polymorphisms. Expressed polymorphisms in X-linked genes can be used to determine the inactivation status of the genes, and polymorphisms in genes that are subject to inactivation can then be used as tools to examine X-chromosome inactivation status in heterozygous females. In this study, we have identified six new X-linked single-nucleotide polymorphisms and

determined the inactivation status of these genes by examination of **expression patterns** in female cells previously demonstrated to have skewed inactivation, as well as by analysis of somatic cell hybrids retaining the inactive human X chromosome.

Expression was seen from both alleles in females heterozygous for the RPS4X gene, confirming the previously reported expression from the inactive X chromosome. Expression of only a single allele was seen in females heterozygous for polymorphisms in the BGN, TM4SF2, ATP6S1, VBP1, and

PDHA1 genes, suggesting that these genes are subject to X-chromosome inactivation.

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L56 ANSWER 6 OF 9 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2000:39117 BIOSIS

DOCUMENT NUMBER: PREV200000039117

TITLE: The Gene Expression **Database** for mouse development.

AUTHOR(S): Begley, Dale A. (1); Baldock, R.; Bard, J.; Beal, J. (1); Corradi, J. (1); Davidson, D.; Davis, G. (1); Eppig, J. T. (1); Frazer, K. (1); Hill, D. P. (1); Kadin, J. (1); Kaufman, M.; Palazola, R. (1); Richardson, J. (1); Sasner, M. (1); Trepanier, L. (1); Ringwald, Martin (1)

CORPORATE SOURCE: (1) Jackson Laboratory, 600 Main Street, Bar Harbor, ME USA

SOURCE: Molecular Biology of the Cell, (Nov., 1999) Vol. 10, No. SUPPL., pp. 102a.

Meeting Info.: 39th Annual Meeting of the American Society for Cell Biology Washington, D.C., USA December 11-15,

1999

The American Society for Cell Biology
. ISSN: 1059-1524.

DOCUMENT TYPE: Conference

LANGUAGE: English

L56 ANSWER 7 OF 9

MEDLINE

DUPLICATE 4

ACCESSION NUMBER: 1999063661 MEDLINE

DOCUMENT NUMBER: 99063661 PubMed ID: 9847150

TITLE: The Mouse Genome **Database** (MGD): genetic and genomic information about the laboratory mouse. The Mouse Genome **Database** Group.

AUTHOR: Blake J A; Richardson J E; Davisson M T; Eppig J T

CORPORATE SOURCE: The Jackson Laboratory, 600 Main Street, Bar Harbor, ME 04609, USA.. jblake@informatics.jax.org

CONTRACT NUMBER: HG00330 (NHGRI)

SOURCE: NUCLEIC ACIDS RESEARCH, (1999 Jan 1) 27 (1) 95-8.
Journal code: 0411011. ISSN: 0305-1048.

PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199903

ENTRY DATE: Entered STN: 19990326
Last Updated on STN: 20000303
Entered Medline: 19990316

AB The Mouse Genome Database (MGD) focuses on the integration of mapping, homology, polymorphism and molecular data about the laboratory mouse. Detailed descriptions of genes including their chromosomal location, gene function, disease associations, mutant phenotypes, molecular polymorphisms and links to representative sequences including **ESTs** are integrated within MGD. The association of information from experiment to gene to genome requires careful coordination and implementation of standardized vocabularies, unique nomenclature constructions, and detailed information derived from multiple sources. This information is linked to other public databases that focus on additional information such as **expression patterns**, sequences, bibliographic details and large mapping panel data. Scientists participate in the curation of MGD data by generating the Chromosome Committee Reports, consulting on gene family nomenclature revisions, and providing descriptions of mouse strain characteristics and of new mutant phenotypes. MGD is accessible at <http://www.informatics.jax.org>

L56 ANSWER 8 OF 9 MEDLINE DUPLICATE 5

ACCESSION NUMBER: 97049974 MEDLINE

DOCUMENT NUMBER: 97049974 PubMed ID: 8894702

TITLE: Characterization of the human ABC superfamily: isolation and mapping of 21 new genes using the expressed **sequence tags database**.

AUTHOR: Allikmets R; Gerrard B; Hutchinson A; Dean M

CORPORATE SOURCE: Laboratory of Viral Carcinogenesis, National Cancer Institute, Frederick Cancer Research and Development Center, MD 21702, USA.

SOURCE: HUMAN MOLECULAR GENETICS, (1996 Oct) 5 (10) 1649-55.
Journal code: 9208958. ISSN: 0964-6906.

PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-U66672; GENBANK-U66692

ENTRY MONTH: 199702

ENTRY DATE: Entered STN: 19970219
Last Updated on STN: 19970219
Entered Medline: 19970204

AB As an approach to characterizing all human ATP-binding cassette (ABC) superfamily genes, a search of the human expressed **sequence tag (EST)** database was performed using sequences from known ABC genes. A total of 105 clones, containing sequences of potential ABC genes, were identified, representing 21 distinct genes. This brings the total number of characterized human ABC genes from 12 to 33. The new ABC genes were mapped by PCR on somatic cell and radiation hybrid panels and yeast artificial chromosomes (YACs). The genes are located on human chromosomes 1, 2, 3, 4, 6, 7, 10, 12, 13, 14, 16, 17 and X; at locations distinct from previously mapped members of the superfamily. The characterized genes display extensive diversity in sequence and

expression pattern and this information was utilized to determine potential structural, functional and evolutionary relationships to previously characterized members of the ABC superfamily.

L56 ANSWER 9 OF 9 MEDLINE DUPLICATE 6
ACCESSION NUMBER: 95284468 MEDLINE
DOCUMENT NUMBER: 95284468 PubMed ID: 7766993
TITLE: Characterization and mapping of three new mammalian ATP-binding transporter genes from an **EST database**.
AUTHOR: Allikmets R; Gerrard B; Glavac D; Ravnik-Glavac M; Jenkins N A; Gilbert D J; Copeland N G; Modi W; Dean M
CORPORATE SOURCE: Laboratory of Viral Carcinogenesis, National Cancer Institute, Frederick Cancer Research and Development Center, Maryland 21702-1201, USA.
CONTRACT NUMBER: NO-CO-74101 (NCI)
SOURCE: MAMMALIAN GENOME, (1995 Feb) 6 (2) 114-7.
Journal code: 9100916. ISSN: 0938-8990.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U18235; GENBANK-U18236; GENBANK-U18237
ENTRY MONTH: 199507
ENTRY DATE: Entered STN: 19950713
Last Updated on STN: 19950713
Entered Medline: 19950705

AB Analysis of the human expressed **sequence tag** (**EST**) database identified four clones that contain sequences of previously uncharacterized genes, members of the ATP-binding cassette (ABC) superfamily. Two new ABC genes (EST20237, 31252) are located at Chromosome (Chr) 1q42 and 1q25 respectively in humans, as determined by FISH; at locations distinct from previously mapped genes of this superfamily. Two additional clones, **EST** 600 and **EST** 1596, were found to represent different ATP-binding domains of the same gene, ABC2. This gene was localized to 9q34 in humans by FISH and to the proximal region of Chr 2 in mice by linkage analysis. All genes display extensive diversity in sequence and **expression pattern**. We present several approaches to characterizing **EST** clones and demonstrate that the analysis of **EST** clones from different tissues is a powerful approach to identify new members of important gene families. Some drawbacks of using **EST** databases, including chimerism of cDNA clones, are discussed.

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
19:04:09
ON 08 JUL 2002

L1 13496 S EST
L2 34 S L1(S) (NO#(W) CORRELAT?)
L3 21 DUP REM L2 (13 DUPLICATES REMOVED)
L4 3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5 1972 S L4(S) (PROTEIN OR PEPTIDE)
L6 1748 S L5(S) (EXPRESS?)
L7 775 S L6(S) DATABASE#
L8 355 DUP REM L7 (420 DUPLICATES REMOVED)
L9 96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN

L10 47 S L8(S)GENBANK
 L11 87 S L8(S) (HEART OR BONE OR BRAIN)
 L12 137 S L11 OR L9
 L13 1 S L12 AND (NO#(W)EXPRESS?)
 L14 67 S L12(S) (TRANSCRI?)
 L15 86 S L8(S)NORTHERN
 L16 50 S L1(S) (NO#(2W)CORRELAT?)
 L17 16 S L16 NOT L2
 L18 12 DUP REM L17 (4 DUPLICATES REMOVED)
 L19 54 S L1(S) (NO#(3W)CORRELAT?)
 L20 0 S L19 NOT L1
 L21 20 S L19 NOT L2
 L22 4 S L21 NOT L16

FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002

L23 13496 S EST OR (SEQUENCE(W)TAG#)
 L24 234 S L23 AND DATABASE#/TI
 L25 0 S L24 AND (NO(3W)CORRELAT?)
 L26 234 S L24(S)DATABASE#
 L27 2221 S L23(S)DATABASE#
 L28 4 S L27(S) (NO#(3W)CORRELAT?)
 L29 1174 S L23(S) (BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVA
 L30 310 S L29(S)NORTHERN
 L31 133 S L30 AND DATABASE#
 L32 78 DUP REM L31 (55 DUPLICATES REMOVED)
 L33 1072 S L23(S) (PREDICT? OR ANTICIPAT?)
 L34 22 S L33 AND DATABASE#/TI
 L35 13 DUP REM L34 (9 DUPLICATES REMOVED)
 L36 22 S L34(S)DATABASE#
 L37 2221 S L23(S)DATABASE#
 L38 612 S L37(S)TISSUE
 L39 58 S L38(S)PROSTATE
 L40 10 S L39 AND PREDICT?
 L41 6 DUP REM L40 (4 DUPLICATES REMOVED)
 L42 1 S L23(S) (CANNOT(3W)PREDICT)
 L43 13596 S L23 OR DBEST
 L44 6719 S L43(S)EXPRESS?
 L45 192 S L44(S)BLAST
 L46 47 S L45(S)PREDICT?
 L47 27 DUP REM L46 (20 DUPLICATES REMOVED)
 L48 2 S L43(S)RELIED
 L49 1 S L43(S) (("NOT" OR CANNOT) (W) PREDICT?)
 L50 0 S L43(S) (CANNOT(W)ANTICIPATE)
 L51 797 S L43(S)TRANSCRIPTS
 L52 28 S L43(S) ((NO(W)EXPRESSION) OR ("NOT"(W)EXPRESSED))
 L53 17 DUP REM L52 (11 DUPLICATES REMOVED)
 L54 546 S L43 AND (EXPRESSION(A)PATTERN#)
 L55 15 S L54 AND DATABASE#/TI
 L56 9 DUP REM L55 (6 DUPLICATES REMOVED)

=> s l43 and database#/ti
 L57 239 L43 AND DATABASE#/TI

=> s l57 and predict
 L58 5 L57 AND PREDICT

=> dup rem l58
 PROCESSING COMPLETED FOR L58
 L59 3 DUP REM L58 (2 DUPLICATES REMOVED)

=> d ibib abs tot

L59 ANSWER 1 OF 3 MEDLINE DUPLICATE 1

ACCESSION NUMBER: 2002081897 MEDLINE

DOCUMENT NUMBER: 21666988 PubMed ID: 11808872

TITLE: **Database** and analysis system for cDNA clones obtained from full-length enriched cDNA libraries.

AUTHOR: Nishikawa Tetsuo; Ota Toshio; Kawai Yuri; Ishii Shizuko; Saito Kaoru; Yamamoto Jun-ichi; Wakamatsu Ai; Ozawa Masashi; Suzuki Yutaka; Sugano Sumio; Isogai Takao

CORPORATE SOURCE: Helix Research Institute, Chiba, Japan.

SOURCE: In Silico Biol, (2002) 2 (1) 5-18.
Journal code: 9815902. ISSN: 1386-6338.

PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200206

ENTRY DATE: Entered STN: 20020128
Last Updated on STN: 20020623
Entered Medline: 20020621

AB We have developed an efficient sequence-analysis system and a database system for clones obtained from full-length enriched cDNA libraries made by using the oligo-capping method. We developed a semi-automatic analysis system for 5'- and 3'-end sequences. It pre-processes raw sequences (vector cut and accurate-sequence region extraction), clusters the sequences, searches for similarities through public databases, annotates completeness of clones and analyzes the ORFs in the sequences. Newly developed or improved programs are used in each step. A new program, ESTiMateFull is used to evaluate and to **predict** the sequence-fullness based on comparisons with mRNA and **EST** sequences, respectively. The ATGpr program is used to **predict** sequence-fullness based on statistical information. The combination of full-length enriched cDNA clones and ATGpr fullness prediction resulted in 70% accuracy in the specificity and the sensitivity of the fullness predictions. For the ORFs predicted by the ATGpr, the signal peptides are predicted and a motif search is performed by our new system. We also developed a program that assembles our sequences with **dbEST** sequences and developed a system to retrieve clones by the characteristics of the ORFs. As keywords, combination of various results of the analyses can be used for retrieval. And various results such as ORF features and database search results can be shown on the same screen by multiple displays. Full-length clones having interesting functions can thus be retrieved efficiently by using this system.

L59 ANSWER 2 OF 3 MEDLINE DUPLICATE 2

ACCESSION NUMBER: 2002188338 MEDLINE

DOCUMENT NUMBER: 21919610 PubMed ID: 11922602

TITLE: Establishment of a root proteome reference map for the model legume *Medicago truncatula* using the expressed **sequence tag database** for peptide mass fingerprinting.

AUTHOR: Mathesius U; Keijzers G; Natera S H; Weinman J J; Djordjevic M A; Rolfe B G

CORPORATE SOURCE: Genomic Interactions Group, Research School of Biological Sciences, Australian National University, Canberra, ACT.

SOURCE: Proteomics, (2001 Nov) 1 (11) 1424-40.
Journal code: 101092707. ISSN: 1615-9853.

PUB. COUNTRY: Germany; Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200206
ENTRY DATE: Entered STN: 20020403
Last Updated on STN: 20020614
Entered Medline: 20020610

AB We have established a proteome reference map for *Medicago truncatula* root proteins using two-dimensional gel electrophoresis combined with peptide mass fingerprinting to aid the dissection of nodulation and root developmental pathways by proteome analysis. *M. truncatula* has been chosen

as a model legume for the study of nodulation-related genes and proteins. Over 2,500 root proteins could be displayed reproducibly across an isoelectric focussing range of 4-7. We analysed 485 proteins by peptide mass fingerprinting, and 179 of those were identified by matching against the current *M. truncatula* expressed **sequence tag** (**EST**) database containing DNA sequences of approximately 105,000 **ESTs**. Matching the **EST** sequences to available plant DNA sequences by BLAST searches enabled us to **predict** protein function. The use of the **EST** database for peptide identification is discussed. The majority of identified proteins were metabolic enzymes and stress response proteins, and 44% of proteins occurred as isoforms, a result that could not have been predicted from sequencing data alone. We identified two nodulins in uninoculated root tissue, supporting evidence for a role of nodulins in normal plant development. This proteome map

will be updated continuously (<http://semele.anu.edu.au/2d/2d.html>) and will be a powerful tool for investigating the molecular mechanisms of root symbioses in legumes.

L59 ANSWER 3 OF 3 MEDLINE
ACCESSION NUMBER: 1999332695 MEDLINE
DOCUMENT NUMBER: 99332695 PubMed ID: 10404616
TITLE: Protein-coding region discovery in organisms underrepresented in **databases**.
AUTHOR: Quentin Y; Voiblet C; Martin F; Fichant G
CORPORATE SOURCE: LCB-IBSM CNRS, Marseille, France.
SOURCE: COMPUTERS AND CHEMISTRY, (1999 Jun 15) 23 (3-4) 209-17.
Journal code: 7607706. ISSN: 0097-8485.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199907
ENTRY DATE: Entered STN: 19990806
Last Updated on STN: 19990806
Entered Medline: 19990728

AB The prediction of coding sequences has received a lot of attention during the last decade. We can distinguish two kinds of methods, those that rely on training with sets of example and counter-example sequences, and those that exploit the intrinsic properties of the DNA sequences to be analyzed.

The former are generally more powerful but their domains of application are limited by the availability of a training set. The latter avoid this drawback but can only be applied to sequences that are long enough to allow computation of the statistics. Here, we present a method that fills the gap between the two approaches. A learning step is applied using a

set of sequences that are assumed to contain coding and non-coding regions, but with the boundaries of these regions unknown. A test step then uses the discriminant function obtained during the learning to **predict**

coding regions in sequences from the same organism. The learning relies upon a correspondence analysis and prediction is presented on a graphical display. The method has been evaluated on a sample of yeast sequences, and the analysis of a set of expressed **sequence tags** from the *Eucalyptus globulus*-*Pisolithus tinctorius* ectomycorrhiza illustrates the relevance of the approach in its biological context.

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
19:04:09
ON 08 JUL 2002

L1 13496 S EST
L2 34 S L1(S) (NO#(W)CORRELAT?)
L3 21 DUP REM L2 (13 DUPLICATES REMOVED)
L4 3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5 1972 S L4(S) (PROTEIN OR PEPTIDE)
L6 1748 S L5(S) (EXPRESS?)
L7 775 S L6(S)DATABASE#
L8 355 DUP REM L7 (420 DUPLICATES REMOVED)
L9 96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
L10 47 S L8(S)GENBANK
L11 87 S L8(S) (HEART OR BONE OR BRAIN)
L12 137 S L11 OR L9
L13 1 S L12 AND (NO#(W)EXPRESS?)
L14 67 S L12(S) (TRANSCRI?)
L15 86 S L8(S)NORTHERN
L16 50 S L1(S) (NO#(2W)CORRELAT?)
L17 16 S L16 NOT L2
L18 12 DUP REM L17 (4 DUPLICATES REMOVED)
L19 54 S L1(S) (NO#(3W)CORRELAT?)
L20 0 S L19 NOT L1
L21 20 S L19 NOT L2
L22 4 S L21 NOT L16

FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002

L23 13496 S EST OR (SEQUENCE(W)TAG#)
L24 234 S L23 AND DATABASE#/TI
L25 0 S L24 AND (NO(3W)CORRELAT?)
L26 234 S L24(S)DATABASE#
L27 2221 S L23(S)DATABASE#
L28 4 S L27(S) (NO#(3W)CORRELAT?)
L29 1174 S L23(S) (BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVA
L30 310 S L29(S)NORTHERN
L31 133 S L30 AND DATABASE#
L32 78 DUP REM L31 (55 DUPLICATES REMOVED)
L33 1072 S L23(S) (PREDICT? OR ANTICIPAT?)
L34 22 S L33 AND DATABASE#/TI
L35 13 DUP REM L34 (9 DUPLICATES REMOVED)
L36 22 S L34(S)DATABASE#
L37 2221 S L23(S)DATABASE#
L38 612 S L37(S)TISSUE
L39 58 S L38(S)PROSTATE
L40 10 S L39 AND PREDICT?
L41 6 DUP REM L40 (4 DUPLICATES REMOVED)
L42 1 S L23(S) (CANNOT(3W)PREDICT)
L43 13596 S L23 OR DBEST

```

L44      6719 S L43(S)EXPRESS?
L45      192 S L44(S)BLAST
L46      47 S L45(S)PREDICT?
L47      27 DUP REM L46 (20 DUPLICATES REMOVED)
L48      2 S L43(S)RELIED
L49      1 S L43(S) (("NOT" OR CANNOT) (W) PREDICT?)
L50      0 S L43(S) (CANNOT(W)ANTICIPATE)
L51      797 S L43(S)TRANSCRIPTS
L52      28 S L43(S) ((NO(W)EXPRESSION) OR ("NOT"(W)EXPRESSED))
L53      17 DUP REM L52 (11 DUPLICATES REMOVED)
L54      546 S L43 AND (EXPRESSION(A)PATTERN#)
L55      15 S L54 AND DATABASE#/TI
L56      9 DUP REM L55 (6 DUPLICATES REMOVED)
L57      239 S L43 AND DATABASE#/TI
L58      5 S L57 AND PREDICT
L59      3 DUP REM L58 (2 DUPLICATES REMOVED)

```

```

=> s s l43(s)librar?
MISSING OPERATOR S L43
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

```

```

=> s l43(s)librar?
L60      1735 L43(S) LIBRAR?

```

```

=> s l60(s)predict
L61      34 L60(S) PREDICT

```

```

=> dup rem l61
PROCESSING COMPLETED FOR L61
L62      19 DUP REM L61 (15 DUPLICATES REMOVED)

```

```

=> d ibib abs tot

```

```

L62  ANSWER 1 OF 19      MEDLINE      DUPLICATE 1
ACCESSION NUMBER: 2002081897      MEDLINE
DOCUMENT NUMBER: 21666988      PubMed ID: 11808872
TITLE: Database and analysis system for cDNA clones obtained from
full-length enriched cDNA libraries.
AUTHOR: Nishikawa Tetsuo; Ota Toshio; Kawai Yuri; Ishii Shizuko;
Saito Kaoru; Yamamoto Jun-ichi; Wakamatsu Ai; Ozawa
Masashi; Suzuki Yutaka; Sugano Sumio; Isogai Takao
CORPORATE SOURCE: Helix Research Institute, Chiba, Japan.
SOURCE: In Silico Biol, (2002) 2 (1) 5-18.
Journal code: 9815902. ISSN: 1386-6338.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200206
ENTRY DATE: Entered STN: 20020128
Last Updated on STN: 20020623
Entered Medline: 20020621

```

```

AB  We have developed an efficient sequence-analysis system and a database
system for clones obtained from full-length enriched cDNA
libraries made by using the oligo-capping method. We developed a
semi-automatic analysis system for 5'- and 3'-end sequences. It
pre-processes raw sequences (vector cut and accurate-sequence region
extraction), clusters the sequences, searches for similarities through
public databases, annotates completeness of clones and analyzes the ORFs
in the sequences. Newly developed or improved programs are used in each

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step. A new program, ESTiMateFull is used to evaluate and to **predict** the sequence-fullness based on comparisons with mRNA and **EST** sequences, respectively. The ATGpr program is used to **predict** sequence-fullness based on statistical information. The combination of full-length enriched cDNA clones and ATGpr fullness prediction resulted in 70% accuracy in the specificity and the sensitivity of the fullness predictions. For the ORFs predicted by the ATGpr, the signal peptides are predicted and a motif search is performed by our new system. We also developed a program that assembles our sequences with **dbEST** sequences and developed a system to retrieve clones by the characteristics of the ORFs. As keywords, combination of various results of the analyses can be used for retrieval. And various results such as ORF features and database search results can be shown on the same screen by multiple displays. Full-length clones having interesting functions can thus be retrieved efficiently by using this system.

L62 ANSWER 2 OF 19 MEDLINE DUPLICATE 2
 ACCESSION NUMBER: 2001495498 MEDLINE
 DOCUMENT NUMBER: 21429094 PubMed ID: 11544195
 TITLE: Identification of alternate polyadenylation sites and analysis of their tissue distribution using EST data.
 AUTHOR: Beaudoin E; Gautheret D
 CORPORATE SOURCE: Centre d'Immunologie de Marseille-Luminy, Institut National de la Sante et de la Recherche Medicale, Centre National de la Recherche Scientifique, Marseille Cedex 09, France.
 SOURCE: GENOME RESEARCH, (2001 Sep) 11 (9) 1520-6.
 Journal code: 9518021. ISSN: 1088-9051.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200110
 ENTRY DATE: Entered STN: 20010910
 Last Updated on STN: 20011008
 Entered Medline: 20011004
 AB Alternate polyadenylation affects a large fraction of higher eucaryote mRNAs, producing mature transcripts with 3' ends of variable length. This variation is poorly represented in the current transcript catalogs derived from whole genome sequences, mostly because such posttranscriptional events are not detectable directly at the DNA level. Alternate polyadenylation of an mRNA is better understood by comparison to **EST** databases. Comparing **ESTs** to mRNAs, however, is a difficult task subjected to the pitfalls of internal priming, presence of intron sequences, repeated elements, chimerical **ESTs** or matches with **EST** from paralogous genes. We present here a computer program that addresses these problems and displays **ESTs** matches to a query mRNA sequence to **predict** alternate polyadenylation and to suggest **library**-specific forms. The output highlights effective polyadenylation signals, possible sources of artifacts such as A-rich stretches in the mRNA sequences, and allows for a direct visualization of **EST libraries** using color codes. Statistical biases in the distribution of alternative mRNA forms among **EST libraries** were systematically sought. About 1450 human and 200 mouse mRNAs displayed such biases, suggesting in each case a tissue- or disease-specific regulation of polyadenylation.

L62 ANSWER 3 OF 19

MEDLINE

DUPLICATE 3

ACCESSION NUMBER: 2001323353 MEDLINE
DOCUMENT NUMBER: 21135671 PubMed ID: 11238394
TITLE: Analysis of expressed sequence tags from two starvation,
time-of-day-specific libraries of *Neurospora crassa*
reveals novel clock-controlled genes.
AUTHOR: Zhu H; Nowrousian M; Kupfer D; Colot H V; Berrocal-Tito G;
Lai H; Bell-Pedersen D; Roe B A; Loros J J; Dunlap J C
CORPORATE SOURCE: Department of Chemistry and Biochemistry, Advanced Center
for Genome Technology, University of Oklahoma, Norman,
Oklahoma 73019, USA.
CONTRACT NUMBER: MH44651 (NIMH)
R37-GM 34985 (NIGMS)
SOURCE: GENETICS, (2001 Mar) 157 (3) 1057-65.
Journal code: 0374636. ISSN: 0016-6731.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF074941; GENBANK-AF277086
ENTRY MONTH: 200106
ENTRY DATE: Entered STN: 20010611
Last Updated on STN: 20010611
Entered Medline: 20010607

AB In an effort to determine genes that are expressed in mycelial cultures
of *Neurospora crassa* over the course of the circadian day, we have sequenced
13,000 cDNA clones from two time-of-day-specific **libraries**
(morning and evening **library**) generating approximately 20,000
sequences. Contig analysis allowed the identification of 445 unique
expressed **sequence tags (ESTs)** and 986
ESTs present in multiple cDNA clones. For approximately 50% of the
sequences (710 of 1431), significant matches to sequences in the National
Center for Biotechnology Information database (of known or unknown
function) were detected. About 50% of the **ESTs** (721 of 1431)
showed no similarity to previously identified genes. We hybridized
Northern blots with probes derived from 26 clones chosen from contigs
identified by multiple cDNA clones and **EST** sequences. Using
these sequences, the representation of genes among the morning and
evening
sequences, respectively, in most cases does not reflect their expression
patterns over the course of the day. Nevertheless, we were able to
identify four new clock-controlled genes. On the basis of these data we
predict that a significant proportion of the expressed *Neurospora*
genes may be regulated by the circadian clock. The mRNA levels of all
four
genes peak in the subjective morning as is the case with previously
identified ccgs.

L62 ANSWER 4 OF 19

MEDLINE

DUPLICATE 4

ACCESSION NUMBER: 2001221832 MEDLINE
DOCUMENT NUMBER: 21210945 PubMed ID: 11311134
TITLE: Cloning, expression and localization of human BM88 shows
that it maps to chromosome 11p15.5, a region implicated in
Beckwith-Wiedemann syndrome and tumorigenesis.
AUTHOR: Gaitanou M; Buanne P; Pappa C; Georgopoulou N; Mamalaki A;
Tirone F; Matsas R
CORPORATE SOURCE: Department of Biochemistry, Hellenic Pasteur Institute,
127

SOURCE: Vassilissis Sofias Avenue, 115 21 Athens, Greece.
 BIOCHEMICAL JOURNAL, (2001 May 1) 355 (Pt 3) 715-24.
 Journal code: 2984726R. ISSN: 0264-6021.
 PUB. COUNTRY: England: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF235030; GENBANK-AF243130
 ENTRY MONTH: 200105
 ENTRY DATE: Entered STN: 20010604
 Last Updated on STN: 20010604
 Entered Medline: 20010531

AB Porcine BM88 is a neuron-specific protein that enhances neuroblastoma cell

differentiation in vitro and may be involved in neuronal differentiation in vivo. Here we report the identification, by Western blotting, of homologous proteins in human and mouse brain and the isolation of their respective cDNAs. Several human and mouse clones were identified in the **EST** database using porcine BM88 cDNA as a query. A human and a mouse **EST** clone were chosen for sequencing and were found both to **predict** a protein of 149 amino acids, with 79.9% reciprocal identity, and 76.4% and 70.7% identities to the porcine protein, respectively. This indicated that the clones corresponded to the human

and

mouse BM88 homologues. In vitro expression in a cell-free system as well as transient expression in COS7 cells yielded polypeptide products that were recognized by anti-BM88 antibodies and were identical in size to the native BM88 protein. Northern-blot analysis showed a wide distribution of the gene in human brain whereas immunohistochemistry on human brain sections demonstrated that the expression of BM88 is confined to neurons. The initial mapping assignment of human BM88 to chromosome 11p15.5, a region implicated in Beckwith-Wiedemann syndrome and tumorigenesis, was retrieved from the UniGene database maintained at the National Centre for Biotechnology Information (NCBI, Bethesda, MD, U.S.A.). We confirmed this localization by performing fluorescence in situ hybridization on BM88-positive cosmid clones isolated from a human genomic **library**. These results suggest that BM88 may be a candidate gene for genetic disorders associated with alterations at 11p15.5.

L62 ANSWER 5 OF 19 MEDLINE DUPLICATE 5
 ACCESSION NUMBER: 2001692422 MEDLINE
 DOCUMENT NUMBER: 21602807 PubMed ID: 11738710
 TITLE: Profiling the malaria genome: a gene survey of three species of malaria parasite with comparison to other apicomplexan species.
 AUTHOR: Carlton J M; Muller R; Yowell C A; Fluegge M R; Sturrock K A; Pritt J R; Vargas-Serrato E; Galinski M R; Barnwell J W;
 CORPORATE SOURCE: Mulder N; Kanapin A; Cawley S E; Hide W A; Dame J B
 Computational Biology Branch, National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, MD 20892, USA.. carlton@tigr.org
 CONTRACT NUMBER: N01-A1-65315
 SOURCE: MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (2001 Dec) 118 (2) 201-10.
 Journal code: 8006324. ISSN: 0166-6851.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals

[illegible][illegible]

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[illegible]

[illegible]

[illegible]

GENBANK-AZ522828; GENBANK-AZ522829; GENBANK-AZ522830;
 GENBANK-AZ522831; GENBANK-AZ522832; GENBANK-AZ522833;
 GENBANK-AZ522834; GENBANK-AZ522835; GENBANK-AZ522836;
 GENBANK-AZ522837; GENBANK-AZ522838; GENBANK-AZ522839;
 GENBANK-AZ522840; GENBANK-AZ522841; GENBANK-AZ522842;
 GENBANK-AZ522843; GENBANK-AZ522844; GENBANK-AZ522845;
 GENBANK-AZ522846; GENBANK-AZ522847; GENBANK-AZ522848;
 GENBANK-AZ522849; GENBANK-AZ522850; GENBANK-AZ522851;
 GENBANK-AZ522852; GENBANK-AZ522853; GENBANK-AZ522854;
 GENBANK-AZ522855; GENBANK-AZ522856; GENBANK-AZ522857;
 GENBANK-AZ522858; GENBANK-AZ522859; GENBANK-AZ522860;
 GENBANK-AZ522861; GENBANK-AZ522862; GENBANK-AZ522863;
 GENBANK-AZ522864; GENBANK-AZ522865; GENBANK-AZ522866;
 GENBANK-AZ522867; GENBANK-AZ522868; GENBANK-AZ522869;
 GENBANK-AZ522870; GENBANK-AZ522871; GENBANK-AZ522872;
 GENBANK-AZ522873; GENBANK-AZ522874; GENBANK-AZ522875;
 GENBANK-AZ522876; GENBANK-AZ522877; GENBANK-AZ522878;
 GENBANK-AZ522879; GENBANK-AZ522880; GENBANK-AZ522881;
 GENBANK-AZ522882; GENBANK-AZ522883; GENBANK-AZ522884;
 GENBANK-AZ522885; GENBANK-AZ522886; GENBANK-AZ522887;
 GENBANK-AZ522888; GENBANK-AZ522889; GENBANK-AZ522890;
 GENBANK-AZ522891; GENBANK-AZ522892; GENBANK-AZ522893;
 GENBANK-AZ522894; GENBANK-AZ522895; GENBANK-AZ522896;
 GENBANK-AZ522897; GENBANK-AZ522898; GENBANK-AZ522899;
 GENBANK-AZ522900; GENBANK-AZ522901; GENBANK-AZ522902;
 GENBANK-AZ522903; GENBANK-AZ522904; GENBANK-AZ522905;
 GENBANK-AZ522906; GENBANK-AZ522907; GENBANK-AZ522908;
 GENBANK-AZ522909; GENBANK-AZ522910; GENBANK-AZ522911;
 GENBANK-AZ522912

ENTRY MONTH:

200202

ENTRY DATE:

Entered STN: 20011213

Last Updated on STN: 20020228

Entered Medline: 20020227

AB We have undertaken the first comparative pilot gene discovery analysis of approximately 25,000 random genomic and expressed **sequence tags (ESTs)** from three species of Plasmodium, the infectious agent that causes malaria. A total of 5482 genome survey sequences (GSSs) and 5582 **ESTs** were generated from mung bean nuclease (MBN) and cDNA **libraries**, respectively, of the ANKA line of the rodent malaria parasite Plasmodium berghei, and 10,874 GSSs generated from MBN **libraries** of the Salvador I and Belem lines of Plasmodium vivax, the most geographically wide-spread human malaria pathogen. These tags, together with 2438 Plasmodium falciparum sequences present in GenBank, were used to perform first-pass assembly and transcript reconstruction, and non-redundant consensus sequence datasets created. The datasets were compared against public protein databases and more than 1000 putative new Plasmodium proteins identified based on sequence similarity. Homologs of previously characterized Plasmodium

genes

were also identified, increasing the number of P. vivax and P. berghei sequences in public databases at least 10-fold. Comparative studies with other species of Apicomplexa identified interesting homologs of possible therapeutic or diagnostic value. A gene prediction program, Phat, was

used

to **predict** probable open reading frames for proteins in all three datasets. Predicted and non-redundant BLAST-matched proteins were submitted to InterPro, an integrated database of protein domains, signatures and families, for functional classification. Thus a partial predicted proteome was created for each species. This first comparative analysis of Plasmodium protein coding sequences represents a valuable resource for further studies on the biology of this important pathogen.

L62 ANSWER 6 OF 19 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:311976 BIOSIS
DOCUMENT NUMBER: PREV200100311976
TITLE: The molecular profile of AFT024, a stem cell supporting
stromal cell line.
AUTHOR(S): Moore, Kateri A. (1); Lemischka, Ihor R. (1)
CORPORATE SOURCE: (1) Molecular Biology, Princeton University, Princeton, NJ
USA
SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 1, pp.
570a. print.
Meeting Info.: 42nd Annual Meeting of the American Society
of Hematology San Francisco, California, USA December
01-05, 2000 American Society of Hematology
. ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

AB The Hematopoietic Microenvironment (HME) provides a complex molecular
milieu that mediates and balances the self-renewal and commitment
potentials of Hematopoietic Stem Cells (HSCs) as well as stimuli of
differentiation, proliferation, and migration. We have undertaken a
comprehensive, molecular screen aimed at identifying candidate molecules
which underlie the stem cell supportive properties of a mouse fetal liver
(FL)-derived stromal cell line, AFT024. We have shown in previous studies
that these cells maintain primitive murine HSCs with long-term
competitive
repopulating ability and also human HSC activity. The hypothesis
underlying our present study is that AFT024 expresses gene-products that
act positively on HSC and those that are not expressed in non-supportive
stromal cell lines obtained from the same tissue source. To date, we have
analyzed 2495 non-redundant and informative sequences from a subtracted
cDNA **library** enriched for molecules preferentially expressed by
AFT024 cells. Collectively, 67% are novel proteins, of these, 30% are
closely homologous to expressed **sequence tags**, while
28% have no match in available databases. More extensive bioinformatic
analyses assigned the remaining 9% to known protein families and revealed
novel, predicted secreted adhesion, matrix, and cytoskeletal proteins.
Other novel proteins contain distinctive motifs that **predict**
roles as effector molecules in intracellular signaling and in
protein-protein interactions. The remaining 33% of the cDNAs are known
murine proteins or are homologs of proteins from other species. Of
interest is that approximately half of the known molecules are in protein
categories that could interact with HSCs. These include cytokines,
chemokines, adhesion molecules, proteoglycans, other matrix molecules,
and
cell surface receptors. Many of these molecules have assigned roles in
other stem cell systems, perhaps indicating conservation and redundancy
of
regulatory molecules in the microenvironments of all stem cells. We are
using available microarrays to analyze gene expression in AFT024 and in
other stromal cell lines, both HSC-supporting and non-supporting. We are
developing our own microarrays with cDNAs from the AFT024-subtracted
library and intend to expand the analysis to other
microenvironmental cell types. We believe that these types of functional
genomics approaches will lead to novel insights into the molecular
mechanisms that define the HME and stem cell microenvironments in
general.

L62 ANSWER 7 OF 19 MEDLINE
ACCESSION NUMBER: 2000133922 MEDLINE

DUPLICATE 6

DOCUMENT NUMBER: 20133922 PubMed ID: 10670462
TITLE: Genes upregulated in the human trabecular meshwork in response to elevated intraocular pressure.
AUTHOR: Gonzalez P; Epstein D L; Borrás T
CORPORATE SOURCE: Department of Ophthalmology, Duke University Medical Center, Durham, North Carolina, USA.
CONTRACT NUMBER: EY01894 (NEI)
EY11906 (NEI)
SOURCE: INVESTIGATIVE OPHTHALMOLOGY AND VISUAL SCIENCE, (2000 Feb) 41 (2) 352-61.
Journal code: 7703701. ISSN: 0146-0404.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200002
ENTRY DATE: Entered STN: 20000229
Last Updated on STN: 20000229
Entered Medline: 20000215

AB PURPOSE: To identify genes upregulated in perfused, intact human trabecular meshwork (TM) in response to elevated intraocular pressure (IOP). METHOD: Two pairs of anterior segments of normal human eyes from postmortem donors were placed in culture and perfused 24 hours at constant flow (3 microl/min). After reaching baseline, the flow of one eye from each pair was raised to obtain an incremental pressure (deltaP) of 50 mm Hg for 6 hours. The anterior segments were then quickly frozen in liquid nitrogen, and their TMs were dissected for RNA extraction. SMART cDNA **libraries** were generated from control and high-pressure human TM RNAs and hybridized to sets of identical high-density cDNA gene arrays. These arrays contained 18,376 human expressed **sequence tags (ESTs)**, corresponding to both characterized and unknown genes. Differentially expressed genes were identified by different-intensity hybridization signals and confirmed by semi-quantitative polymerase chain reaction. RESULTS: Eleven genes were found to be consistently upregulated in the human TM by elevated IOP: interleukin-6, preprotachykinin-1, secretogranin-II, cathepsin-L, stromelysin-1, thymosin-beta4, alpha-tubulin, alphaB-crystallin, glyceraldehyde-3-phosphate dehydrogenase, metallothionein and Cu/Zn superoxide dismutase. The products of these genes are involved in vascular permeability, secretion, extracellular matrix remodeling, cytoskeleton reorganization, and reactive oxygen species scavenging. CONCLUSIONS: Elevated IOP induced specific upregulation of 11 physiologically relevant genes. On the basis of their known activities, the products of each of these genes might **predict** homeostatic mechanisms similar to those involved in the regulation of blood vessel permeability. We hypothesize that similar mechanisms might be involved in regulating flow through Schlemm's Canal endothelium.

L62 ANSWER 8 OF 19

MEDLINE

DUPLICATE 7

ACCESSION NUMBER: 2000256781 MEDLINE
DOCUMENT NUMBER: 20256781 PubMed ID: 10794731
TITLE: Cloning of human Ca²⁺ homeostasis endoplasmic reticulum protein (CHERP): regulated expression of antisense cDNA depletes CHERP, inhibits intracellular Ca²⁺ mobilization and decreases cell proliferation.
AUTHOR: Laplante J M; O'Rourke F; Lu X; Fein A; Olsen A; Feinstein M B
CORPORATE SOURCE: Department of Pharmacology, The University of Connecticut Health Center, Farmington 06032, USA.

CONTRACT NUMBER: HL 18937 (NHLBI)
SOURCE: BIOCHEMICAL JOURNAL, (2000 May 15) 348 Pt 1 189-99.
Journal code: 2984726R. ISSN: 0264-6021.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U94836
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 20000728
Last Updated on STN: 20000728
Entered Medline: 20000717

AB A monoclonal antibody which blocks InsP(3)-induced Ca(2+) release from isolated endoplasmic reticulum was used to isolate a novel 4.0 kb cDNA from a human erythroleukaemia (HEL) cell cDNA expression library. A corresponding mRNA transcript of approx. 4.2 kb was present in all human cell lines and tissues examined, but cardiac and skeletal muscle

had an additional transcript of 6.4 kb. The identification in GenBank(R) of homologous expressed **sequence tags** from many tissues and organisms suggests that the gene is ubiquitously expressed in higher eukaryotes. The gene was mapped to human chromosome 19p13.1. The cDNA **predicts** a 100 kDa protein, designated Ca(2+) homoeostasis endoplasmic reticulum protein (CHERP), with two putative transmembrane domains, multiple consensus phosphorylation sites, a polyglutamine tract of 12 repeats and regions of imperfect tryptophan and histidine octa- and nona-peptide repeats. In vitro translation of the full-length cDNA produced proteins of M(r) 128000 and 100000, corresponding to protein bands detected by Western blotting of many cell types. CHERP was co-localized in HEL cells with the InsP(3) receptor by two-colour immunofluorescence. Transfection of HEL cells with antisense cDNA led to an 80% decline in CHERP within 5 days of antisense induction, with markedly decreased intracellular Ca(2+) mobilization by thrombin, decreased DNA synthesis and growth arrest, indicating that the protein

has an important function in Ca(2+) homoeostasis, growth and proliferation.

L62 ANSWER 9 OF 19 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:299307 BIOSIS

DOCUMENT NUMBER: PREV200100299307

TITLE: Overexpression of ribosomal proteins in chronic lymphocytic

leukemia identified by subtractive hybridization.

AUTHOR(S): Witzens, Mathias (1); Krackhardt, Angela M. (1); Harig, Sabine (1); Donovan, John W. (1); Gribben, John G. (1)

CORPORATE SOURCE: (1) Adult Oncology, Dana-Farber Cancer Institute, Boston, MA USA

SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 2, pp. 168b. print.

Meeting Info.: 42nd Annual Meeting of the American Society of Hematology San Francisco, California, USA December 01-05, 2000 American Society of Hematology
. ISSN: 0006-4971.

DOCUMENT TYPE: Conference

LANGUAGE: English

SUMMARY LANGUAGE: English

AB Chronic lymphocytic leukemia (CLL) is the most common form of leukemia. Although CLL is relatively indolent, it is incurable with current therapies. The idiotype can elicit an autologous T and B cell immune response. However, these responses are relatively weak and the idiotype has to be determined individually in each patient. To identify new tumor

associated antigens in B cell malignancies that could serve as a target antigen for immunotherapy, we performed an analysis of a subtracted cDNA **library**. The **library** was constructed by subtraction of mRNA from healthy B cells (driver) from mRNA of primary CLL tumor cells (tester). Tumor specific cDNA sequences were isolated by subtracting the driver cDNA from the tester cDNA. The remaining cDNA fragments were PCR amplified, cloned and sequenced. 120 sequences were analysed. As expected, we found sequences coding for MHC molecules, since driver and tester mRNA were derived from different individuals, confirming the quality of the constructed **library**. Interestingly, in the remaining tumor specific sequences 9 ribosomal proteins (S2, S6, S9, S10, S15, L12, L13, L18 and L24) were identified. In addition to their overexpression in CLL, systematic analysis of **EST** databases revealed expression of these proteins in wide panel of various human tumors, including lung, pancreatic, prostate, esophagus, renal and colon cancer as well as lymphoma. Using Northern Blot, we confirmed that the ribosomal protein S2 is overexpressed in CLL tumor cells when compared with healthy PBMC. The expression of ribosomal proteins in a broad variety of malignancies indicates an important role of these proteins in the development and maintenance of the malignant state. However, in spite of the overexpression of ribosomal proteins in CLL, the immune system does not generate a significant antitumor response. To examine whether cellular immune tolerance towards tumors expressing ribosomal proteins can be overcome, we used two independent bioinformatic algorithms to **predict** for HLA class I binding immunogenic peptides. We identified 3 decamer peptides with high prediction scores for binding to HLA-A*0201 within the 221 amino acid long open reading frame of the S2 sequence. Numerous other peptides with high prediction scores for binding to HLA-A*0201 could also be identified in the remaining ribosomal proteins. Ongoing studies are characterizing the immunogenicity of these peptides for both allogeneic and autologous CD8+ T cell responses and will determine the ability of peptide stimulated CD8+ T cells to lyse primary tumor cells that overexpress ribosomal proteins.

L62 ANSWER 10 OF 19 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 2001:290176 BIOSIS
 DOCUMENT NUMBER: PREV200100290176
 TITLE: Specific expression of a novel cytokine-like gene in human CD34+ cells.
 AUTHOR(S): Ye, Zhaohui (1); Sung, Young Kwan (1); Cheng, Linzhao (1)
 CORPORATE SOURCE: (1) Johns Hopkins Oncology Center, Baltimore, MD USA
 SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 2, pp. 142b. print.
 Meeting Info.: 42nd Annual Meeting of the American Society of Hematology San Francisco, California, USA December 01-05, 2000 American Society of Hematology
 . ISSN: 0006-4971.
 DOCUMENT TYPE: Conference
 LANGUAGE: English
 SUMMARY LANGUAGE: English
 AB To elucidate molecular mechanisms governing functional differences between human CD34+ and CD34- cells, we set up a molecular screen to identify genes that are preferentially expressed in CD34+ cells. We recently reported that in a subtracted cDNA **library** (cord blood CD34+ vs. CD34- cells), genes expressed preferentially in CD34+ cells were highly enriched (20% and 10% of the cloned gene fragments were from the c-kit and CD34 gene, respectively). Among the 73 initially sequenced gene fragments,

27 (37%) were novel, or homologous only to entries in **EST** databases (Genomics, 65-283). One of these novel/**EST** clones (C17) was found 4 times (5.5%). The C17 cDNA is 1 kb long, and encodes a protein of 136 amino acids with a putative signal peptide at its N-terminus. Transient expression in transfected human cells demonstrated that the C17 protein is indeed a secreted molecule. To date we have not found any existing molecule that shows significant homology to the amino acid sequence of the C17 gene. A secondary structure analysis **predicts** that the C17 peptide contains 4 alpha-helices, a characteristics of hematopoietic cytokines and interleukins. In order to determine functions and regulation of C17 gene, we first examined its expression profile in over 50 human tissues and many types of primary and cultured human cells. C17 expression is largely restricted to tissues associated with hematopoiesis and the blood/lymph circulation. At cellular level, C17 expression is highly restricted to CD34+ cells. By RT-PCR and Northern blot analyses, C17 gene expression was detected in human CD34+ cells from cord blood, adult bone marrow (ABM) and G-CSF mobilized peripheral blood (mPB), but not in bulk CD34- cells, PBL or marrow stromal cells. C17 gene is also expressed in sorted Thy+CD34+Lin- cells from ABM and mPB. Second, we mapped the location of C17 gene in the human genome. It is uniquely mapped to chromosome 4p15-16 where the AC133 and CD38 gene reside. Third, we obtained an upstream 129 kb genomic fragment overlapping with the C17 cDNA sequence. The proximal 1.5 kb fragment flanking sequence was first tested for its ability as a promoter to drive GFP or luciferase reporter expression. We found that the 1.5 kb fragment is functional to direct either transgene expression in transfected human cells. Since lentiviral vectors with self-inactivating (SIN) modification allow transgene expression in stably transduced cells from a non-LTR promoter, we are constructing SIN lentiviral vectors containing the C17 promoter. These vectors may allow specific expression of a transgene (C17 or MDR) in cultured and primary human CD34+ cells.

L62 ANSWER 11 OF 19 MEDLINE DUPLICATE 8
 ACCESSION NUMBER: 2000130112 MEDLINE
 DOCUMENT NUMBER: 20130112 PubMed ID: 10662543
 TITLE: A novel family of bromodomain genes.
 AUTHOR: Jones M H; Hamana N; Nezu J i; Shimane M
 CORPORATE SOURCE: Chugai Research Institute for Molecular Medicine, 153-2
 Nagai, Niihari, Ibaraki, 300-4101, Japan.. mike@cimmed.com
 SOURCE: GENOMICS, (2000 Jan 1) 63 (1) 40-5.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AB032252; GENBANK-AB032253; GENBANK-AB032254;
 GENBANK-AB032255
 ENTRY MONTH: 200004
 ENTRY DATE: Entered STN: 20000421
 Last Updated on STN: 20000421
 Entered Medline: 20000411
 AB The bromodomain is a structural motif characteristic of proteins involved in chromatin-dependent regulation of transcription. Bromodomain proteins have been identified as integral components of chromatin remodeling complexes and frequently possess histone acetyltransferase activity.
 Their

encoding genes have been identified at translocation breakpoints, and at least one, CBP, is a tumor suppressor gene. We have identified a series of novel bromodomain genes by **EST** database and cDNA library screening. Comparison of sequences for four clones indicated that they represent genes belonging to a novel bromodomain family. Full-length sequences for these genes, which are widely expressed, **predict** encoded proteins of between 1527 and 1972 amino acids. In addition to a carboxy-terminal bromodomain, an adjacent PHD finger, and a WACZ motif, at least four other conserved novel motifs are present in each protein. The genes contain regions conserved with Drosophila Acf1 and Caenorhabditis elegans ZK783.4. The novel genes, termed BAZ1A, BAZ1B, BAZ2A, and BAZ2B, localize to chromosomes 14q12-q13, 7q11-q21, 12q24.3-qter, and 2q23-q24, respectively. Conservation of multiple domains throughout these genes with Acf1 indicates that they are likely to be components of chromatin remodeling complexes.
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L62 ANSWER 12 OF 19 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:223827 BIOSIS
DOCUMENT NUMBER: PREV200200223827
TITLE: Cloning and functional characterization of a cation-Cl cotransporter interacting protein.
AUTHOR(S): Isenring, Paul (1); Gagnon, Edith (1); Caron, Luc (1)
CORPORATE SOURCE: (1) Groupe de Nephrologie de L'Hotel-Dieu de Quebec, Departement de Medecine, Faculte de Medecine, Universite Laval, Quebec, PQ Canada
SOURCE: Journal of the American Society of Nephrology, (September, 2000) Vol. 11, No. Program and Abstract Issue, pp. 30A-31A.
<http://www.jasn.org/>. print.
Meeting Info.: 33rd Annual Meeting of the American Society of Nephrology and the 2000 Renal Week Toronto, Ontario, Canada October 10-16, 2000
ISSN: 1046-6673.
DOCUMENT TYPE: Conference
LANGUAGE: English
AB The cation-Cl cotransporters (CCC) mediate the coupled movement of Na and/or K to that of Cl across the plasmalemma of animal cells. In polarized tissues, cation-Cl cotransport is involved in net transepithelial water and salt movement, and in non-polarized tissues, cation-Cl cotransport modulates the water and the electrolyte content of cells. To date, the CCC family comprises two branches of homologous membrane proteins. One branch includes the Na-K-Cl cotransporters (NKCC1 and 2) and the Na-Cl cotransporter (NCC1), and the other branch, the K-Cl cotransporters (KCC1, 2, 3, and 4). Here, we have isolated the first member of a third CCC family branch. This member was first identified in human and mouse expressed **sequence tag (EST)** databases as a 500-bp sequence homologous to a region in the carboxy-terminus of the CCCs. We isolated corresponding cDNAs from a human heart cDNA library, and the full-length clone, termed WO3.3, was found to encode a 914-residue polypeptide having a calculated molecular mass of 96.2 kDa. Overall, WO3.3 shares approx25% identity in amino acid sequence with each of the known CCCs. Sequence analyses **predict** a 12-transmembrane domain (tm) region, two N-linked glycosylation sites between tm5 and tm6, and a large intracellular carboxy-terminus containing protein kinase C phosphorylation sites. Northern blot analysis uncovers a

apprx3.7-kb transcript present in muscle, placenta, brain, and kidney. With regard to function, WO3.3 expressed either in HEK-293 cells or *Xenopus laevis* oocytes does not increase Rb-, Na- and Cl-coupled transport during 5-min or 6-hour fluxes, respectively. In the oocyte, however, WO3.3 specifically inhibits human NKCC1-mediated 86Rb flux. In addition, coimmunoprecipitation studies using lysates from WO3.3-transfected HEK-293 cells suggest a direct interaction of WO3.3 with endogenous NKCC. Thus, we have cloned and characterized the first putative heterologous CCC interacting protein (CIP) known at present. CIP1 may be part of a novel family of proteins that modifies the activity or kinetics of CCCs through heterodimer formation.

L62 ANSWER 13 OF 19 MEDLINE DUPLICATE 9
 ACCESSION NUMBER: 2000099032 MEDLINE
 DOCUMENT NUMBER: 20099032 PubMed ID: 10620048
 TITLE: Cloning and analysis of cDNAs encoding the hypusine-containing protein eIF5A of two lepidopteran insect species.
 AUTHOR: van Oers M M; van Marwijk M; Kwa M S; Vlak J M; Thomas A A
 CORPORATE SOURCE: Department of Molecular Cell Biology, University of Utrecht, The Netherlands..
 monique.vanoers@medew.viro.wau.n
 SOURCE: 1
 INSECT MOLECULAR BIOLOGY, (1999 Nov) 8 (4) 531-8.
 Journal code: 9303579. ISSN: 0962-1075.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF109730; GENBANK-AF109731
 ENTRY MONTH: 200002
 ENTRY DATE: Entered STN: 20000229
 Last Updated on STN: 20000229
 Entered Medline: 20000214
 AB Eukaryotic initiation factor eIF5A is essential for cell viability and contains a characteristic post-translational modification of a specific lysine residue into a hypusine. cDNAs with similarity to eIF5A sequences were derived from *Spodoptera exigua* and *S. frugiperda* cDNA libraries. The deduced amino acid sequences are identical for both species and predict a protein with a molecular mass of 17.5 kDa. The *Drosophila melanogaster* eIF5A cDNA sequence was retrieved from the *Drosophila* EST Project. The predicted protein is 80% similar to *Spodoptera* eIF5A. A single eIF5A gene copy is present in the *S. frugiperda* genome, which is transcribed into four different transcripts. Infection of *S. frugiperda* cells with a baculovirus resulted in a strong decline of all four transcripts already at 12 h after infection. In contrast, the eIF5A protein was fairly stable up to 48 h post infection.

L62 ANSWER 14 OF 19 MEDLINE DUPLICATE 10
 ACCESSION NUMBER: 1999403001 MEDLINE
 DOCUMENT NUMBER: 99403001 PubMed ID: 10471707
 TITLE: An exploration of the sequence of a 2.9-Mb region of the genome of *Drosophila melanogaster*: the Adh region.
 AUTHOR: Ashburner M; Misra S; Roote J; Lewis S E; Blazej R; Davis

Harvey T; Doyle C; Galle R; George R; Harris N; Hartzell G;
D; Hong L; Houston K; Hoskins R; Johnson G; Martin C;
Moshrefi A; Palazzolo M; Reese M G; Spradling A; Tsang G;
Wan K; Whitelaw K; Celniker S; +
CORPORATE SOURCE: Department of Genetics, University of Cambridge,
Cambridge,
CB2 3EH, England.. m.ashburner@gen.cam.ac.uk
CONTRACT NUMBER: P50 HG00750 (NHGRI)
SOURCE: GENETICS, (1999 Sep) 153 (1) 179-219.
Journal code: 0374636. ISSN: 0016-6731.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AE003407; GENBANK-AE003408; GENBANK-AE003409;
GENBANK-AE003410; GENBANK-AE003411; GENBANK-AE003412;
GENBANK-AE003413; GENBANK-AE003414; GENBANK-AE003415;
GENBANK-AE003416
ENTRY MONTH: 199910
ENTRY DATE: Entered STN: 20000111
Last Updated on STN: 20000111
Entered Medline: 19991028
AB A contiguous sequence of nearly 3 Mb from the genome of *Drosophila melanogaster* has been sequenced from a series of overlapping P1 and BAC clones. This region covers 69 chromosome polytene bands on chromosome arm 2L, including the genetically well-characterized "Adh region." A computational analysis of the sequence **predicts** 218 protein-coding genes, 11 tRNAs, and 17 transposable element sequences. At least 38 of the protein-coding genes are arranged in clusters of from 2 to 6 closely related genes, suggesting extensive tandem duplication. The gene density is one protein-coding gene every 13 kb; the transposable element density is one element every 171 kb. Of 73 genes in this region identified by genetic analysis, 49 have been located on the sequence; P-element insertions have been mapped to 43 genes. Ninety-five (44%) of the known and predicted genes match a *Drosophila* **EST**, and 144 (66%) have clear similarities to proteins in other organisms. Genes known to have mutant phenotypes are more likely to be represented in cDNA **libraries**, and far more likely to have products similar to proteins of other organisms, than are genes with no known mutant phenotype. Over 650 chromosome aberration breakpoints map to this chromosome region, and their nonrandom distribution on the genetic map reflects variation in gene spacing on the DNA. This is the first large-scale analysis of the genome of *D. melanogaster* at the sequence level. In addition to the direct results obtained, this analysis has allowed us to develop and test methods that will be needed to interpret the complete sequence of the genome of this species. Before beginning a Hunt, it is wise to ask someone what you are looking for before you begin looking for it. Milne 1926

L62 ANSWER 15 OF 19 MEDLINE DUPLICATE 11
ACCESSION NUMBER: 1998139902 MEDLINE
DOCUMENT NUMBER: 98139902 PubMed ID: 9473515
TITLE: Cloning and characterization of a novel human chemokine receptor.
AUTHOR: Fan P; Kyaw H; Su K; Zeng Z; Augustus M; Carter K C; Li Y
CORPORATE SOURCE: Human Genome Sciences, Inc, Rockville, Maryland 20850, USA.

SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (1998
Feb 4) 243 (1) 264-8.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U97123
ENTRY MONTH: 199803
ENTRY DATE: Entered STN: 19980326
Last Updated on STN: 20000303
Entered Medline: 19980316

AB The present study reports the identification of a human gene, HCR, which encodes a novel human chemokine receptor. The partial sequence of the HCR gene was first found in a human neutrophil cDNA library. With the use of an expressed sequence tag (EST) probe from the neutrophil library, the full length HCR cDNA was isolated. The open reading frame of HCR cDNA predicts a protein of 345 amino acids with seven transmembrane domain topography. The HCR gene exhibits good homology to human MIP-1a receptor with 43.1% amino acid identity and 64.4% amino acid similarity and also shows considerable sequence homology to other human chemokine receptors such as the MCP-3 receptor, MCP-5 receptor, and MCP-1 receptor. Northern blot analysis suggests that HCR gene is expressed abundantly in immunal tissues such as spleen, fetal liver, lymph node, and bone marrow. Strong expression was also found in human lung and heart. A chromosome mapping study indicated that HCR gene is positioned within human chromosome band Xq13. Our result suggests that HCR gene is a novel putative chemokine receptor.

L62 ANSWER 16 OF 19 MEDLINE DUPLICATE 12
ACCESSION NUMBER: 1998008921 MEDLINE
DOCUMENT NUMBER: 98008921 PubMed ID: 9344656
TITLE: Identification of two novel human putative
serine/threonine

kinases, VRK1 and VRK2, with structural similarity to vaccinia virus B1R kinase.

AUTHOR: Nezu J; Oku A; Jones M H; Shimane M
CORPORATE SOURCE: Gene Search Program, Chugai Research Institute for
Molecular Medicine, 153-2 Nagai, Niihari, Ibaraki, 300-41,
Japan.. nezuj@tk.chugai-pharm.co.jp
SOURCE: GENOMICS, (1997 Oct 15) 45 (2) 327-31.
Journal code: 8800135. ISSN: 0888-7543.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB000449; GENBANK-AB000450
ENTRY MONTH: 199802
ENTRY DATE: Entered STN: 19980224
Last Updated on STN: 19990129
Entered Medline: 19980212

AB A cDNA library enriched for human fetal-specific liver genes was constructed by suppressive subtractive hybridization. EST fls223 generated from this library was found to represent a novel putative serine/threonine (Ser/Thr) kinase. A full-length clone isolated for this gene encodes a protein of 396 amino acids. The amino acid sequence has 40% identity over 305 amino acids with the B1R Ser/Thr protein kinase of vaccinia virus. This gene has therefore been named VRK1 (vaccinia virus B1R kinase related kinase). VRK1 was also found to have sequence identity (62.0% over 481 nucleotides) to a database EST

. A full-length clone for this **EST** was isolated and sequenced. Conceptual translation **predicts** a protein of 508 amino acids that, like VRK1, has similarity to B1R kinase (38.7% identity over 300 amino acids). This gene has been named VRK2. Comparison of VRK1 with VRK2 indicates that they encode structurally related putative Ser/Thr protein kinases. Northern analysis shows that expression of both genes is widespread and elevated in highly proliferative cells, such as testis, thymus, and fetal liver. B1R kinase is reported to be essential for DNA replication of vaccinia virus. The similarity of VRK1 and VRK2 to B1R indicates that these genes may have similar functions.
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L62 ANSWER 17 OF 19 MEDLINE DUPLICATE 13
 ACCESSION NUMBER: 97480717 MEDLINE
 DOCUMENT NUMBER: 97480717 PubMed ID: 9339362
 TITLE: Cloning of GPR37, a gene located on chromosome 7 encoding a putative G-protein-coupled peptide receptor, from a human frontal brain EST library.
 AUTHOR: Marazziti D; Golini E; Gallo A; Lombardi M S; Matteoni R; Tocchini-Valentini G P
 CORPORATE SOURCE: Istituto di Biologia Cellulare, Consiglio Nazionale delle Ricerche, Rome, Italy.
 SOURCE: GENOMICS, (1997 Oct 1) 45 (1) 68-77.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-Y12476; GENBANK-Y12477
 ENTRY MONTH: 199711
 ENTRY DATE: Entered STN: 19971224
 Last Updated on STN: 20000303
 Entered Medline: 19971120
 AB A cDNA sequence encoding a putative peptide-specific G-protein-coupled receptor (GPR37) was isolated from a set of human brain frontal lobe expressed **sequence tags**. The GPR37 cDNA **predicts** a single open reading frame coding for a 613-amino-acid protein with seven hydrophobic transmembrane domains. The GPR37 genomic sequence was mapped to chromosome 7q31, and it was isolated upon screening of a chromosome 7-specific genomic **library**. The GPR37 gene spans more than 25 kb and contains two exons and a single intron which interrupts the GPR37 cDNA within the sequence encoding the presumed third transmembrane domain. Northern blot analysis with GPR37 probes revealed a main 3.8-kb mRNA and a less abundant 8-kb mRNA, both expressed in human brain tissues, particularly in corpus callosum, medulla, putamen, and caudate nucleus. The lowest level of expression was detected in cerebellum. The 3.8-kb mRNA is also less abundantly expressed in liver and placenta. Although the ligand for the putative GPR37 receptor has not been identified, its deduced amino acid sequence shows a high degree of homology (approximately 40% in the transmembrane regions) with most mammalian peptide-specific G-protein-coupled receptors and particularly with the human endothelin-B, bombesin-BB1, and bombesin-BB2 receptors.

L62 ANSWER 18 OF 19 MEDLINE DUPLICATE 14
 ACCESSION NUMBER: 96216112 MEDLINE
 DOCUMENT NUMBER: 96216112 PubMed ID: 8662638
 TITLE: Isolation of inositol 1,3,4-trisphosphate 5/6-kinase, cDNA

cloning and expression of the recombinant enzyme.

AUTHOR: Wilson M P; Majerus P W

CORPORATE SOURCE: Division of Hematology-Oncology, Washington University
School of Medicine, St. Louis, Missouri 63110, USA.

CONTRACT NUMBER: HL 07088 (NHLBI)
HL 14147 (NHLBI)
HL 16634 (NHLBI)

SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1996 May 17) 271 (20)
11904-10.
Journal code: 2985121R. ISSN: 0021-9258.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-U51336

ENTRY MONTH: 199608

ENTRY DATE: Entered STN: 19960911
Last Updated on STN: 19960911
Entered Medline: 19960829

AB Inositol 1,3,4-trisphosphate 5/6-kinase was purified 12,900-fold from calf

brain using chromatography on heparin-agarose and affinity elution with inositol hexakisphosphate. The final preparation contained proteins of 48 and 36-38 kDa. All of these proteins had the same amino-terminal sequence and were enzymatically active. The smaller species represent proteolysis products with carboxyl-terminal truncation. The Km of the enzyme for inositol 1,3,4-trisphosphate was 80 nM with a Vmax of 60 nmol of product/min/mg of protein. The amino acid sequence of the tryptic peptide HSKLLARPAGGLVGERTCNAXP matched the protein sequence encoded by a human expressed **sequence tag** clone (GB T09063) at 16 of 22 residues. The expressed **sequence tag** clone was used to screen a human fetal brain cDNA **library** to obtain a cDNA clone of 1991 base pairs (bp) that **predicts** a protein of 46 kDa. The clone encodes the amino-terminal amino acid sequence obtained from the purified calf brain preparation, suggesting that it represents its human homologue. The cDNA was expressed as a fusion protein in Escherichia coli and was found to have inositol 1,3,4-trisphosphate 5/6-kinase activity. Remarkably, both the purified calf brain and recombinant proteins produced

both inositol 1,3,4,6-tetrakisphosphate and inositol 1,3,4,5-tetrakisphosphate as products in a ratio of 2.3-5:1. This finding proves that a single kinase phosphorylates inositol in both the D5 and D6 positions. Northern blot analysis identified a transcript of 3.6 kilobases

in all tissues with the highest levels in brain. The composite cDNA isolated contains 3054 bp with a poly(A) tail, suggesting that 500-600 bp of 5' sequence remains to be identified.

L62 ANSWER 19 OF 19 MEDLINE DUPLICATE 15

ACCESSION NUMBER: 97115998 MEDLINE

DOCUMENT NUMBER: 97115998 PubMed ID: 8957090

TITLE: Molecular characterization and modular analysis of human MyD88.

AUTHOR: Hardiman G; Rock F L; Balasubramanian S; Kastelein R A; Bazan J F

CORPORATE SOURCE: Department of Molecular Biology, DNAX Research Institute, Palo Alto, California 94304-1104, USA.

SOURCE: ONCOGENE, (1996 Dec 5) 13 (11) 2467-75.
Journal code: 8711562. ISSN: 0950-9232.

PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U70451
ENTRY MONTH: 199701
ENTRY DATE: Entered STN: 19970128
Last Updated on STN: 19970128
Entered Medline: 19970113

AB MyD88 was first characterized as a myeloid differentiation primary response gene in mice, activated in M1 myeloleukemic cells following interleukin-6 (IL-6) induced growth arrest and terminal differentiation. Analysis of expressed **sequence tags (ESTs)** from activated dendritic cell **libraries** led to the indentification of cDNAs encoding the human homolog (hMyD88). The

original

description of MyD88 as a 243 aa protein may reflect a truncated mouse cDNA since the 2682 nt hMyD88 cDNA **predicts** a 296 aa cytoplasmic protein. Consistent with this proposal is the detection of a 33 kDa protein in human heart, kidney and liver tissue. The expression pattern

of

MyD88 is also more widespread than originally believed: a 2.6 kb hMyD88 mRNA species was found to be constitutively expressed in many adult human tissues; in addition MyD88 expression was observed in monocyte, T, B, NK and dendritic cells. The MyD88 protein has a modular structure composed

of

an N-terminal 'death domain' (DD) similar to the intracellular segments

of

TNF receptor 1 (TNFR1) and FAS and a C-terminal region related to the signaling domains of vertebrate interleukin-1 receptors (IL-1R) and the Drosophila morphogen Toll. This intriguing structural framework may endow MyD88 with unique signaling capabilities.

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
19:04:09
ON 08 JUL 2002

L1 13496 S EST
L2 34 S L1(S) (NO#(W) CORRELAT?)
L3 21 DUP REM L2 (13 DUPLICATES REMOVED)
L4 3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5 1972 S L4(S) (PROTEIN OR PEPTIDE)
L6 1748 S L5(S) (EXPRESS?)
L7 775 S L6(S) DATABASE#
L8 355 DUP REM L7 (420 DUPLICATES REMOVED)
L9 96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
L10 47 S L8(S) GENBANK
L11 87 S L8(S) (HEART OR BONE OR BRAIN)
L12 137 S L11 OR L9
L13 1 S L12 AND (NO#(W) EXPRESS?)
L14 67 S L12(S) (TRANSCRI?)
L15 86 S L8(S) NORTHERN
L16 50 S L1(S) (NO#(2W) CORRELAT?)
L17 16 S L16 NOT L2
L18 12 DUP REM L17 (4 DUPLICATES REMOVED)
L19 54 S L1(S) (NO#(3W) CORRELAT?)
L20 0 S L19 NOT L1
L21 20 S L19 NOT L2
L22 4 S L21 NOT L16

FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002

L23 13496 S EST OR (SEQUENCE(W)TAG#)
L24 234 S L23 AND DATABASE#/TI
L25 0 S L24 AND (NO(3W)CORRELAT?)
L26 234 S L24(S)DATABASE#
L27 2221 S L23(S)DATABASE#
L28 4 S L27(S) (NO#(3W)CORRELAT?)
L29 1174 S L23(S) (BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVA
L30 310 S L29(S)NORTHERN
L31 133 S L30 AND DATABASE#
L32 78 DUP REM L31 (55 DUPLICATES REMOVED)
L33 1072 S L23(S) (PREDICT? OR ANTICIPAT?)
L34 22 S L33 AND DATABASE#/TI
L35 13 DUP REM L34 (9 DUPLICATES REMOVED)
L36 22 S L34(S)DATABASE#
L37 2221 S L23(S)DATABASE#
L38 612 S L37(S)TISSUE
L39 58 S L38(S)PROSTATE
L40 10 S L39 AND PREDICT?
L41 6 DUP REM L40 (4 DUPLICATES REMOVED)
L42 1 S L23(S) (CANNOT(3W)PREDICT)
L43 13596 S L23 OR DBEST
L44 6719 S L43(S)EXPRESS?
L45 192 S L44(S)BLAST
L46 47 S L45(S)PREDICT?
L47 27 DUP REM L46 (20 DUPLICATES REMOVED)
L48 2 S L43(S)RELIED
L49 1 S L43(S) (("NOT" OR CANNOT) (W)PREDICT?)
L50 0 S L43(S) (CANNOT(W)ANTICIPATE)
L51 797 S L43(S)TRANSCRIPTS
L52 28 S L43(S) ((NO(W)EXPRESSION) OR ("NOT" (W)EXPRESSED))
L53 17 DUP REM L52 (11 DUPLICATES REMOVED)
L54 546 S L43 AND (EXPRESSION(A)PATTERN#)
L55 15 S L54 AND DATABASE#/TI
L56 9 DUP REM L55 (6 DUPLICATES REMOVED)
L57 239 S L43 AND DATABASE#/TI
L58 5 S L57 AND PREDICT
L59 3 DUP REM L58 (2 DUPLICATES REMOVED)
L60 1735 S L43(S)LIBRAR?
L61 34 S L60(S)PREDICT
L62 19 DUP REM L61 (15 DUPLICATES REMOVED)

=> s l43(s) (mRNA or northern or cDNA or transcript#)

L63 4276 L43(S) (MRNA OR NORTHERN OR CDNA OR TRANSCRIPT#)

=> s l63(s) (expression(a)pattern#)

L64 335 L63(S) (EXPRESSION(A) PATTERN#)

=> s l64(s) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN or heart)

L65 86 L64(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
OR HEART)

=> dup rem l65

PROCESSING COMPLETED FOR L65

L66 49 DUP REM L65 (37 DUPLICATES REMOVED)

=> d ibib abs tot

L66 ANSWER 1 OF 49

MEDLINE

ACCESSION NUMBER: 2002353498

IN-PROCESS

DOCUMENT NUMBER: 22091578 PubMed ID: 12096622
 TITLE: Mapping and expression analysis of a different expression
 cDNA fragment from lung adenocarcinoma cell line.
 AUTHOR: Fan Hong; Li Yu; Feng Hui-Chen; Lu Bing-Jie; Fu Song-Bin;
 Zhang Gui-Yin; Li Pu
 CORPORATE SOURCE: Laboratory of Medical Genetics, Ha'erbin Medical
 University, Ha'erbin 150086, China.
 SOURCE: I CHUAN HSUEH PAO. ACTA GENETICA SINICA, (2002 Jun) 29 (6)
 476-80.
 Journal code: 7900784. ISSN: 0379-4172.
 PUB. COUNTRY: China
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: Chinese
 FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
 ENTRY DATE: Entered STN: 20020705
 Last Updated on STN: 20020705

AB Lung cancer is one of the most common malignant tumors in humans. Metastasis is the basic biological feature of malignant tumors, which is the main cause of death. Molecular mechanism of metastasis is still unclear, although lots of studies have been done in tumor metastasis. To study and explore the molecular basis of metastasis in lung cancer, and isolate tumor metastasis-related genes, two human lung adenocarcinoma cell lines AGZY 83-a and Anip 973 were chosen as research materials. The Anip973 was derived from AGZY83-a, but manifested much higher metastasis potential than the parent line. Using mRNA differential display technique, an unknown cDNA fragment, OPB7-1, which is over-expressive in Anip973 cell line, was obtained. It was used as a template to isolate its corresponding cDNA through dbEST searching and PCR. To search and clone lung adenocarcinoma metastasis-related candidate gene, and to explore the molecular basis of development of lung carcinoma, differential expression of OPB7-1 cDNA fragment among 9 human lung adenocarcinoma cell lines and 12 normal human tissues were detected using cell culture, cDNA clone, Northern blot analysis and bioinformation technology. Results showed that there were significant differences in OPB7-1 expression among 9 human lung adenocarcinoma cell lines. High expression tendency was observed in Anip973 cell line with high metastasis potential, TKB-18 cell line with high invasion potential and GLC-82 cell line with low differentiation potential. Besides, a bigger fragment can be found in Anip973 cell line

on

the Northern blot hybridization. The 3.0 kb transcriptions were found in various tissues. Over-expression in heart and skeletal muscle could be observed, whereas expression in spleen, liver, kidney, placental and lung could be found except colon, thyroid gland and small intestine. These manifests indicate that OPB7-1 gene has a wide-range expression in human multiple tissues. A 1.0 kb cDNA fragment was acquired by linking up EST fragments homologous match 5' end and PCR. BLAST analysis revealed that OPB7-1 gene has extremely low sequence identity with any known genes from GenBank and any sequences from EST database. The chromosomal localization of it was determined by RH location method. The OPB7-1 fragment was localized to chromosome 1p31-34. That OPB7-1 gene has an extensive expression pattern, may be a novel tumor gene related to lung carcinoma. Further research needs to be done to obtain the full-length cDNA of OPB7-1 gene. It will be helpful to investigate the expression in lung cancer cases and other tumor tissues for further determining the function of OPB7-1 gene in development of tumor.

L66 ANSWER 2 OF 49 MEDLINE
 ACCESSION NUMBER: 2002318854 MEDLINE
 DOCUMENT NUMBER: 22041134 PubMed ID: 12045295
 TITLE: Microarray analysis of global changes in gene expression during cardiac myocyte differentiation.
 COMMENT: Comment in: Physiol Genomics. 2002;9(3):131-3
 AUTHOR: Peng Chang-Fu; Wei Yi; Levsky Jeffrey M; McDonald Thomas V;
 CORPORATE SOURCE: Childs Geoffrey; Kitsis Richard N
 Department of Medicine (Molecular Cardiology), Albert Einstein College of Medicine, Bronx, New York 10461, USA.
 CONTRACT NUMBER: R01-HL-60665 (NHLBI)
 R01-HL-61550 (NHLBI)
 R01-NS-40329 (NINDS)
 T32-GM-07491 (NIGMS)
 SOURCE: PHYSIOLOGICAL GENOMICS, (2002) 9 (3) 145-55.
 Journal code: 100894125. ISSN: 1094-8341.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200207
 ENTRY DATE: Entered STN: 20020614
 Last Updated on STN: 20020704
 Entered Medline: 20020703

AB Significant progress has been made in defining pathways that mediate the formation of the mammalian heart. Little is known, however, about the genetic program that directs the differentiation of cardiac myocytes from their precursor cells. A major hindrance to this kind of investigation has been the absence of an appropriate cell culture model of cardiac myocyte differentiation. Recently, a subline of P19 cells (P19CL6) was derived that, following dimethyl sulfoxide (DMSO) treatment, differentiate efficiently over 10 days into spontaneously beating cardiac myocytes. We demonstrate that these cells are indeed cardiac myocytes as they express cell type-specific markers and exhibit electrophysiological properties indicative of cardiac myocytes. The requirement for DMSO stimulation in this paradigm was shown to be limited to the first 4 days, suggesting that critical events in the differentiation process occur over this interval. To uncover relationships among known genes and identify novel genes that mediate cardiac myocyte differentiation, a detailed time course of changes in global gene expression was carried out using cDNA microarrays. In addition to the activation of genes encoding cardiac transcription factors and structural proteins, increases were noted in the expression of multiple known genes and expressed **sequence tags (ESTs)**. Analysis of the former suggested the involvement of a variety of signaling pathways in cardiac myocyte differentiation. The 16 **ESTs** whose expression was increased during the early, stimulus-dependent phase of cardiac myocyte differentiation may be novel regulators of this process. Thus this first report of large-scale changes in gene expression during cardiac myocyte differentiation has delineated relationships among the **expression patterns** of known genes and identified a number of novel genes that merit further study.

L66 ANSWER 3 OF 49 MEDLINE DUPLICATE 1
 ACCESSION NUMBER: 2002204654 IN-PROCESS
 DOCUMENT NUMBER: 21935106 PubMed ID: 11937755
 TITLE: Generation of kidney transcriptomes using serial analysis

of gene expression.

AUTHOR: Schelling J R; El-Meanawy M A; Barathan S; Dodig T; Iyengar S K; Sedor J R

CORPORATE SOURCE: Department of Medicine, Case Western Reserve University, Rammelkamp Center for Education and Research, MetroHealth Medical Center Campus, Cleveland, Ohio, USA.

SOURCE: EXPERIMENTAL NEPHROLOGY, (2002) 10 (2) 82-92.
Journal code: 9302239. ISSN: 1018-7782.

PUB. COUNTRY: Switzerland
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals

ENTRY DATE: Entered STN: 20020409
Last Updated on STN: 20020409

AB Chronic renal disease initiation and progression remain incompletely understood. Genomewide expression monitoring should clarify the mechanisms which cause progressive renal disease by determining how clusters of genes coordinately change their activity. Serial analysis of gene expression (SAGE) is a technique of expression profiling which permits simultaneous and quantitative analysis of 9- to 13-bp **sequence tags** that correspond to unique **mRNAs**. Key principles of the technique are use of PCR in a manner to minimize distortion and serial concatenation of tags which facilitates sequencing and permits identification of many expressed genes in a single **cDNA** molecule. Tags are extracted from many concatenated sequences, counted using software, and identified by comparison with existing gene databases. In aggregate, gene expression profiles generated from a tag library comprise a transcriptome which represents a comprehensive and quantitative profile of genes expressed at the time of analysis. These global snapshots of gene **expression patterns** can better define basic cell biology and provide insights into disease pathogenesis by simultaneously determining the net consequences of gene-gene and gene-environment interactions on expression of thousands of genes. Rather than applying a priori assumptions (i.e., hypothesis testing), transcriptome analysis is hypothesis generating and requires no prior knowledge of gene expression. SAGE **kidney** transcriptomes, from normal animals and animals with progressive **kidney** disease, are being produced and can be analyzed for novel pathogenetic mechanisms. The use of SAGE and other genomic and proteomic tools should result in a better understanding of **kidney** disease pathogenesis and in identification of new therapeutic targets.
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L66 ANSWER 4 OF 49 MEDLINE DUPLICATE 2

ACCESSION NUMBER: 2002132101 MEDLINE

DOCUMENT NUMBER: 21856794 PubMed ID: 11867260

TITLE: Digital expression profiles of the prostate androgen-response program.

AUTHOR: Clegg Nigel; Eroglu Burak; Ferguson Camari; Arnold Hugh; Moorman Alec; Nelson Peter S

CORPORATE SOURCE: Division of Human Biology, Fred Hutchinson Cancer Research Center, 1100 Fairview Avenue North, Seattle, WA 98109, USA.

CONTRACT NUMBER: CA75173 (NCI)

SOURCE: JOURNAL OF STEROID BIOCHEMISTRY AND MOLECULAR BIOLOGY, (2002 Jan) 80 (1) 13-23.
Journal code: 9015483. ISSN: 0960-0760.

PUB. COUNTRY: England: United Kingdom

Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200205
ENTRY DATE: Entered STN: 20020228
Last Updated on STN: 20020515
Entered Medline: 20020514

AB The androgen receptor (AR) and cognate ligands regulate vital aspects of **prostate** cellular growth and function including proliferation, differentiation, apoptosis, lipid metabolism, and secretory action. In addition, the AR pathway also influences pathological processes of the **prostate** such as benign prostatic hypertrophy and **prostate** carcinogenesis. The pivotal role of androgens and the AR in **prostate** biology prompted this study with the objective of identifying molecular mediators of androgen action. Our approach was designed to compare transcriptomes of the LNCaP **prostate** cancer cell line under conditions of androgen depletion and androgen stimulation by generating and comparing collections of expressed **sequence tags (ESTs)**. A total of 4400 **ESTs** were produced from LNCaP **cDNA** libraries and these **ESTs** assembled into 2486 distinct **transcripts**. Rigorous statistical analysis of the expression profiles indicated that 17 genes exhibited a high probability ($P > 0.9$) of androgen-regulated expression. **Northern** analysis confirmed that the expression of KLK3/PSA, FKBP5, KRT18, DKFZP564K247, DDX15, and HSP90 is regulated by androgen exposure. Of these, only KLK3/PSA is known to be androgen-regulated while the other genes represent new members of the androgen-response program in **prostate** epithelium. LNCaP gene expression profiles defined by two independent experiments using the serial analysis of gene expression (SAGE) method were compared with the **EST** profiles. Distinctly different **expression patterns** were produced from each dataset. These results are indicative of the sensitivity of the methods to experimental conditions and demonstrate the power and the statistical limitations of digital expression analyses.

L66 ANSWER 5 OF 49 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:372790 BIOSIS
DOCUMENT NUMBER: PREV200200372790
TITLE: Cloning and characterization of human ubiquitin binding enzyme 2 cDNA.
AUTHOR(S): Li Guangtao; Lu Hongyan; Zhou Yan; Jin Jian; Jiang Keyi; Peng Xiaozhong; Yuan Jiangang (1); Qiang Boqin
CORPORATE SOURCE: (1) National Laboratory of Medical Molecular Biology, Institute of Basic Medical Sciences, CAMS and PUMC, Chinese
SOURCE: National Human Genome Center, Beijing, 100005 China
Chinese Medical Sciences Journal, (March, 2002) Vol. 17, No. 1, pp. 7-12. print.
ISSN: 1001-9294.
DOCUMENT TYPE: Article
LANGUAGE: English
AB Objective: To clone and identify the gene encoding human ubiquitin binding enzyme 2 and study its **expression pattern**. Methods: According to the sequence of human **EST**, which is highly homologous to the mouse ubiquitin binding/conjugating enzyme (E2), primers were synthesized to screen the human fetal brain **cDNA** library. The gene was analyzed by bioinformatics technique and its **expression pattern** was studied by using multiple-tissue

Northern blot. Results: Two **cDNA** clones encoding human ubiquitin conjugating enzyme have been isolated and identified. Both containing the ubiquitin conjugating domain, the 2 **cDNA** clones are 88% identical in amino acid sequences and splicing isoforms to each other only with an exon excised to form the short sequence. They belong to a highly conserved and widely expressed E2 enzyme family. **Northern blot** shows that they are expressed exclusively in adult human **heart**, placenta, and pancreas but no **transcripts** can be detected in brain, **lung**, liver, skeletal muscle or **kidney**. Conclusions: The gene encoding human ubiquitin binding enzyme is expressed under temporal control. As a key enzyme in the degradation of proteins, ubiquitin conjugating enzymes play a central role in the expression regulation on the level of post-translation.

L66 ANSWER 6 OF 49 MEDLINE DUPLICATE 3
 ACCESSION NUMBER: 2001374577 MEDLINE
 DOCUMENT NUMBER: 21324347 PubMed ID: 11431363
 TITLE: Global analysis of gene expression in invasion by a lung cancer model.
 AUTHOR: Chen J J; Peck K; Hong T M; Yang S C; Sher Y P; Shih J Y; Wu R; Cheng J L; Roffler S R; Wu C W; Yang P C
 CORPORATE SOURCE: Department of Clinical Research, National Taiwan University
 SOURCE: Hospital, Taipei, Taiwan 100, Republic of China. CANCER RESEARCH, (2001 Jul 1) 61 (13) 5223-30. Journal code: 2984705R. ISSN: 0008-5472.
 PUB. COUNTRY: United States
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200107
 ENTRY DATE: Entered STN: 20010723
 Last Updated on STN: 20010723
 Entered Medline: 20010719

AB Metastasis is a complicated multistep process that involves interactions between cancer cells and their surrounding microenvironments. Previously, we have established a series of **lung** adenocarcinoma cell lines with varying degrees of invasiveness. Tracheal graft assay confirmed that cell lines with higher in vitro invasiveness had greater in vivo invasive potential. In this study, we used these model cell lines to identify invasion-associated genes using **cDNA** microarray with colorimetric detection. A more invasive subline, CL 1-5-F 4, derived from metastatic **lung** tumor of severe combined immunodeficient mice inoculated with CL 1-5 cells, was combined with CL 1-0, CL 1-1, and CL

1-5 in **cDNA** microarray screening. **cDNA** microarray membranes, each containing 9600 nonredundant expressed **sequence tag** clones, were used to identify differentially expressed genes in these cell lines. For statistical analysis, self-organizing map algorithm was performed to identify the **expression patterns**. Positive correlation between gene expression levels and cell line invasiveness was found in 2.9% of the 9600 putative genes. On the other hand, negative correlation was found in 3.3% of the genes. The trends of expression of some of the genes were also confirmed by **Northern** hybridization and flow cytometry. Our data demonstrated that genes related to cell adhesion, motility, angiogenesis, signal transduction, and some other expressed **sequence tag** genes may play significant roles in the metastasis process. These results substantiate the model system with which one can identify

invasion-associated genes by using **cdna** microarray and cancer cell lines of different invasiveness. This technique may allow us to explore complex interactions between multiple genes that orchestrate the process of cancer metastasis.

L66 ANSWER 7 OF 49 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 2001536214 MEDLINE
DOCUMENT NUMBER: 21467656 PubMed ID: 11583946
TITLE: Molecular signatures of sepsis: multiorgan gene expression profiles of systemic inflammation.
AUTHOR: Chinnaiyan A M; Huber-Lang M; Kumar-Sinha C; Barrette T R; Shankar-Sinha S; Sarma V J; Padgaonkar V A; Ward P A
CORPORATE SOURCE: Department of Pathology, University of Michigan Medical School, Ann Arbor, Michigan 48109-0620, USA..
arul@umich.edu
CONTRACT NUMBER: GM-29507 (NIGMS)
HL-31963 (NHLBI)
SOURCE: AMERICAN JOURNAL OF PATHOLOGY, (2001 Oct) 159 (4)
1199-209.
PUB. COUNTRY: Journal code: 0370502. ISSN: 0002-9440.
United States
Journal; Article; (JOURNAL ARTICLE)
(VALIDATION STUDIES)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20011004
Last Updated on STN: 20020122
Entered Medline: 20011204

AB During sepsis the host's system-wide response to microbial invasion seems dysregulated. Here we explore the diverse multiorgan transcriptional programs activated during systemic inflammation in a cecal ligation/puncture model of sepsis in rats. Using DNA microarrays representing 7398 genes, we examined the temporal sequence of sepsis-induced gene **expression patterns** in major organ systems including lung, liver, kidney, thymus, spleen, and brain. Although genes known to be associated with systemic inflammation were identified by our global **transcript** analysis, many genes and expressed **sequence tags** not previously linked to the septic response were also elucidated. Taken together, our results suggest activation of a highly complex transcriptional response

in individual organs of the septic animal. Several overlying themes emerged from our genome-scale analysis that includes 1) the sepsis response elicited gene expression profiles that were either organ-specific, common to more than one organ, or distinctly opposite in some organs; 2) the brain is protected from sepsis-induced gene activation relative to other organs; 3) the thymus and spleen have an interesting cohort of genes with opposing gene **expression patterns**; 4) genes with proinflammatory effects were often balanced by genes with anti-inflammatory effects (eg, interleukin-1beta/decoy receptor, xanthine oxidase/superoxide dismutase, Ca²⁺-dependent PLA₂/Ca²⁺-independent PLA₂); and 5) differential gene expression was observed in proteins responsible for preventing tissue injury and promoting homeostasis including anti-proteases (TIMP-1, Cpi-26), oxidant neutralizing enzymes (metallothionein), cytokine decoy receptors (interleukin-1RII), and tissue/vascular permeability factors (aquaporin 5, vascular endothelial growth factor). This global perspective of the sepsis response should provide a molecular framework for future research into the pathophysiology of systemic inflammation. Understanding, on a genome scale, how an

organism responds to infection, may facilitate the development of enhanced detection and treatment modalities for sepsis.

L66 ANSWER 8 OF 49 MEDLINE DUPLICATE 5
ACCESSION NUMBER: 2001228125 MEDLINE
DOCUMENT NUMBER: 21139743 PubMed ID: 11243851
TITLE: Effect of serial passage on gene expression in MC3T3-E1 preosteoblastic cells: a microarray study.
AUTHOR: Huang W; Carlsen B; Rudkin G H; Shah N; Chung C; Ishida K; Yamaguchi D T; Miller T A
CORPORATE SOURCE: Plastic Surgery Section, VA Greater Los Angeles Healthcare System, Los Angeles, California, 90073, USA.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2001 Mar16) 281 (5) 1120-6.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200104
ENTRY DATE: Entered STN: 20010502
Last Updated on STN: 20010502
Entered Medline: 20010426

AB The osteoblastic function of mouse preosteoblastic MC3T3-E1 cells, as measured by alkaline phosphatase activity and osteocalcin secretion, decreases after serial passage. To uncover genes responsible for decreased osteoblastic function in high-passage cells, we have studied passage-dependent change of gene expression in MC3T3-E1 cells. Changes in the **expression pattern** of 2000 selected genes were examined simultaneously by comparing **mRNA** levels between MC3T3-E1 cells at passage 20 and passage 60 using the **cdna** microarray analysis. Significant changes in the steady-state abundance of 27 **mRNAs** were observed in response to different passage numbers, including 17 known genes, 4 **ESTs** with homology to known genes, and 6 genes with no previously described function or homology. **Northern** blot analysis was used to verify and quantify the expression of selected genes, and revealed a significant higher level of up- and down-regulation compared to microarray data. These results indicate the existence of a significant change in gene expression in osteoblastic cells undergoing serial passages. Such changes might be responsible for a reduction in **bone** regeneration in older osteoblasts. Potential roles of selected genes in **bone** aging are discussed.
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L66 ANSWER 9 OF 49 MEDLINE DUPLICATE 6
ACCESSION NUMBER: 2001485446 MEDLINE
DOCUMENT NUMBER: 21418781 PubMed ID: 11527381
TITLE: Analysis of the mammalian talin2 gene TLN2.
AUTHOR: Monkley S J; Pritchard C A; Critchley D R
CORPORATE SOURCE: Department of Biochemistry, University of Leicester, University Road, Leicester, LE1 7RH, United Kingdom.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2001 Sep 7) 286 (5) 880-5.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals

ENTRY MONTH: 200110
ENTRY DATE: Entered STN: 20010903
Last Updated on STN: 20011015
Entered Medline: 20011011

AB We have utilised genomic and **EST** databases to assemble the sequence of the human talin2 (TLN2) gene. Talin2 protein is similar in size and sequence to talin1 throughout its length (74% identity, 86% similarity). The major differences are in (i) the size of the genes, the TLN2 gene is >200 kb compared with approximately 30 kb for TLN1 due to a difference in intron size, although intron/exon boundaries, with the exception of two, are strictly conserved; (ii) the **expression patterns**, TLN1 gives rise to an approximately 8-kb **mRNA** which is observed in all tissues, whereas TLN2 gives rise to multiple **transcripts** with the highest levels in **heart**.
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L66 ANSWER 10 OF 49 MEDLINE DUPLICATE 7

ACCESSION NUMBER: 2001699402 MEDLINE
DOCUMENT NUMBER: 21614690 PubMed ID: 11748832
TITLE: In situ hybridization screen in zebrafish for the selection of genes encoding secreted proteins.
AUTHOR: Crosier P S; Bardsley A; Horsfield J A; Krassowska A K; Lavallie E R; Collins-Racie L A; Postlethwait J H; Yan Y L;
McCoy J M; Crosier K E
CORPORATE SOURCE: Division of Molecular Medicine, Faculty of Medical and Health Sciences, University of Auckland, Auckland, New Zealand.. ps.crosier@auckland.ac.nz
SOURCE: DEVELOPMENTAL DYNAMICS, (2001 Dec) 222 (4) 637-44.
Journal code: 9201927. ISSN: 1058-8388.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200203
ENTRY DATE: Entered STN: 20011219
Last Updated on STN: 20020307
Entered Medline: 20020305

AB An in situ hybridization expression screen using a signal sequence trap system has been conducted in zebrafish to isolate **cdNAs** that encode secreted proteins. Random clones (secreted expressed **sequence tags**; sESTs) were sequenced from zebrafish embryonic (18-24 hr postfertilization) and adult **kidney** libraries. From the two RNA sources, 627 random sEST **cdNAs** were identified as being homologous or identical to known genes and 166 clones encode currently unidentified genes. The sESTs represent a broad range of enzymes and other regulatory molecules. Whole-mount in situ hybridization analysis was carried out by using antisense probes generated from 244 selected sESTs, and a range of **expression patterns** was obtained. Genetic mapping undertaken with sEST sequences demonstrated that assignment of map position was attainable by using 5' primers. The signal sequence trap system used in this work has yielded a range of **cdNAs** that encode secreted proteins and, together with analysis of patterns of expression and genetic mapping, has the potential to facilitate analysis of signaling pathways central to development and physiology.
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L66 ANSWER 11 OF 49 MEDLINE

ACCESSION NUMBER: 2001531731 MEDLINE
 DOCUMENT NUMBER: 21461573 PubMed ID: 11577827
 TITLE: Microarray-based genetics of cardiac malformations.
 AUTHOR: Miertus J; Amoroso A
 CORPORATE SOURCE: Department of Reproductive and Developmental Sciences,
 University of Trieste, Italy.
 SOURCE: ITALIAN HEART JOURNAL, (2001 Aug) 2 (8) 565-7.
 Journal code: 100909716. ISSN: 1129-471X.
 PUB. COUNTRY: Italy
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200201
 ENTRY DATE: Entered STN: 20011002
 Last Updated on STN: 20020125
 Entered Medline: 20020109

AB One of the most revolutionary approaches in human genomics is DNA
 microarray technology. Latest developments have brought this technology
 to
 a widespread use. In this paper we discuss its usefulness especially for
 the study of the genetic component in congenital **heart** disease
 as a model of multifactorial disease and the possible clinical
 applications in the near future. Malformations of the **heart** and
 blood vessels account for the largest number of human birth defects. The
 susceptibility of the **heart** to developmental anomalies reflects
 the complexity of the morphogenetic events responsible for the
heart formation. The genetics of congenital **heart**
 disease points to the existence of powerful disease modifiers. Tissue
 analysis of gene expression with **cDNA** microarrays provides a
 measure of transcriptional or posttranscriptional regulation. Large-scale
 partial sequencing of **cDNA** libraries generating expressed
sequence tags is an effective means of discovering novel
 genes and characterizing transcription patterns in different organs and
 tissues. The qualitative and quantitative analysis of genes expressed in
 cardiac tissue by means of comparison of **expression**
patterns related to the normal and to the pathological tissue may
 be of great importance for the study of cardiac pathologies. The
 variation
 in phenotypic penetrance and severity suggests that if we can identify
 high-risk individuals, a reduction in infant morbidity might be possible
 by altering environmental or maternal factors.

L66 ANSWER 12 OF 49 MEDLINE DUPLICATE 8
 ACCESSION NUMBER: 2001182376 MEDLINE
 DOCUMENT NUMBER: 21092856 PubMed ID: 11181079
 TITLE: Identification and tissue distribution of the novel human
 cytochrome P450 2S1 (CYP2S1).
 AUTHOR: Rylander T; Neve E P; Ingelman-Sundberg M; Oscarson M
 CORPORATE SOURCE: Division of Molecular Toxicology, Institute of
 Environmental Medicine, Karolinska Institutet, SE-171 77
 Stockholm, Sweden.. tove.rylander@imm.ki.se
 SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2001
 Feb 23) 281 (2) 529-35.
 Journal code: 0372516. ISSN: 0006-291X.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF335278
 ENTRY MONTH: 200103
 ENTRY DATE: Entered STN: 20010404

Last Updated on STN: 20010404

Entered Medline: 20010329

AB With the aid of the htgs and dbEST databases, a novel cytochrome P450 cDNA was found by homology searches, and the corresponding gene was identified on chromosome 19. Nested PCR was used to amplify a full-length sequence of 1515 bp. The predicted 504 amino acid sequence displays 38--49% identity with CYP2 family members and the protein was designated CYP2S1. mRNA dot blot analysis demonstrated high expression levels in trachea, lung, stomach, small intestine, and spleen. The expression pattern was confirmed by Northern blot, which also revealed a single transcript of approximately 2.4 kb. Western blot analysis, using an antiserum directed against the C-terminus of the enzyme, detected a protein in human lung with the same mobility as recombinant CYP2S1. Subcellular fractionation and immunostaining revealed that CYP2S1 was localized in the endoplasmic reticulum. We conclude that CYP2S1 represents a novel abundantly expressed human P450 with potential importance for extrahepatic xenobiotic metabolism.
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L66 ANSWER 13 OF 49 MEDLINE DUPLICATE 9
ACCESSION NUMBER: 2001235535 MEDLINE
DOCUMENT NUMBER: 21134366 PubMed ID: 11237856
TITLE: Expression pattern and localization of beta,beta-carotene 15,15'-dioxygenase in different tissues.
AUTHOR: Wyss A; Wirtz G M; Woggon W D; Brugger R; Wyss M; Friedlein
CORPORATE SOURCE: A; Riss G; Bachmann H; Hunziker W
F. Hoffmann-La Roche Ltd., Vitamins & Fine Chemicals Division, 4070 Basel, Switzerland.. adrian.wyss@roche.com
SOURCE: BIOCHEMICAL JOURNAL, (2001 Mar 15) 354 (Pt 3) 521-9.
Journal code: 2984726R. ISSN: 0264-6021.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AJ271386; GENBANK-AW278064
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010517
Last Updated on STN: 20010517
Entered Medline: 20010503

AB Beta,beta-carotene 15,15'-dioxygenase cleaves beta,beta-carotene into two molecules of retinal, and is the key enzyme in the metabolism of beta,beta-carotene to vitamin A. The enzyme has been known for more than 40 years, yet all attempts to purify the protein to homogeneity have failed. Recently, the successful cloning and sequencing of an enzyme with beta,beta-carotene 15,15'-dioxygenase activity from chicken, as well as from Drosophila, has been reported. Here, we describe in detail our attempt to enrich the chicken beta,beta-carotene 15,15'-dioxygenase to such an extent as to allow determination of partial amino acid sequences, which were then used to design degenerate oligonucleotides. Screening of a chicken duodenal expression library yielded a full-length clone containing a coding sequence of 1578 bp. Functional expression in Escherichia coli and in eukaryotic cell lines confirmed that we had cloned the first vertebrate dioxygenase that cleaves beta,beta-carotene at the central 15,15'-double bond. By performing a sequence homology search, the

cDNA sequence of the mouse homologue was found as an expressed sequence tag (EST) in the gene bank. At the amino-acid level, the degree of homology between the chicken and mouse sequences is 81%. Thus beta,beta-carotene 15,15'-dioxygenase can be considered as being an enzyme that is evolutionarily rather well conserved. We established the expression pattern of beta,beta-carotene 15,15'-dioxygenase in chicken and mouse tissues with a combination of Northern blots and in situ hybridization. The mRNA for beta,beta-carotene 15,15'-dioxygenase was localized primarily in duodenal villi, as well as in liver and in tubular structures of lung and kidney. These new findings demonstrate that beta,beta-carotene 15,15'-dioxygenase is also expressed in epithelial structures, where it serves to provide the tissue-specific vitamin A supply.

L66 ANSWER 14 OF 49 MEDLINE
ACCESSION NUMBER: 2002037162 IN-PROCESS
DOCUMENT NUMBER: 21608823 PubMed ID: 11764985
TITLE: Functional genomics of oxidant-induced lung injury.
AUTHOR: Leikauf G D; McDowell S A; Bachurski C J; Aronow B J; Gammon K; Wesselkamper S C; Hardie W; Wiest J S; Leikauf J E; Korfhagen T R; Prows D R
CORPORATE SOURCE: Department of Environmental Health, University of Cincinnati, Ohio, USA.. leikaugd@uc.edu
CONTRACT NUMBER: ES06096 (NIEHS)
ES10562 (NIEHS)
HL65213 (NHLBI)
HL65612 (NHLBI)
SOURCE: ADVANCES IN EXPERIMENTAL MEDICINE AND BIOLOGY, (2001) 500 479-87.
Journal code: 0121103. ISSN: 0065-2598.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020124
Last Updated on STN: 20020124

AB In summary, acute lung injury is a severe (>40% mortality) respiratory disease associated with numerous precipitating factors. Despite extensive research since its initial description over 30 years ago, questions remain about the basic pathophysiological mechanisms and their relationship to therapeutic strategies. Histopathology reveals surfactant disruption, epithelial perturbation and sepsis, either as initiating factors or as secondary complications, which in turn increase the expression of cytokines that sequester and activate inflammatory cells, most notably, neutrophils. Concomitant release of reactive oxygen and nitrogen species subsequently modulates endothelial function.

Together

these events orchestrate the principal clinical manifestations of the syndrome, pulmonary edema and atelectasis. To better understand the gene-environmental interactions controlling this complex process, we examined the relative sensitivity of inbred mouse strains to acute lung injury induced by ozone, ultrafine PTFE, or fine particulate NiSO₄ (0.2 microm MMAD, 15-150 microg/m³). Measuring survival time, protein and neutrophils in bronchoalveolar lavage, lung wet: dry weight, and histology, we found that these responses varied between inbred

mouse strains, and susceptibility is heritable. To assess the molecular progression of NiSO₄-induced acute lung injury, temporal

relationships of 8734 genes and expressed **sequence tags** were assessed by **cDNA** microarray analysis. Clustering of co-regulated genes (displaying similar temporal **expression patterns**) revealed the altered expression of relatively few genes. Enhanced expression occurred mainly in genes associated with oxidative stress, anti-proteolytic function, and repair of the extracellular matrix.

Concomitantly, surfactant proteins and Clara cell secretory protein **mRNA** expression decreased. Genome wide analysis of 307 mice generated from the backcross of resistant B6xA F1 with susceptible A strain identified significant linkage to a region on chromosome 6 (proposed as Aliq4) and suggestive linkages on chromosomes 1, 8, and 12. Combining of these QTLs with two additional possible modifying loci (chromosome 9 and 16) accounted for the difference in survival time noted in the A and B6 parental strains. Combining these findings with those of the microarray analysis has enabled prioritization of candidate genes. These candidates, in turn, can be directed to the **lung** epithelium in transgenic mice or abated in inducible and constitutive gene-targeted mice. Initial results are encouraging and suggest that several of these mice vary in their susceptibility to oxidant-induced **lung** injury. Thus, these combined approaches have led to new insights into functional genomics of **lung** injury and diseases.

L66 ANSWER 15 OF 49 MEDLINE DUPLICATE 10
ACCESSION NUMBER: 2001285314 MEDLINE
DOCUMENT NUMBER: 21240211 PubMed ID: 11342109
TITLE: Human Ca2+/calmodulin-dependent phosphodiesterase PDE1A: novel splice variants, their specific expression, genomic organization, and chromosomal localization.
AUTHOR: Michibata H; Yanaka N; Kanoh Y; Okumura K; Omori K
CORPORATE SOURCE: Discovery Research Laboratory, Tanabe Seiyaku Co. Ltd., 2-50 Kawagishi-2-chome, Toda, Saitama 335-8505, Japan.
SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (2001 Jan 26) 1517 (2) 278-87.
Journal code: 0217513. ISSN: 0006-3002.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB038227; GENBANK-AB038228
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010529
Last Updated on STN: 20010529
Entered Medline: 20010524

AB We report here the identification of novel human PDE1A splice variants, their tissue distribution patterns, genomic structure, and chromosomal localization of the gene. We identified one N-terminus (N3) and one C-terminus (C3) by **cDNA** library screening and **dbEST** database search. These N- and C-termini, including the reported N-termini (N1 and N2) and C-termini (C1 and C2), combined to generate nine different

PDE1A **cDNAs**. N1 and N2 are similar to the 5' ends of the bovine PDE1A proteins of 61 kDa and 59 kDa, respectively, and C1 and C2 are the 3' ends of the reported human PDE1A variants. The results of PCR and Southern blot analysis show that nine PDE1A splice variants exhibit distinctive tissue distribution patterns by the difference of the N-terminus. PDE1As with N2 were widely expressed in various tissues, mainly in the **kidney**, liver, and pancreas. On the other hand, PDE1As with N1 and N3 were particularly expressed at a high level in the brain and testis, respectively. These findings suggest that the distinct **expression patterns** among PDE1A variants depend on the

several promoters situated upstream of exons encoding 5' ends of the variants. The PDE1A gene spans over 120 kb of genomic DNA, and consists of at least 17 exons and 16 introns. The PDE1A gene was located on human chromosome 2q32 by fluorescent in situ hybridization analysis.

L66 ANSWER 16 OF 49 MEDLINE DUPLICATE 11
ACCESSION NUMBER: 2001221850 MEDLINE
DOCUMENT NUMBER: 21210966 PubMed ID: 11311935
TITLE: Cloning and characterization of a human orphan family C G-protein coupled receptor GPRC5D.
AUTHOR: Brauner-Osborne H; Jensen A A; Sheppard P O; Brodin B; Krogsgaard-Larsen P; O'Hara P
CORPORATE SOURCE: NeuroScience PharmaBiotec Research Centre, Department of Medicinal Chemistry, Royal Danish School of Pharmacy, 2 Universitetsparken, DK-2100 Copenhagen, Denmark.. hbo@dfh.dk
SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (2001 Apr 16) 1518 (3) 237-48.
PUB. COUNTRY: Netherlands
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF207989; GENBANK-AF209923; GENBANK-AF218809
ENTRY MONTH: 200106
ENTRY DATE: Entered STN: 20010625
Last Updated on STN: 20010625
Entered Medline: 20010621

AB Recently three orphan G-protein coupled receptors, RAIG1, GPRC5B and GPRC5C, with homology to members of family C (metabotropic glutamate receptor-like) have been identified. Using the protein sequences of these receptors as queries we identified overlapping expressed **sequence tags** which were predicted to encode an additional subtype. The full length coding regions of mouse mGprc5d and human GPRC5D were cloned and shown to contain predicted open reading frames of 300 and 345 amino acids, respectively. GPRC5D has seven putative transmembrane segments and is expressed in the cell membrane. The four human receptor subtypes, which we assign to group 5 of family C GPCRs, show 31-42% amino acid sequence identity to each other and 20-25% sequence identity to the transmembrane domains of metabotropic glutamate receptor subtypes 2 and 3 and other family C members. In contrast to the remaining family C members, the group 5 receptors have short amino terminal domains of some 30-50 amino acids. GPRC5D was shown to be clustered with RAIG1 on chromosome 12p13.3 and like RAIG1 and GPRC5B to consist of three exons, the first exon being the largest containing all seven transmembrane segments. GPRC5D **mRNA** is widely expressed in the peripheral system but all four receptors show distinct **expression patterns**. Interestingly, **mRNA** levels of all four group 5 receptors were found in medium to high levels in the **kidney**, pancreas and **prostate** and in low to medium levels in the colon and the small intestine, whereas other organs only express a subset of the genes. In an attempt to delineate the signal transduction pathway(s) of the orphan receptors, a series of chimeric receptors containing the amino terminal domain of the calcium sensing receptor or metabotropic glutamate receptor subtype 1, and the seven transmembrane domain of the orphan receptors were constructed and tested in binding and functional assays.

L66 ANSWER 17 OF 49

MEDLINE

DUPLICATE 12

ACCESSION NUMBER: 2001231031 MEDLINE
DOCUMENT NUMBER: 21218927 PubMed ID: 11318611
TITLE: Cloning and characterization of 13 novel transcripts and the human RGS8 gene from the 1q25 region encompassing the hereditary prostate cancer (HPC1) locus.
AUTHOR: Sood R; Bonner T I; Makalowska I; Stephan D A; Robbins C M;
Connors T D; Morgenbesser S D; Su K; Faruque M U; Pinkett H; Graham C; Baxevanis A D; Klinger K W; Landes G M; Trent J M; Carpten J D
CORPORATE SOURCE: Cancer Genetics Branch, National Human Genome Research Institute, Bethesda, MD 20892, USA.. rsood@nhgri.nih.gov
SOURCE: GENOMICS, (2001 Apr 15) 73 (2) 211-22.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF288399; GENBANK-AF297014; GENBANK-AF297015; GENBANK-AF297016; GENBANK-AF297017; GENBANK-AF297018; GENBANK-AF297019; GENBANK-AF297020; GENBANK-AF297021; GENBANK-AF297022; GENBANK-AF297023; GENBANK-AF312863; GENBANK-AF312864; GENBANK-AF312865; GENBANK-AF338436
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010827
Last Updated on STN: 20010827
Entered Medline: 20010823

AB The aim of this study was to develop a saturated **transcript** map of the region encompassing the HPC1 locus to identify the susceptibility genes involved in hereditary **prostate** cancer (OMIM 176807) and hyperparathyroidism-jaw tumor syndrome (OMIM 145001). We previously reported the generation of a 6-Mb BAC/PAC contig of the candidate region and employed various strategies, such as database searching, exon-trapping, direct **cDNA** hybridization, and sample sequencing of BACs, to identify all potential **transcripts**. These efforts led to the identification and precise localization on the BAC contig of

59

transcripts representing 22 known genes and 37 potential **transcripts** represented by **ESTs** and exon traps. Here we report the detailed characterization of these **ESTs** into full-length **transcript** sequences, their **expression pattern** in various tissues, their genomic organization, and their homology to known genes. We have also identified an Alu insertion polymorphism in the intron of one of the **transcripts**. Overall, data on 13 novel **transcripts** and the human RGS8 gene (homologue of the rat RGS8 gene) are presented in this paper. Ten of the 13 novel **transcripts** are expressed in **prostate** tissue and represent positional candidates for HPC1.
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L66 ANSWER 18 OF 49

MEDLINE

DUPLICATE 13

ACCESSION NUMBER: 2001297501 MEDLINE
DOCUMENT NUMBER: 21272509 PubMed ID: 11376952
TITLE: The cloning, genomic structure, localization, and expression of human deoxyribonuclease IIbeta.
AUTHOR: Krieser R J; MacLea K S; Park J P; Eastman A
CORPORATE SOURCE: Department of Pharmacology and Toxicology, Dartmouth Medical School, 7650 Remsen, Hanover, NH 03755, USA.
CONTRACT NUMBER: CA23108 (NCI)

SOURCE: CA50224 (NCI)
GENE, (2001 May 16) 269 (1-2) 205-16.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF274571
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010806
Last Updated on STN: 20010806
Entered Medline: 20010802

AB Acidic endonuclease activity is present in all cells in the body and much of this can be attributed to the previously cloned and ubiquitously expressed deoxyribonuclease II (DNase II). Database analysis revealed the existence of expressed **sequence tags** and genomic segments coding for a protein with considerable homology to DNase II.

This report describes the cloning of this **cDNA**, which we term deoxyribonuclease IIbeta (DNase IIbeta) and comparison of its expression to that of the originally cloned DNase II (now termed DNase IIalpha). The **cDNA** encodes a 357 amino acid protein. This protein exhibits extensive homology to DNase IIalpha including an amino-terminal signal peptide and a conserved active site, and has many of the regions of identity that are conserved in homologs in other mammals as well as *C. elegans* and *Drosophila*. The gene encoding DNase IIbeta has identical splice sites to DNase IIalpha. Human DNase IIbeta is highly expressed in the salivary gland, and at low levels in trachea, **lung**, **prostate**, lymph node, and testis, whereas DNase IIalpha is ubiquitously expressed in all tissues. The **expression pattern** of human DNase IIbeta suggests that it may function primarily as a secreted enzyme. Human saliva was found to contain DNase IIalpha, but after immunodepletion, considerable acid-active endonuclease remained which we presume is DNase IIbeta. We have localized the gene for human DNase IIbeta to chromosome 1p22.3 adjacent (and in opposing orientation) to the human uricase pseudogene. Interestingly, murine DNase IIbeta is highly expressed in the liver. Uricase is also highly expressed in mouse but not human liver and this may explain the difference in **expression patterns** between human and mouse DNase IIbeta.

L66 ANSWER 19 OF 49 MEDLINE DUPLICATE 14
ACCESSION NUMBER: 2002184690 MEDLINE
DOCUMENT NUMBER: 21914855 PubMed ID: 11917942
TITLE: Identification of a gene frequently mutated in prostate tumors.
AUTHOR: Reding D J; Zhang K Q; Salzman S A; Thomalla J V; Riepe R E; Suarez B K; Catalona W J; Burmester J K
CORPORATE SOURCE: Department of Hematology, Marshfield Clinic, WI, USA.
CONTRACT NUMBER: MH31302 (NIMH)
SOURCE: MEDICAL ONCOLOGY, (2001) 18 (3) 179-87.
Journal code: 9435512. ISSN: 1357-0560.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200204
ENTRY DATE: Entered STN: 20020403
Last Updated on STN: 20020424
Entered Medline: 20020423

AB Although **prostate** cancer is the second leading cause of cancer

death for men in the United States, the genetics of tumor development are poorly understood. Several expressed sequence tagged genes (**ESTs**) that are expressed predominantly in the **prostate** have recently been identified, although their role in the development and maintenance of the **prostate** is unknown. Here, we demonstrate that the gene identified as UNIGENE cluster Hs. 104215, which codes for a message found predominantly in the **prostate**, may be important in tumor development. We name this gene PCan1 for **Prostate Cancer gene 1**. **Northern** blot experiments were performed using RNA isolated from tumor-derived cell lines and human **prostate** to determine the **expression pattern** of the gene. DNA sequencing was used to identify mutations that occurred in tumor tissue. By **Northern** blot analysis, this gene product was not detectable in LNCaP, DU 145, or PC-3 **prostate** cancer cell lines, although it was readily observed in RNA isolated from total **prostate** and from dissected central and peripheral regions of **prostate**. Sequence analysis of genomic DNA from LNCaP, DU 145, or PC-3 cells demonstrated a G/A polymorphism at position 193. Analysis of matched tumor-derived DNA and blood-derived DNA samples from 11 of 13 patients who had undergone a radical prostatectomy and who were homozygous for A in blood-derived DNA demonstrated mutation of position 193 in matched tumor samples resulting in G/A polymorphism. Sixteen additional patient samples were G/A polymorphic in both blood-derived DNA and tumor-derived DNA and two samples were GG in both blood-derived and tumor-derived DNA. Our results suggest that this gene may be a hot spot for mutation in **prostate** cancer, especially because our radiation hybrid mapping located this gene within a region identified in linkage mapping studies of affected families with **prostate** cancer. Loss of heterozygosity in **prostate** tumors has also been reported at the location of PCan1. Further studies to determine the functional role of this candidate tumor suppressor gene are warranted.

L66 ANSWER 20 OF 49 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 2002:151849 BIOSIS
 DOCUMENT NUMBER: PREV200200151849
 TITLE: Gene expression profiling in kidney of zebrafish's hematopoietic tissue.
 AUTHOR(S): Song, Huai-Dong (1); Liu, Ting-Xi; Wu, Xin-Yan (1); Shun, Xiao-Jian (1); Zhang, Qing-Hua (1); Chen, Sai-Juan (1); Zhou, Yi; Chen, Zhu (1); Look, Thomas A.; Zon, Leonard I.
 CORPORATE SOURCE: (1) Shanghai Institute of Hematology, Rui Jin Hospital, SSMU, Shanghai China
 SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 2, pp. 121b. <http://www.bloodjournal.org/>. print.
 Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 2 Orlando, Florida, USA December 07-11, 2001
 ISSN: 0006-4971.
 DOCUMENT TYPE: Conference
 LANGUAGE: English
 AB The zebrafish, *Danio rerio*, was previously viewed as a model to bridge the gap between fly/worm and mouse/human for the understanding of embryonic development. Recent studies have indicated that the zebrafish has a great potential to serve as a model for the study of human disease, especially hematopoiesis. The **kidney** is the hematopoietic tissue of zebrafish, so the gene expression profiling in the zebrafish

kidney was studied by generating a large amount of expressed **sequence-tags (ESTs)**. Totally, 7,199 sequences of good quality were obtained from 10,239 clones (70.4%) to form **cdna** library of the zebrafish **kidney**. After bioinformatics analysis, 686 **ESTs** homologous to the repetitive elements and mtDNA were put aside. The remaining 6,513 **ESTs** could be assembled into 2,808 clusters, of which 39.6% matched zebrafish known genes or human orthologs and 19.2% matched zebrafish **ESTs**, while 41.2% showed no match with any **ESTs** or known genes. A total of 1,111 unique known genes were used to analyze the gene **expression patterns** in the **kidney** of zebrafish hematopoietic tissue. These known genes were categorized into 8 categories according to the basis of gene function, the largest class of which represented those involved in gene/protein expression. Some of genes involved in the hematopoiesis were expressed in the zebrafish's **kidney**. All of these data may contribute to the understanding of the function of the zebrafish's **kidney**.

L66 ANSWER 21 OF 49 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 2002:151838 BIOSIS
 DOCUMENT NUMBER: PREV200200151838
 TITLE: Gene expression patterns in primary and cultured bone marrow cells.
 AUTHOR(S): Ma, Xianrong (1); Degar, Barbara; Wang, Lin (1); Krause, Diane S. (1); Perkins, Archibald S.
 CORPORATE SOURCE: (1) Dept. of Laboratory Medicine, Yale University School of Medicine, New Haven, CT USA
 SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 2, pp. 118b. <http://www.bloodjournal.org/>. print.
 Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 2 Orlando, Florida, USA December

07-11,
 2001
 ISSN: 0006-4971.

DOCUMENT TYPE: Conference
 LANGUAGE: English

AB With the goal of creating a resource for in-depth study of myelopoiesis, we have executed a two-pronged strategy to obtain a **cdna** clone set enriched in myeloid genes. First, we enriched two hematopoietic **cdna** libraries for low copy genes. Libraries were prepared from EML cells and their differentiated counterparts, and from Lin-Hoechstlow Rhodaminelow primary murine **bone** marrow cells. The subtractions were performed using 10,000 known genes and **ESTs** as driver, the ssDNA were purified by hydroxyl appetite chromatography column and used to

construct the subtracted **cdna** library. 3228 randomly picked clones from the subtracted **cdna** libraries represent 1456 distinct genes, of which 649 (45%) are known named genes, 417 (29%) match uncharacterized **ESTs**, and 345 (24%) are novel sequences. The second aspect of our strategy was to complement this subtracted library with genes known to be involved in myeloid cell differentiation and function. The resulting **cdnas** were arrayed on polylysine-coated glass slides. Microarrays were used to analyze changes in gene **expression patterns** during myeloid differentiation. Mouse primary **bone** marrow cells were fractionated into Lin+, Lin-, (Lin- Hoechst low/Rhodamine Bright), and (Lin- Hoechst low/Rhodamine low) sub-populations. **cdna** was prepared from these populations, labeled with Cy3-dCTP or Cy5-dCTP fluorescent nucleotides by PCR amplification, and then hybridized to microarray slides to assess gene

expression patterns. Cluster and tree view programs were used to arrange the gene **expression pattern**. Northern blot or pseudo-Northern blot was used to confirm the microarray data. Analysis indicated that there were abundant changes in gene expression during differentiation. 226 novel genes and 1320 known genes (e.g. DKFZ, SOX4, Ftp-3, Her, Tpd52, Wnt1, FWD2) were down regulated, and 88 novel genes and 1052 known genes (e.g. Agx-1, Mint, Granzyme A, PEBP2aB2, LKLF, ATRN) were up regulated. We focused on several novel genes that we identified as being downregulated very early in hematopoiesis. One of them was cloned and identified as a new member of receptor activity modifying proteins (RAMPs) family called RAMP4, which is highly homologous to RAMP2. However, the **transcript** is significant larger (apprx7.5kb). When EML (myeloid stem cell line) cells are induced to differentiate with all-trans retinoic acid and IL3, RAMP4 expression levels decrease dramatically within 6 hrs and expression levels remains low thereafter. Consistent with this, Epro (myeloid progenitor cell line) cells express RAMP4 at very low levels. RAMP family members assist in intracellular trafficking of calcitonin receptor and G protein-coupled receptor proteins to the cell surface and thus help dictate the expression of unique cellular phenotypes. Therefore these results suggest the new RAMP may play an important role in myeloid stem cell differentiation and blood cell development. The study for complete physical map and biological function of RAMP-4 are progressing.

L66 ANSWER 22 OF 49 MEDLINE DUPLICATE 15
 ACCESSION NUMBER: 2001357490 MEDLINE
 DOCUMENT NUMBER: 21311398 PubMed ID: 11418467
 TITLE: Highly abundant genes in the transcriptosome of human and baboon CD34 antigen-positive bone marrow cells.
 AUTHOR: Gomes I; Sharma T T; Mahmud N; Kapp J D; Edassery S; Fulton
 N; Liang J; Hoffman R; Westbrook C A
 CORPORATE SOURCE: Department of Medicine, University of Illinois at Chicago, USA.
 CONTRACT NUMBER: P01-75 606 (NCI)
 R01-CA-72593
 SOURCE: BLOOD, (2001 Jul 1) 98 (1) 93-9.
 Journal code: 7603509. ISSN: 0006-4971.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
 ENTRY MONTH: 200107
 ENTRY DATE: Entered STN: 20010730
 Last Updated on STN: 20010730
 Entered Medline: 20010726

AB Nonhuman primates are useful large animal model systems for the in vivo study of hematopoietic stem cell biology. To better understand the degree of similarity of the hematopoietic systems between humans and baboons, and to explore the relevance of such studies in nonhuman primates to humans, this study was designed to compare the global gene expression profile of bone marrow CD34(+) cells isolated from these 2 species. Human complementary DNA (cDNA) filter arrays containing 25 920 human cDNAs were surveyed for this purpose. The **expression pattern** and relative gene abundance of the 2 RNA sources were similar, with a correlation coefficient of 0.87. A total of 15 970 of

these **cdNAs** were expressed in human CD34(+) cells, of which the majority (96%) varied less than 3-fold in their relative level of expression between human and baboon. Reverse transcriptase-polymerase chain reaction analysis of selected genes confirmed that expression was comparable between the 2 species. No species-restricted **transcripts** have been identified, further reinforcing the high degree of similarity between the 2 populations. A subset of 1554 **cdNAs**, which are expressed at levels 100-fold and greater than background, is described, which includes 959 expressed **sequence tags** and uncharacterized **cdNAs**, and 595 named genes, including many that are clearly involved in hematopoiesis. The **cdNAs** reported here represent a selection of some of the most highly abundant genes in hematopoietic cells and provide a starting point to develop a profile of the transcriptome of CD34(+) cells.

L66 ANSWER 23 OF 49 MEDLINE DUPLICATE 16
 ACCESSION NUMBER: 2001105545 MEDLINE
 DOCUMENT NUMBER: 20568482 PubMed ID: 11116087
 TITLE: Identification, characterization, and mapping of expressed sequence tags from an embryonic zebrafish heart cDNA library.
 AUTHOR: Ton C; Hwang D M; Dempsey A A; Tang H C; Yoon J; Lim M; Mably J D; Fishman M C; Liew C C
 CORPORATE SOURCE: Department of Laboratory Medicine and Pathobiology, University of Toronto, Toronto, Ontario M5G 1L5, Canada.
 SOURCE: GENOME RESEARCH, (2000 Dec) 10 (12) 1915-27.
 Journal code: 9518021. ISSN: 1088-9051.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-BE693120; GENBANK-BE693121; GENBANK-BE693122;
 GENBANK-BE693123; GENBANK-BE693124; GENBANK-BE693125;
 GENBANK-BE693126; GENBANK-BE693127; GENBANK-BE693128;
 GENBANK-BE693129; GENBANK-BE693130; GENBANK-BE693131;
 GENBANK-BE693132; GENBANK-BE693133; GENBANK-BE693134;
 GENBANK-BE693135; GENBANK-BE693136; GENBANK-BE693137;
 GENBANK-BE693138; GENBANK-BE693139; GENBANK-BE693140;
 GENBANK-BE693141; GENBANK-BE693142; GENBANK-BE693143;
 GENBANK-BE693144; GENBANK-BE693145; GENBANK-BE693146;
 GENBANK-BE693147; GENBANK-BE693148; GENBANK-BE693149; +
 ENTRY MONTH: 200102
 ENTRY DATE: Entered STN: 20010322
 Last Updated on STN: 20010322
 Entered Medline: 20010208
 AB The generation of expressed **sequence tags** (**ESTs**) has proven to be a rapid and economical approach by which to identify and characterize expressed genes. We generated 5102 **ESTs** from a 3-d-old embryonic zebrafish **heart cDNA** library. Of these, 57.6% matched to known genes, 14.2% matched only to other **ESTs**, and 27.8% showed no match to any **ESTs** or known genes. Clustering of all **ESTs** identified 359 unique clusters comprising 1771 **ESTs**, whereas the remaining 3331 **ESTs** did not cluster. This estimates the number of unique genes identified in the data set to be approximately 3690. A total of 1242 unique known genes were used to analyze the gene **expression patterns** in the zebrafish embryonic **heart**. These were categorized into seven categories on the basis of gene function. The largest class of genes represented those involved in gene/protein expression (25.9% of known **transcripts**). This class was followed by genes involved in metabolism (18.7%), cell structure/motility (16.4%), cell signaling and

communication (9.6%), cell/organism defense (7.1%), and cell division (4.4%). Unclassified genes constituted the remaining 17.91%. Radiation hybrid mapping was performed for 102 **ESTs** and comparison of map positions between zebrafish and human identified new syteny groups. Continued comparative analysis will be useful in defining the boundaries of conserved chromosome segments between zebrafish and humans, which will facilitate the transfer of genetic information between the two organisms and improve our understanding of vertebrate evolution.

L66 ANSWER 24 OF 49 MEDLINE DUPLICATE 17
 ACCESSION NUMBER: 2000195242 MEDLINE
 DOCUMENT NUMBER: 20195242 PubMed ID: 10733104
 TITLE: Isolation of MYADM, a novel hematopoietic-associated marker
 gene expressed in multipotent progenitor cells and up-regulated during myeloid differentiation.
 AUTHOR: Pettersson M; Dannaeus K; Nilsson K; Jonsson J I
 CORPORATE SOURCE: Department of Genetics and Pathology, University Hospital, University of Uppsala, Sweden.
 SOURCE: JOURNAL OF LEUKOCYTE BIOLOGY, (2000 Mar) 67 (3) 423-31. Journal code: 8405628. ISSN: 0741-5400.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200004
 ENTRY DATE: Entered STN: 20000413
 Last Updated on STN: 20000413
 Entered Medline: 20000405

AB A large number of hematopoietic cytokines and their receptors as well as transcription factors have been shown to be involved in maturation of blood cells. However, many of the genes important for the differentiation of multipotent stem cells to specific cellular lineages are still unknown.
 To identify novel genes involved in lineage selection of myeloid cells, we have applied differential display analysis during commitment toward granulocytes and macrophages of an IL-3-dependent multipotent progenitor cell line, FDCP-mix. One regulated **cDNA** represented a novel gene with restricted **expression pattern** within the hematopoietic system and was strongly up-regulated when FDCP-mix cells differentiated in GM-CSF, G-CSF, and M-CSF. The expression appears to be differentiation stage-specific in myeloid cells and is absent in B and T lymphocytes. Thus we found expression in normal mouse **bone marrow** enriched for stem cells and multipotent progenitors (c-kit+Sca-1+Lin- cells). When these cells were induced to differentiate toward myeloid cells, MYADM was up-regulated. In contrast, during conditions known to favor the development of B cell progenitors, the gene was down-regulated. The gene, termed MYADM for myeloid-associated differentiation marker gene, shows 100% identity to expressed **sequence tags** from early mouse embryonic development as well as from the mouse **lung** and from activated mouse macrophages. The predicted 32-kDa MYADM protein contains multiple hydrophobic putative transmembrane segments and has several potential consensus sites for phosphorylation. In view of its **expression pattern**, MYADM could serve as a new marker gene for hematopoietic differentiation. Although the function is unknown, antisense oligonucleotides were able to inhibit colony formation of c-kit+ Lin- **bone marrow** cells, suggesting an important role for MYADM in myeloid differentiation.

L66 ANSWER 25 OF 49 MEDLINE DUPLICATE 18
 ACCESSION NUMBER: 2001019682 MEDLINE
 DOCUMENT NUMBER: 20438252 PubMed ID: 10980418
 TITLE: A subtractive PCR-based cDNA library from human odontoblast cells: identification of novel genes expressed in tooth forming cells.
 AUTHOR: Buchaille R; Couble M L; Magloire H; Bleicher F
 CORPORATE SOURCE: Laboratoire du Developpement des Tissus Dentaires, E.A. 1892, Faculte d'Odontologie, UCBL, Rue G. Paradin, 69372 cedex 08, Lyon, France.
 SOURCE: MATRIX BIOLOGY, (2000 Sep) 19 (5) 421-30. Journal code: 9432592. ISSN: 0945-053X.
 PUB. COUNTRY: GERMANY: Germany, Federal Republic of Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200011
 ENTRY DATE: Entered STN: 20010322
 Last Updated on STN: 20010322
 Entered Medline: 20001107

AB Odontoblasts are highly specialized cells aligned at the edge of the dental pulp. As a step towards understanding the complex mechanisms underlying their terminal differentiation, the gene **expression pattern** was examined in human cultured odontoblast cells. Suppression subtractive hybridization (SSH) was used to establish a subtracted **cDNA** library specific for human odontoblasts. For this purpose, **cDNAs** from human cultured fibroblastic pulp cells were subtracted to **cDNA** from human cultured odontoblasts. The nucleotide sequence of 154 subtracted **cDNA** clones was determined. We identified 130 preferentially expressed gene fragments in odontoblasts as compared with the fibroblastic pulp cells. Ten of them were already identified in odontoblasts such as DSPP, BSP, enamelysin and CollA1. We confirmed their overexpression by RT-PCR on the cultured cells and in vivo by in situ hybridization on human molars. Another 64 clones corresponded to known genes. Among them, two clones were of particular interest: reelin, which was first detected in the brain and osteoadherin, which was first located in **bone**. Fifty-six clones were unknown genes even though 82% matched expressed **sequence tags** or genomic clones. A reverse **Northern** dot blot showed that 96% of them were overexpressed at different rates in cultured odontoblasts. These latest results indicate that there are still unknown genes that are associated with the control of the odontoblast phenotype. Thus, cloning

of odontoblast differentiation-associated genes not only opens up new methods of elucidating the normal development but also the recruitment of odontoblasts when required to initiate repair of dentin.

L66 ANSWER 26 OF 49 MEDLINE DUPLICATE 19
 ACCESSION NUMBER: 2000426879 MEDLINE
 DOCUMENT NUMBER: 20379301 PubMed ID: 10919859
 TITLE: Use of serial analysis of gene expression to generate kidney expression libraries.
 AUTHOR: El-Meanawy M A; Schelling J R; Pozuelo F; Churpek M M; Ficker E K; Iyengar S; Sedor J R
 CORPORATE SOURCE: Department of Medicine, School of Medicine, Case Western Reserve University, MetroHealth Medical Center, Cleveland, Ohio 44109, USA.
 CONTRACT NUMBER: DK-02281 (NIDDK)
 DK-07470 (NIDDK)
 DK-38558 (NIDDK)

SOURCE: + AMERICAN JOURNAL OF PHYSIOLOGY. RENAL PHYSIOLOGY, (2000 Aug) 279 (2) F383-92.
 Journal code: 100901990. ISSN: 0363-6127.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200009
 ENTRY DATE: Entered STN: 20000922
 Last Updated on STN: 20000922
 Entered Medline: 20000912

AB Chronic renal disease initiation and progression remain incompletely understood. Genome-wide expression monitoring should clarify mechanisms that cause progressive renal disease by determining how clusters of genes coordinately change their activity. Serial analysis of gene expression (SAGE) is a technique of expression profiling, which permits simultaneous, comparative, and quantitative analysis of gene-specific, 9- to 13-bp **sequence tags**. Using SAGE, we have constructed a tag expression library from ROP-+/+ mouse **kidney**. Tag sequences were sorted by abundance, and identity was determined by sequence homology searching. Analyses of 3,868 tags yielded 1,453 unique **kidney transcripts**. Forty-two percent of these **transcripts** matched **mRNA** sequence entries with known function, 35% of the **transcripts** corresponded to expressed **sequence tag (EST)** entries or cloned genes, whose function has not been established, and 23% represented unidentified genes. Previously characterized **transcripts** were clustered into functional groups, and those encoding metabolic enzymes, plasma membrane proteins (transporters/receptors), and ribosomal proteins were most abundant (39, 14, and 12% of known **transcripts**, respectively). The most common, **kidney-specific transcripts** were **kidney** androgen-regulated protein (4% of all **transcripts**), sodium-phosphate cotransporter (0.3%), renal cytochrome P-450 (0.3%), parathyroid hormone receptor (0.1%), and **kidney-specific cadherin** (0.1%). Comprehensively characterizing and contrasting gene **expression patterns** in normal and diseased **kidneys** will provide an alternative strategy to identify candidate pathways, which regulate nephropathy susceptibility and progression, and novel targets for therapeutic intervention.

L66 ANSWER 27 OF 49 MEDLINE
 ACCESSION NUMBER: 2002187485 MEDLINE
 DOCUMENT NUMBER: 21917126 PubMed ID: 11920191
 TITLE: Gene expression in CD34(+) cells from normal bone marrow and leukemic origins.
 AUTHOR: Gu J; Zhang Q H; Huang Q H; Ren S X; Wu X Y; Ye M; Huang C H; Fu G; Zhou J; Niu C; Han Z G; Chen S J; Chen Z
 CORPORATE SOURCE: Chinese National Human Genome Center at Shanghai, Shanghai 201203, PR China.
 SOURCE: Hematol J, (2000) 1 (3) 206-17.
 Journal code: 100965523. ISSN: 1466-4860.
 PUB. COUNTRY: England: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200205
 ENTRY DATE: Entered STN: 20020403
 Last Updated on STN: 20020509
 Entered Medline: 20020508

AB INTRODUCTION: To address the molecular regulation of hematopoiesis and the complex mechanism in leukemogenesis, we established the first catalogs of genes expressed in normal **bone** marrow and leukemia CD34(+) cells. MATERIALS AND METHODS: CD34(+) cell **cDNA** libraries were constructed using **mRNA** from adult **bone** marrow and from a case of acute myeloid leukemia-M5 transformed from myelodysplastic syndrome (MDS-AML). Expressed **sequence tags** (**ESTs**) and full-length **cDNAs** were generated by sequencing and were annotated using bioinformatic tools. RESULTS: From a total of 4142 **ESTs** obtained from normal **bone** marrow, 3424 meaningful tags were integrated into 1630 clusters, representing 622 known genes, 522 **dbEST** entries and 486 novel sequences. Out of 5382 **ESTs** from MDS-AML, 1985 clusters were produced based on the analysis of 4321 useful **ESTs**, including 711 known genes, 657 known **ESTs** and 617 novel sequences. Among 251 **transcripts** found in both **bone** marrow and MDS-AML **EST** datasets and those present in only one dataset, 58 showed statistically significant differences in **EST** copy numbers between the two tissues ($P < 0.05$). Twenty putative full-length **cDNAs** for novel genes were also cloned from the MDS-AML library. CONCLUSION: The distinct gene **expression patterns** in MDS-AML-CD34(+) cells as compared to normal control cells may contribute to the development and/or maintenance of the malignant phenotypes of leukemia cells.

L66 ANSWER 28 OF 49 MEDLINE DUPLICATE 20
 ACCESSION NUMBER: 2000195627 MEDLINE
 DOCUMENT NUMBER: 20195627 PubMed ID: 10729223
 TITLE: The region on 9p associated with 46,XY sex reversal contains several transcripts expressed in the urogenital system and a novel doublesex-related domain.
 AUTHOR: Ottolenghi C; Veitia R; Quintana-Murci L; Torchard D; Scapoli L; Souleyreau-Therville N; Beckmann J; Fellous M; McElreavey K
 CORPORATE SOURCE: Unite d'Immunogenetique humaine, INSERM U276, Institut Pasteur, 25 rue du Docteur Roux, Paris, 75724, France.
 SOURCE: GENOMICS, (2000 Mar 1) 64 (2) 170-8.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200005
 ENTRY DATE: Entered STN: 20000518
 Last Updated on STN: 20000518
 Entered Medline: 20000511

AB Deletions of 9p have been associated with 46,XY gonadal dysgenesis, and the smallest region of overlap has been mapped to the tip of chromosome 9.
 9. Two candidate genes (DMRT1 and 2) have been found in the region. Despite intensive mutation searches, no mutations have been detected in these genes. To gain insights into the genomics of the region and to isolate other candidate genes for the phenotype, we have constructed a P1 artificial chromosome (PAC)/bacterial artificial chromosome (BAC) contig spanning over 500 kb and covering the consensus critical region. We have analyzed the **expression pattern** of several **ESTs** mapped or sublocalized within the framework of the contig. In addition, a sample shotgun sequencing of a PAC containing the mentioned

DM

genes led to the detection of novel **transcripts** displaying an **expression pattern** specific to testis and kidney, consistent with a role in the development of the urogenital system. One of them, expressed in adult testis and human embryos aged 4-5 weeks, encodes a potential polypeptide and is located immediately downstream of

a sequence capable of encoding a novel DM domain. The region was partially screened for mutations in sex-reversed patients by Southern blot, sequencing, and FISH. No mutations were found. Our results suggest that the critical region on 9p involved in male-to-female sex reversal displays

greater gene density and genomic complexity than previously anticipated. Future investigations will include functional and mutational studies of the novel **transcripts** mapped or sublocalized within the critical region by this study as well as cloning efforts to isolate additional candidate genes.

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L66 ANSWER 29 OF 49 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:299309 BIOSIS

DOCUMENT NUMBER: PREV200100299309

TITLE: Comparison of mRNA expression patterns at diagnosis and relapse in acute lymphoblastic leukemia by differential display analysis.

AUTHOR(S): Yuge, M. (1); Nagai, H. (1); Naoe, T.; Horibe, K.; Saito, H. (1); Kinoshita, T. (1)

CORPORATE SOURCE: (1) First Department of Internal Medicine, Nagoya University School of Medicine, Nagoya, Aichi Japan

SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 2, pp. 169b. print.

Meeting Info.: 42nd Annual Meeting of the American Society of Hematology San Francisco, California, USA December 01-05, 2000 American Society of Hematology . ISSN: 0006-4971.

DOCUMENT TYPE: Conference

LANGUAGE: English

SUMMARY LANGUAGE: English

AB One of the major clinical problems in the treatment of acute lymphoblastic

leukemia (ALL) is relapse after chemotherapy. Although some possibilities such as MDR1 over-expression were supposed, the mechanism of relapse is still unclear. To address these points, we compared **mRNA expression patterns** of leukemic cells in adult ALL patients at diagnosis with those at relapse by fluorescence differential display-PCR analysis. **cDNA** were synthesized from total RNA of mononuclear cells of **bone marrow** at diagnosis and relapse of 3 ALL cases using 9 anchor primers. After PCR amplification of these **cDNA** as templates with each anchor primer and 24 arbitrary primers, the expression profiles were analyzed by comparison of the intensity of bands separated on 6% polyacrylamide gels using digital scanning. We have identified about 50 **transcripts**, which showed differences in expression at least three times, including about 10 **ESTs**. The **transcripts** that have motifs such as runt-domain or WD-repeat were over-expressed at relapse and some phosphatases were down regulated at relapse, compared with at diagnosis. The changes of expression of these **transcripts** were also examined in additional nine primary cases of the lymphoid malignancies.

We

are investigating the biological significance of the expression of these **transcripts**.

L66 ANSWER 30 OF 49 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:299208 BIOSIS

DOCUMENT NUMBER: PREV200100299208

TITLE: The gene expression profile in murine long-term pluripotent

hematopoietic stem cells.

AUTHOR(S): Zhao, Yi (1); Zhu, Lunjian (1); Yan, Chunli (1); Zhan, Iris

(1); Lin, Gloria (1); Chang, Adam (1); Gallaher, Tim (1); Anderson, W. French (1)

CORPORATE SOURCE: (1) Gene Therapy Laboratories, Keck School of Medicine, University of Southern California, Los Angeles, CA USA

SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 2, pp. 130b. print.

Meeting Info.: 42nd Annual Meeting of the American Society of Hematology San Francisco, California, USA December 01-05, 2000 American Society of Hematology . ISSN: 0006-4971.

DOCUMENT TYPE: Conference

LANGUAGE: English

SUMMARY LANGUAGE: English

AB It is known that murine hematopoietic stem cells (HSC) reside in the Lin- Sca-1+ c-kit+ **bone** marrow cells. We subfractionated these cells based on the surface expression profile of CD38 and CD34 (Blood, in press). With competitive long term repopulation assays, we demonstrated that the primitive long-term mouse HSC in adult **bone** marrow are cells with the surface markers: Lin- Sca+ kit+ CD38+ CD34-, abbreviated 38+34-; these cells are present at a level of 2 per 100,000 **bone** marrow cells. Although the other subsets, i.e., the 38+34+, 38-34+, and 38-34- cells, give multilineage reconstitution in short term and low activity in long term in primary lethally irradiated recipients, only 38+34- cells are able to reconstitute second and third lethally irradiated

bone marrow transplant recipients 2.5 years after the first **bone** marrow transplantation. Thus, we have fractionated the HSC into what appears to be a relatively pure population of long-term repopulating cells, specifically the 38+34- subset (Blood, in press). Furthermore, we have shown that the maturation pathway is from 38+34- to 38+34+ to 38-34+. Of great interest is to determine the unique gene expression profile of the 38+34- cells, i.e., to determine those genes which are highly expressed in the 38+34- cells but not in the immediate downstream cell types, namely the 38+34+ and 38-34+ cells. We compared

the gene **expression patterns** between these three subsets with Differential Display PCR (DD-PCR). 1395 fragments were isolated from DD-PCR; reverse **Northern**s were performed to confirm the unique expression in the 38+34- subset. 184 genes, which had been selected by reverse **Northern**, were sequenced and analyzed with database searches. 72 genes (39%) show significant homologies to known genes involved in different cell functions, including signal transduction, anti-apoptosis, adhesion, metabolism, etc. 15 genes (8%) show high similarity with the genes in **EST** databases, and 97 fragments (53%) did not match to any of the databases examined. Ongoing projects

are to identify the relationships of the anti-apoptosis and signal transduction proteins with stem cell biological functions, to identify unique cell surface markers, and to attempt to identify the unknown genes that have been isolated.

L66 ANSWER 31 OF 49 MEDLINE

ACCESSION NUMBER: 2000247251 MEDLINE

DUPLICATE 21

DOCUMENT NUMBER: 20247251 PubMed ID: 10783259
TITLE: Sequence and expression pattern of a novel human orphan G-protein-coupled receptor, GPRC5B, a family C receptor with a short amino-terminal domain.
AUTHOR: Brauner-Osborne H; Krogsgaard-Larsen P
CORPORATE SOURCE: NeuroScience PharmaBiotec Research Centre, Department of Medical Chemistry, The Royal Danish School of Pharmacy, 2 Universitetsparken, Copenhagen, DK-2100, Denmark.. hbo@dfh.dk
SOURCE: GENOMICS, (2000 Apr 15) 65 (2) 121-8. Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF202640
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 20000728
Last Updated on STN: 20000728
Entered Medline: 20000720

AB Query of GenBank with the amino acid sequence of human metabotropic glutamate receptor subtype 2 (mGluR2) identified a predicted gene product of unknown function on BAC clone CIT987SK-A-69G12 (located on chromosome band 16p12) as a homologous protein. The **transcript**, entitled GPRC5B, was cloned from an expressed **sequence tag** clone that contained the entire open reading frame of the **transcript** encoding a protein of 395 amino acids. Analysis of the protein sequence reveal that GPRC5B contains a signal peptide and seven transmembrane alpha-helices, which is a hallmark of G-protein-coupled receptors (GPCRs). GPRC5B displays homology to retinoic acid-inducible gene 1 (RAIG1, 33% sequence identity) and to several family C (mGluR-like) GPCRs (20-25% sequence identity). Both RAIG1 and GPRC5B have short extracellular amino-terminal domains (ATDs) that contrast the very long ATDs characterizing the receptors currently assigned to family C. However, our results strongly indicate that RAIG1 and GPRC5B form a new subgroup of family C characterized by short ATDs. GPRC5B **mRNA** is widely expressed in peripheral and central tissues with highest abundance in **kidney**, **pancreas**, and **testis**. This **mRNA expression pattern** is markedly different from that of RAIG1, which shows a slightly more restricted **expression pattern** with highest abundance in **lung** tissue.
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L66 ANSWER 32 OF 49 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:299167 BIOSIS
DOCUMENT NUMBER: PREV200100299167
TITLE: The CD34+ transcriptosome: Highly expressed genes in human and baboon bone marrow.
AUTHOR(S): Gomes, Ignatius (1); Le, Tiffany (1); Kapp, Jeffrey (1); Edassery, Seby (1); Fulton, Noreen (1); Liang, Jie; Hoffman, Ronald (1); Westbrook, Carol A. (1)
CORPORATE SOURCE: (1) Medicine, University of Illinois, Chicago, IL USA
SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 2, pp. 119b. print.
Meeting Info.: 42nd Annual Meeting of the American Society of Hematology San Francisco, California, USA December 01-05, 2000 American Society of Hematology . ISSN: 0006-4971.

DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Although recent studies have greatly advanced our knowledge of the genes expressed in murine **bone** marrow stem cells, relatively little is known about comparable cells in the human. In the present study we attempt to describe the human CD34+ transcriptosome, and compare it to that of the baboon (*Papio anubis*). The baboon is of interest because it is widely used as an experimental large animal for **bone** marrow studies, is closely related to humans, and shows cross reactivity with many of the reagents used to study human hematopoiesis. Filter arrays containing 25,920 human **cDNAs**, an estimated 33% of all human genes, were hybridized to RNA-based probes prepared from human and baboon **bone** marrow cells which were positive for the CD34 antigen (CD34+ cells) to establish the expression profiles and compare the two populations. The **expression pattern** and relative gene abundance of the two RNA sources was similar, with a correlation coefficient of 0.87. A total of 15,970 of these **cDNAs** were expressed in human CD34+ cells, of which the majority (96%) varied less than 3-fold in their relative abundance between human and baboon. RT-PCR analysis of selected genes confirmed that expression was comparable between the two species.

No species-restricted **transcripts** were identified, further reinforcing the high degree of similarity between the two populations, and validating the utility of human **cDNA** arrays for baboon studies. A subset is described consisting of the most abundant human **cDNAs**, expressed at levels 100-fold and more over baseline, including 853 **ESTs** and 701 named genes from all categories of proteins, including transcription factors, cytokines, and receptors. The **ESTs** are of particular interest because they comprise partially- or uncharacterized genes, and thus may represent novel biological pathways. Overall, this list of **cDNAs** provides a potential wealth of new information about **bone** marrow hematopoietic progenitor cells, representing a selection of some of the most abundant genes in hematopoietic cells which describe the CD34+ transcriptosome.

L66 ANSWER 33 OF 49 MEDLINE DUPLICATE 22
ACCESSION NUMBER: 2000304749 MEDLINE
DOCUMENT NUMBER: 20304749 PubMed ID: 10843801
TITLE: Transcription mapping of the 5q- syndrome critical region: cloning of two novel genes and sequencing, expression, and mapping of a further six novel cDNAs.
AUTHOR: Boultwood J; Fidler C; Strickson A J; Watkins F; Kostrzewa M; Jaju R J; Muller U; Wainscoat J S
CORPORATE SOURCE: Leukaemia Research Fund Molecular Haematology Unit, John Radcliffe Hospital, Headington, OX3 9DU, United Kingdom.. jrboultwo@enterprise.molbiol
SOURCE: GENOMICS, (2000 May 15) 66 (1) 26-34.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF156165; GENBANK-AF157115; GENBANK-AF157116; GENBANK-AF159165; GENBANK-AF159700
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 20000728

Last Updated on STN: 20000728

Entered Medline: 20000720

AB The 5q- syndrome is a myelodysplastic syndrome with the 5q deletion del(5q) as the sole karyotypic abnormality. We are using the expressed **sequence tag (EST)** resource as our primary approach to identifying novel candidate genes for the 5q- syndrome. Seventeen **ESTs** were identified from the Human Gene Map at the National Center for Biotechnology Information that had no significant homology to any known genes and were assigned between DNA markers D5S413 and D5S487, flanking the critical region of the 5q- syndrome at 5q31-q32. Eleven of the 17 **cDNAs** from which the **ESTs** were derived (65%) were shown to map to the critical region of the 5q- syndrome by gene dosage analysis and were then sublocalized by PCR screening to a YAC contig encompassing the critical region. Eight of the 11 **cDNA** clones, upon full sequencing, had no significant homology to any known genes. Each of the 8 **cDNA** clones was shown to be expressed in human **bone marrow**. The complete coding sequence was obtained for 2 of the novel genes, termed C5orf3 and C5orf4. The 2.6-kb **transcript** of C5orf3 encodes a putative 505-amino-acid protein and contains an ATP/GTP-binding site motif A (P loop), suggesting that this novel gene encodes an ATP- or a GTP-binding protein. The novel gene C5orf4 has a **transcript** of 3.1 kb, encoding a putative 144-amino-acid protein. We describe the cloning of 2 novel human genes and the sequencing, **expression patterns**, and mapping to the critical region of the 5q- syndrome of a further 6 novel **cDNA** clones. Genomic localization and **expression patterns** would suggest that the 8 novel **cDNAs** described in this report represent potential candidate genes for the 5q- syndrome. Copyright 2000 Academic Press.

L66 ANSWER 34 OF 49 MEDLINE DUPLICATE 23
ACCESSION NUMBER: 1999143102 MEDLINE
DOCUMENT NUMBER: 99143102 PubMed ID: 9988682
TITLE: Control of O-glycan branch formation. Molecular cloning of human cDNA encoding a novel beta1,6-N-acetylglucosaminyltransferase forming core 2 and core 4.
AUTHOR: Schwientek T; Nomoto M; Lavery S B; Merckx G; van Kessel A G; Bennett E P; Hollingsworth M A; Clausen H
CORPORATE SOURCE: School of Dentistry, University of Copenhagen, Norre Alle 20, 2200 Copenhagen N, Denmark.
CONTRACT NUMBER: 1 RO1 CA66234 (NCI)
1RO1 CA66234 (NCI)
5 P41 RR05351 (NCRR)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1999 Feb 19) 274 (8) 4504-12.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF038650
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990326
Last Updated on STN: 20000303
Entered Medline: 19990318
AB A novel human UDP-GlcNAc:Gal/GlcNAc beta1-3GalNAc alpha beta1,6GlcNAc-transferase, designated C2/4GnT, was identified by BLAST analysis of expressed **sequence tags**. The sequence of C2/4GnT encoded a putative type II transmembrane protein with significant sequence

similarity to human C2GnT and IGnT. Expression of the secreted form of C2/4GnT in insect cells showed that the gene product had UDP-N-acetyl-alpha-D-glucosamine:acceptor beta1, 6-N-acetylglucosaminyltransferase (beta1,6GlcNAc-transferase) activity. Analysis of substrate specificity revealed that the enzyme catalyzed O-glycan branch formation of the core 2 and core 4 type. NMR analyses of the product formed with core 3-para-nitrophenyl confirmed the product core 4-para-nitrophenyl. The coding region of C2/4GnT was contained in a single exon and located to chromosome 15q21.3. Northern analysis revealed a restricted **expression pattern** of C2/4GnT mainly in colon, **kidney**, pancreas, and small intestine. No expression of C2/4GnT was detected in brain, **heart**, liver, ovary, placenta, spleen, thymus, and peripheral blood leukocytes. The expression of core 2 O-glycans has been correlated with cell differentiation processes and cancer. The results confirm the predicted existence of a beta1,6GlcNAc-transferase that functions in both core 2 and core 4 O-glycan branch formation. The redundancy in beta1,6GlcNAc-transferases capable of forming core 2 O-glycans is important for understanding the mechanisms leading to specific changes in core 2 branching during cell development and malignant transformation.

L66 ANSWER 35 OF 49 MEDLINE DUPLICATE 24
 ACCESSION NUMBER: 1999400797 MEDLINE
 DOCUMENT NUMBER: 99400797 PubMed ID: 10471358
 TITLE: Chromosomal, in silico and in vitro expression analysis of cardiovascular-based genes encoding zinc finger proteins.
 AUTHOR: Dai K S; Liew C C
 CORPORATE SOURCE: The Cardiac Gene Unit, Institute of Medical Science
 Department of Laboratory Medicine and Pathobiology,
 University of Toronto, Ontario, Canada.
 SOURCE: JOURNAL OF MOLECULAR AND CELLULAR CARDIOLOGY, (1999 Sep)
 31
 (9) 1749-69.
 Journal code: 0262322. ISSN: 0022-2828.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199910
 ENTRY DATE: Entered STN: 19991014
 Last Updated on STN: 19991014
 Entered Medline: 19991004
 AB Three hundred and sixty expressed **sequence tags** (**ESTs**) from human **heart cDNA** libraries corresponding to one hundred and twenty six unique zinc finger proteins (ZFPs) were annotated and classified into seven types of ZFPs as reported previously. Among these 126 cvbZFPs (cardiovascular-based ZFPs), the C(2)H(2)-type and the C(2)C(2)-type are the two major ZFP types which account for more than 80% of ZFP genes present in the cardiovascular system. The **expression patterns** of 11 randomly selected ZFP genes (at least one for each type) in normal fetal, adult and hypertrophic adult **hearts**, respectively, were determined using reverse transcriptase-polymerase chain reaction (RT-PCR) analysis. The results suggest that ZFPs may be involved in the processes of either developmental control (downregulated or upregulated expression) or basic cellular functional regulation (constant expression). Interestingly,

(peroxisome assembly factor-1), a C(3)HC(4)-type ZFP (RING domain-containing ZFP) showing a downregulated **expression pattern** in normal tissues was found to be upregulated in hypertrophic adult **heart**, suggesting a possible role for this fetal gene in the pathogenesis of cardiac hypertrophy. In silico **Northern** analysis of 15 tissues showed that over 90% of cvbZFPs demonstrate widespread tissue distribution, suggesting the vast majority of ZFPs are functionally shared among tissues. The potential importance of transcriptional repressors in cardiovascular development and disease, such as HFHZ, was supported by the observation that one-third (39 of 126) of cvbZFPs possess this function. Of these, 26 are C(2)H(2)-type and the remaining 13 included 8 C(2)C(2)-type, 1 C(3)HC(4)-type, 1 C(2)HC(4)C(HD)-type, 2 C(3)H-type and 1 combination type. Of particular interest was the observation that ZFPs which contain a KRAB domain are the major subtype present (51.3% of the total repressors in cvbZFPs). Chromosomal distribution analysis showed that mapping loci of cvbZFP genes are concentrated on chromosomes 1, 3, 6, 8, 10, 11, 12, 19 and X. In particular, chromosome 19 appears to be enriched in ZFP genes with C(2)H(2)-type as the predominant type present. Overall, this report provides a fundamental initial step toward understanding the potential role of ZFPs in regulating cardiac development and disease. Copyright 1999 Academic Press.

L66 ANSWER 36 OF 49 MEDLINE DUPLICATE 25
 ACCESSION NUMBER: 1999313187 MEDLINE
 DOCUMENT NUMBER: 99313187 PubMed ID: 10386616
 TITLE: The human cadherin-10 gene: complete coding sequence, predominant expression in the brain, and mapping on chromosome 5p13-14.
 AUTHOR: Kools P; Vanhalst K; Van den Eynde E; van Roy F
 CORPORATE SOURCE: Department of Molecular Biology, Flanders Interuniversity Institute for Biotechnology (VIB)-University of Ghent, Belgium.
 SOURCE: FEBS LETTERS, (1999 Jun 11) 452 (3) 328-34.
 Journal code: 0155157. ISSN: 0014-5793.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
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 OTHER SOURCE: GENBANK-AF039747
 ENTRY MONTH: 199907
 ENTRY DATE: Entered STN: 19990727
 Last Updated on STN: 19990727
 Entered Medline: 19990712

AB In a quest for novel cadherin gene family members in the human **dbEST** database, an interesting **EST** clone was identified and chosen for subsequent analysis. Using the technique of 5' rapid amplification of **cdNA** ends, we isolated the complete coding sequence and a large part of the UTRs of a novel gene. The sequence appeared to correspond to the human cadherin-10 gene, whose sequence was only partially known before. The **expression pattern** of this cadherin was found to be largely brain-specific, with additional expression in both adult and fetal **kidney**, and with minor expression in **prostate** and fetal **lung**. By FISH analysis the genomic location was determined at human chromosome 5p13-14, which is nearby the reported positions of the human cadherin-6, -12, and cadherin-14 (CDH18) genes. Cadherin-10 shows high relationship to the

human cadherin-6 gene.

L66 ANSWER 37 OF 49 MEDLINE DUPLICATE 26
ACCESSION NUMBER: 1999339982 MEDLINE
DOCUMENT NUMBER: 99339982 PubMed ID: 10409429
TITLE: Prostate cancer expression profiling by cDNA sequencing analysis.
AUTHOR: Huang G M; Ng W L; Farkas J; He L; Liang H A; Gordon D; Yu J; Hood L
CORPORATE SOURCE: Department of Molecular Biotechnology, University of Washington, Seattle, Washington 98195, USA..
huanggm@yahoo.com
SOURCE: GENOMICS, (1999 Jul 15) 59 (2) 178-86.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AI524829; GENBANK-AI524830; GENBANK-AI524831;
GENBANK-AI524832; GENBANK-AI524833; GENBANK-AI524834;
GENBANK-AI524835; GENBANK-AI524836; GENBANK-AI524837;
GENBANK-AI524838; GENBANK-AI524839; GENBANK-AI524840;
GENBANK-AI524841; GENBANK-AI524842; GENBANK-AI524843;
GENBANK-AI524844; GENBANK-AI524845; GENBANK-AI524846;
GENBANK-AI524847; GENBANK-AI524848; GENBANK-AI524849;
GENBANK-AI524850; GENBANK-AI524851; GENBANK-AI524852;
GENBANK-AI524853; GENBANK-AI524854; GENBANK-AI524855;
GENBANK-AI524856; GENBANK-AI524857; GENBANK-AI524858; +
ENTRY MONTH: 199909
ENTRY DATE: Entered STN: 19990921
Last Updated on STN: 19990921
Entered Medline: 19990908

AB **Prostate** cancer is a frequently diagnosed solid tumor that is originated mostly from **prostate** epithelium. One of the key issues in **prostate** cancer research is to develop molecular markers that can effectively detect and distinguish the progression and malignancy of **prostate** tumors. Automated, single-pass **cDNA** sequencing was utilized to rapidly identify expressed genes in a number of **cDNA** libraries constructed from various normal and tumor prostatic tissues. These included cell lines as well as short-term epithelial culture. A total of 6604 expressed **sequence tags (ESTs)** were generated and searched against on-line nucleotide and protein databases. A relational database centric software system was constructed to process, store, and analyze **EST** data rapidly. **cDNA** contigs were also obtained by assembly of multiple **EST** sequences. Protein structural signatures were annotated using motif analysis tools including BLOCKS and an in-house-designed neural network. Cross-library comparisons revealed their unique gene expression profiles. Several differentially expressed **cDNA** clones were identified, and their **expression patterns** were confirmed by RNA dot blot and RT-PCR analyses.
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L66 ANSWER 38 OF 49 MEDLINE DUPLICATE 27
ACCESSION NUMBER: 1999110977 MEDLINE
DOCUMENT NUMBER: 99110977 PubMed ID: 9892814
TITLE: mRNA differential display analysis of nephrotic kidney glomeruli.
AUTHOR: Haltia A; Solin M; Luimula P; Kretzler M; Holthofer H
CORPORATE SOURCE: Haartman Institute, Division of Bacteriology and Immunology, University of Helsinki, Finland.

SOURCE: EXPERIMENTAL NEPHROLOGY, (1999 Jan-Feb) 7 (1) 52-8.
Journal code: 9302239. ISSN: 1018-7782.
PUB. COUNTRY: Switzerland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990316
Last Updated on STN: 20020420
Entered Medline: 19990301

AB BACKGROUND: Differential display RT-PCR (DDRT-PCR) is a new powerful technique for identification and characterization of altered gene expression in eukaryotic cells and tissues. We studied here changes in **kidney** glomerular gene expression in patients with congenital nephrotic syndrome of the Finnish type (CNF), an inherited **kidney** disease with heavy proteinuria already in utero. METHODS: Using the DDRT-PCR approach and isolated glomeruli from removed human **kidneys**, we compared the gene **expression patterns** of normal human and CNF glomeruli. Differential expression of candidate genes was verified by **Northern** blotting, and the corresponding PCR fragments were sequenced and compared to known sequences in databanks. RESULTS: We found several genes and **sequence tags** with altered expression in nephrotic glomeruli including fragments with close homologies to cytochrome c oxidase subunit I, integrin-linked kinase, insulin-like growth factor II receptor and eotaxin, and also clones resembling ankyrin and cadherin-like consensus sequences. CONCLUSION: All the sequences identified are of interest in respect to pathogenesis of proteinuria. Furthermore, this study reveals potentially new members to known gene families with tissue and cell type-specific expression.

L66 ANSWER 39 OF 49 MEDLINE DUPLICATE 28

ACCESSION NUMBER: 1998250717 MEDLINE
DOCUMENT NUMBER: 98250717 PubMed ID: 9582303
TITLE: A family of human beta3-galactosyltransferases.
Characterization of four members of a

UDP-galactose:beta-N-

acetyl-glucosamine/beta-nacetyl-galactosamine
beta-1,3-galactosyltransferase family.

AUTHOR: Amado M; Almeida R; Carneiro F; Levery S B; Holmes E H;
Nomoto M; Hollingsworth M A; Hassan H; Schwientek T;
Nielsen P A; Bennett E P; Clausen H

CORPORATE SOURCE: School of Dentistry, University of Copenhagen, Norre Alle
20, 2200 Copenhagen N, Denmark.

CONTRACT NUMBER: 1 RO1 CA66234 (NCI)
RO1 CA41521 (NCI)
RO1 CA70740 (NCI)

SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1998 May 22) 273 (21)
12770-8.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-Y15060; GENBANK-Y15061; GENBANK-Y15062
ENTRY MONTH: 199806
ENTRY DATE: Entered STN: 19980708
Last Updated on STN: 19980708
Entered Medline: 19980625

AB BLAST analysis of expressed **sequence tags** (

ESTs) using the coding sequence of a human UDP-galactose:beta-N-acetyl-glucosamine beta-1, 3-galactosyltransferase, designated beta3Gal-T1, revealed no **ESTs** with identical sequences but a large number with similarity. Three different sets of overlapping **ESTs** with sequence similarities to beta3Gal-T1 were compiled, and complete coding regions of these genes were obtained. Expression of two of these genes in the Baculo virus system showed that one represented a UDP-galactose:beta-N-acetyl-glucosamine beta-1, 3-galactosyltransferase (beta3Gal-T2) with similar kinetic properties as beta3Gal-T1. Another gene represented a UDP-galactose:beta-N-acetyl-galactosamine beta-1, 3-galactosyltransferase (beta3Gal-T4) involved in GM1/GD1 ganglioside synthesis, and this gene was highly similar to a recently reported rat GD1 synthase (Miyazaki, H., Fukumoto, S., Okada, M., Hasegawa, T., and Furukawa, K. (1997) J. Biol. Chem. 272, 24794-24799). **Northern** analysis of **mRNA** from human organs with the four homologous **cDNA** revealed different **expression patterns**. beta3Gal-T1 **mRNA** was expressed in brain, beta3Gal-T2 was expressed in brain and **heart**, and beta3Gal-T3 and -T4 were more widely expressed. The coding regions for each of the four genes were contained in single exons. beta3Gal-T2, -T3, and -T4 were localized to 1q31, 3q25, and 6p21.3, respectively, by **EST** mapping. The results demonstrate the existence of a family of homologous beta3-galactosyltransferase genes.

L66 ANSWER 40 OF 49 MEDLINE
 ACCESSION NUMBER: 1998349389 MEDLINE
 DOCUMENT NUMBER: 98349389 PubMed ID: 9686600
 TITLE: Cytokine-like factor-1, a novel soluble protein, shares homology with members of the cytokine type I receptor family.
 AUTHOR: Elson G C; Graber P; Losberger C; Herren S; Gretener D; Menoud L N; Wells T N; Kosco-Vilbois M H; Gauchat J F
 CORPORATE SOURCE: Department of Immunology, Geneva Biomedical Research Institute, Glaxo Wellcome Research and Development, Plan-les-Ouates, Switzerland.
 SOURCE: JOURNAL OF IMMUNOLOGY, (1998 Aug 1) 161 (3) 1371-9. Journal code: 2985117R. ISSN: 0022-1767.
 PUB. COUNTRY: United States
 LANGUAGE: English
 FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
 OTHER SOURCE: GENBANK-AF059293
 ENTRY MONTH: 199808
 ENTRY DATE: Entered STN: 19980820
 Last Updated on STN: 20000303
 Entered Medline: 19980812

AB In this report we describe the identification, cloning, and **expression pattern** of human cytokine-like factor 1 (hCLF-1) and the identification and cloning of its murine homologue. They were identified from expressed **sequence tags** using amino acid sequences from conserved regions of the cytokine type I receptor family. Human CLF-1 and murine CLF-1 shared 96% amino acid identity and significant homology with many cytokine type I receptors. CLF-1 is a secreted protein, suggesting that it is either a soluble subunit within a cytokine receptor complex, like the soluble form of the IL-6R alpha-chain, or a subunit of a multimeric cytokine, e.g., IL-12

p40. The highest levels of hCLF-1 **mRNA** were observed in lymph node,

spleen, thymus, appendix, placenta, stomach, **bone** marrow, and fetal **lung**, with constitutive expression of CLF-1 **mRNA** detected in a human **kidney** fibroblastic cell line. In fibroblast primary cell cultures, CLF-1 **mRNA** was up-regulated by TNF-alpha, IL-6, and IFN-gamma. Western blot analysis of recombinant forms of hCLF-1 showed that the protein has the tendency to form covalently linked di- and tetramers. These results suggest that CLF-1 is a novel soluble cytokine receptor subunit or part of a novel cytokine complex, possibly playing a regulatory role in the immune system and during fetal development.

L66 ANSWER 41 OF 49 MEDLINE DUPLICATE 29
ACCESSION NUMBER: 1998103635 MEDLINE
DOCUMENT NUMBER: 98103635 PubMed ID: 9443398
TITLE: Hevin, an antiadhesive extracellular matrix protein, is down-regulated in metastatic prostate adenocarcinoma.
AUTHOR: Nelson P S; Plymate S R; Wang K; True L D; Ware J L; Gan L;
CORPORATE SOURCE: Liu A Y; Hood L
Department of Molecular Biotechnology, University of Washington, Seattle 98195, USA.
SOURCE: CANCER RESEARCH, (1998 Jan 15) 58 (2) 232-6.
Journal code: 2984705R. ISSN: 0008-5472.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199802
ENTRY DATE: Entered STN: 19980217
Last Updated on STN: 19980217
Entered Medline: 19980204

AB Hevin, a gene closely related to the extracellular matrix protein SPARC, is an acidic cysteine-rich glycoprotein shown to be important for the adhesion and trafficking of cells through the endothelium. Through the use of differential display and differential **EST** analysis, we identified Hevin as a gene whose transcription is down-regulated in transformed **prostate** epithelial cell lines and metastatic **prostate** adenocarcinoma. These results were confirmed by comparing expression levels between normal and neoplastic human **prostate** tissues using **Northern** analysis. In situ hybridization with an 35S-labeled antisense riboprobe demonstrated the loss of Hevin expression in metastatic **prostate** carcinoma. The **expression pattern** of Hevin in transformed and metastatic epithelium may provide further insights into the complex cell adhesion events involved in the metastatic progression of **prostate** carcinoma.

L66 ANSWER 42 OF 49 MEDLINE DUPLICATE 30
ACCESSION NUMBER: 1998234542 MEDLINE
DOCUMENT NUMBER: 98234542 PubMed ID: 9570947
TITLE: Divergently transcribed overlapping genes expressed in liver and kidney and located in the 11p15.5 imprinted domain.
AUTHOR: Cooper P R; Smilnich N J; Day C D; Nowak N J; Reid L H; Pearsall R S; Reece M; Prawitt D; Landers J; Housman D E; Winterpacht A; Zabel B U; Pelletier J; Weissman B E; Shows T B; Higgins M J
CORPORATE SOURCE: Department of Human Genetics, Roswell Park Cancer Institute, Buffalo, New York 14263, USA.
CONTRACT NUMBER: CA63176 (NCI)

SOURCE: CA63333 (NCI)
 HG00333 (NHGRI)
 GENOMICS, (1998 Apr 1) 49 (1) 38-51.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AC001228; GENBANK-AF087428
 ENTRY MONTH: 199806
 ENTRY DATE: Entered STN: 19980708
 Last Updated on STN: 20000512
 Entered Medline: 19980625

AB Human chromosomal band 11p15.5 has been shown to contain genes involved in

the development of several pediatric and adult tumors and in Beckwith-Wiedemann syndrome (BWS). Overlapping P1 artificial chromosome clones from this region have been used as templates for genomic sequencing

in an effort to identify candidate genes for these disorders. PowerBLAST identified several matches with expressed **sequence tags** (**ESTs**) from fetal brain and liver **cDNA** libraries.

Northern blot analysis indicated that two of the genes identified by these **ESTs** encode **transcripts** of 1-1.5 kb with predominant expression in fetal and adult liver and **kidney**. With RT-PCR and RACE, full-length **transcripts** were isolated for these two genes, with the largest open reading frames encoding putative

proteins of 253 and 424 amino acids. Database comparison of the predicted amino acid sequence of the larger **transcript** indicated homology to integral membrane organic cation transporters; hence, we designate this gene ORCTL2 (organic cation transporter-like 2). An expressed sequence polymorphism provided evidence that the ORCTL2 gene exhibits "leaky" imprinting in both human fetal **kidney** and human fetal liver. The mouse orthologue (Orctl2) was identified, and a similar polymorphism was used to demonstrate maternal-specific expression of this gene in fetal liver from interspecific F1 mice. The predicted protein of the smaller gene showed no significant similarity in the database. **Northern** and RACE analyses suggest that this gene may have multiple transcription start sites. Determination of the genomic structure in humans indicated that the 5'-end of this **transcript** overlaps in divergent orientation with the first two exons of ORCTL2, suggesting a possible

role for antisense regulation of one gene by the other. We, therefore, provisionally name this second **transcript** ORCTL2S (ORCTL2-antisense). The **expression patterns** of these genes and the imprinted expression of ORCTL2 are suggestive of a possible role in the development of Wilms tumor (WT) and hepatoblastoma. Although SSCP analysis of 62 WT samples and 10 BWS patients did not result in the identification of any mutations in ORCTL2 or ORCTL2S, it will be

important to examine their **expression pattern** in tumors and BWS patients, since epigenetic alteration at these loci may play a role in the etiology of these diseases.

L66 ANSWER 43 OF 49 MEDLINE DUPLICATE 31
 ACCESSION NUMBER: 97238863 MEDLINE
 DOCUMENT NUMBER: 97238863 PubMed ID: 9083061
 TITLE: Primary structure and expression of matrilin-2, the closest

relative of cartilage matrix protein within the von Willebrand factor type A-like module superfamily.

AUTHOR: Deak F; Piecha D; Bachrati C; Paulsson M; Kiss I
 CORPORATE SOURCE: Institute of Biochemistry, Biological Research Center of the Hungarian Academy of Sciences, P. O. Box 521, Szeged H-6701, Hungary.

SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1997 Apr 4) 272 (14) 9268-74.
 Journal code: 2985121R. ISSN: 0021-9258.

PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-U69262; GENBANK-U69263
 ENTRY MONTH: 199705
 ENTRY DATE: Entered STN: 19970514
 Last Updated on STN: 19970514
 Entered Medline: 19970508

AB A mouse **cdna** encoding a novel member of the von Willebrand factor type A-like module superfamily was cloned. The protein precursor of 956 amino acids consists of a putative signal peptide, two von Willebrand factor type A-like domains connected by 10 epidermal growth factor-like modules, a potential oligomerization domain, and a unique segment, and it contains potential N-glycosylation sites. A sequence similarity search indicated the closest relation to the trimeric cartilage matrix protein (CMP). Since they constitute a novel protein family, we introduce the term

matrilin-2 for the new protein, reserving matrilin-1 as an alternative name for CMP. A 3.9-kilobase matrilin-2 **mRNA** was detected in a variety of mouse organs, including calvaria, uterus, **heart**, and brain, as well as fibroblast and osteoblast cell lines. Expressed human and rat **cdna sequence tags** indicate a high degree of interspecies conservation. A group of 120-150-kDa bands was, after reduction, recognized specifically with an antiserum against the matrilin-2-glutathione S-transferase fusion protein in media of the matrilin-2-expressing cell lines. Assuming glycosylation, this agrees well with the predicted minimum Mr of the mature protein (104,300). Immunolocalization of matrilin-2 in developing skeletal elements showed reactivity in the perichondrium and the osteoblast layer of trabecular **bone**. CMP binds both collagen fibrils and aggrecan, and because of the similar structure and complementary **expression pattern**, matrilin-2 is likely to perform similar functions in the extracellular matrix assembly of other tissues.

L66 ANSWER 44 OF 49 MEDLINE DUPLICATE 32

ACCESSION NUMBER: 97480719 MEDLINE
 DOCUMENT NUMBER: 97480719 PubMed ID: 9339364
 TITLE: Novel genes mapping to the critical region of the 5q-syndrome.

AUTHOR: Boultonwood J; Fidler C; Soularue P; Strickson A J; Kostrzewa M; Jaju R J; Cotter F E; Fairweather N; Monaco A P; Muller U; Lovett M; Jabs E W; Auffray C; Wainscoat J S

CORPORATE SOURCE: Leukaemia Research Fund Molecular Haematology Unit, University Department of Cellular Science, John Radcliffe Hospital, Oxford, United Kingdom.

SOURCE: GENOMICS, (1997 Oct 1) 45 (1) 88-96.
 Journal code: 8800135. ISSN: 0888-7543.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF010235; GENBANK-AF010236; GENBANK-AF010242;
 GENBANK-AF010244; GENBANK-AF010245
 ENTRY MONTH: 199711
 ENTRY DATE: Entered STN: 19971224
 Last Updated on STN: 20000303
 Entered Medline: 19971120

AB The 5q- syndrome is a myelodysplastic syndrome with specific
 hematological
 features and a good prognosis. Using molecular mapping techniques, we
 have

previously defined the critical region of gene loss of the 5q- chromosome
 in the 5q- syndrome as the approximately 5-Mb region at 5q31-q33 flanked
 by the genes for FGF1 and IL12B. This region is completely represented by
 a series of overlapping YACs, and we are currently generating a
 transcription map with the aim of identifying the tumor-suppressor gene
 associated with the development of the 5q- syndrome. In this study two
 techniques have been used: first, the screening of full-length
cDNA libraries with radiolabeled YACs and second, the mapping of
 chromosome 5-specific expressed **sequence tags** (**ESTs**)
 to a YAC contig. A 1-Mb YAC contig encompassing the CSF1R
 gene has been used to screen a fetal brain **cDNA** library, and
 this has resulted in the identification of two genes comprising one known
 gene previously localized to the region (ADRB2) and one known gene
 previously unlocalized. Six of 135 chromosome 5-specific **ESTs**
 were localized by PCR screening to the YAC contig mapping to the critical
 region of the 5q- syndrome. IMAGE **cDNA** clones for each of the
 six **ESTs** have been obtained. These seven (excluding ADRB2) newly
 assigned **cDNA** clones were subjected to further analysis. The
expression patterns of each of the **cDNA** clones
 have been established in a range of human tissues, including **bone**
 marrow. Six of seven **cDNAs** are expressed in human **bone**
 marrow. Six of seven **cDNAs** have no known homology to any
 deposited human sequences, and one (C29) is dihydropyrimidinase-related
 protein-3, a member of a novel gene family. Genomic localization and
expression patterns would suggest that these newly
 assigned **cDNAs** represent potential candidate genes for the 5q-
 syndrome.

L66 ANSWER 45 OF 49 MEDLINE DUPLICATE 33
 ACCESSION NUMBER: 97094765 MEDLINE
 DOCUMENT NUMBER: 97094765 PubMed ID: 8939999
 TITLE: Molecular cloning and characterization of human tissue
 inhibitor of metalloproteinase 4.
 AUTHOR: Greene J; Wang M; Liu Y E; Raymond L A; Rosen C; Shi Y E
 CORPORATE SOURCE: Human Genome Sciences, Inc., Rockville, Maryland
 20850-3338, USA. aecom.yu.edu.
 CONTRACT NUMBER: CA68064-01 (NCI)
 SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1996 Nov 29) 271 (48)
 30375-80.
 Journal code: 2985121R. ISSN: 0021-9258.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199701
 ENTRY DATE: Entered STN: 19970128
 Last Updated on STN: 20000303
 Entered Medline: 19970107

AB The tissue inhibitors of metalloproteinases (TIMPs) constitute a family of proteins, of which three members have so far been described. Using the expressed **sequence tag** sequencing approach, we have identified a novel TIMP-related **cdna** fragment and subsequently cloned a fourth human TIMP (TIMP-4) from a human **heart cdna** library. The open reading frame encodes a 224-amino acid precursor including a 29-residue secretion signal. The predicted structure of the new protein shares 37% sequence identity with TIMP-1 and 51% identity with TIMP-2 and -3. The protein has a predicted isoelectric point of 7.34. The open reading frame-directed expression of TIMP-4 protein in MDA-MB-435 human breast cancer cells showed metalloproteinase inhibitory activity on reverse zymography. By **Northern** analysis, only the adult **heart** showed abundant TIMP-4 **transcripts** with a 1.4-kilobase predominant **transcript** band; very low levels of the **transcripts** were detected in the **kidney**, placenta, colon, and testes, and no **transcripts** were detected in the liver, brain, **lung**, thymus, and spleen. This unique **expression pattern** suggests that TIMP-4 may function in a tissue-specific fashion in extracellular matrix homeostasis.

L66 ANSWER 46 OF 49 MEDLINE DUPLICATE 34
 ACCESSION NUMBER: 97115998 MEDLINE
 DOCUMENT NUMBER: 97115998 PubMed ID: 8957090
 TITLE: Molecular characterization and modular analysis of human MyD88.
 AUTHOR: Hardiman G; Rock F L; Balasubramanian S; Kastelein R A; Bazan J F
 CORPORATE SOURCE: Department of Molecular Biology, DNAX Research Institute, Palo Alto, California 94304-1104, USA.
 SOURCE: ONCOGENE, (1996 Dec 5) 13 (11) 2467-75.
 Journal code: 8711562. ISSN: 0950-9232.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-U70451
 ENTRY MONTH: 199701
 ENTRY DATE: Entered STN: 19970128
 Last Updated on STN: 19970128
 Entered Medline: 19970113

AB MyD88 was first characterized as a myeloid differentiation primary response gene in mice, activated in M1 myeloleukemic cells following interleukin-6 (IL-6) induced growth arrest and terminal differentiation. Analysis of expressed **sequence tags (ESTs)** from activated dendritic cell libraries led to the identification of **cdnas** encoding the human homolog (hMyD88). The original description of MyD88 as a 243 aa protein may reflect a truncated mouse **cdna** since the 2682 nt hMyD88 **cdna** predicts a 296 aa cytoplasmic protein. Consistent with this proposal is the detection of a 33 kDa protein in human **heart**, **kidney** and liver tissue. The **expression pattern** of MyD88 is also more widespread than originally believed: a 2.6 kb hMyD88 **mrna** species was found to be constitutively expressed in many adult human tissues; in addition MyD88 expression was observed in monocyte, T, B, NK and dendritic cells. The MyD88 protein has a modular structure composed of an N-terminal 'death domain' (DD) similar to the intracellular segments of

TNF receptor 1 (TNFR1) and FAS and a C-terminal region related to the signaling domains of vertebrate interleukin-1 receptors (IL-1R) and the Drosophila morphogen Toll. This intriguing structural framework may endow MyD88 with unique signaling capabilities.

L66 ANSWER 47 OF 49 MEDLINE DUPLICATE 35
ACCESSION NUMBER: 96375776 MEDLINE
DOCUMENT NUMBER: 96375776 PubMed ID: 8782065
TITLE: Identification of genes associated with myocardial development.
AUTHOR: Fung Y W; Liew C C
CORPORATE SOURCE: Department of Clinical Biochemistry, Toronto Hospital, University of Toronto, Canada.
SOURCE: JOURNAL OF MOLECULAR AND CELLULAR CARDIOLOGY, (1996 Jun) 28
(6) 1241-9.
Journal code: 0262322. ISSN: 0022-2828.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199611
ENTRY DATE: Entered STN: 19961219
Last Updated on STN: 19961219
Entered Medline: 19961127
AB We are conducting a **cdna** sequencing project using human **heart cdna** libraries to study expression of genes in the human **heart**. From our human **heart cdna** libraries, we have accumulated over 10,000 partial **cdna** sequences (expressed **sequence tags-ESTs**) representing both the previously uncharacterized and known **transcripts** expressed in the human **heart** (Liew et al., 1994). Currently, we have applied dot blot hybridization as a rapid approach to determine the genes putatively involved in myocardial development. Differential **expression patterns** of gene **transcripts** represented by the **cdna** clones can be revealed by comparing dot intensities on the autoradiographs, after hybridization with **cdna** probes generated from neonatal and adult **heart mRNAs**, **cdna** clones (1505) have been processed by dot blot hybridization, of which 924 and 581 represented novel and known **transcripts** respectively. Among the screened clones, about 1.4% were found to be differentially expressed during **heart** development. Further verification was accomplished by **Northern** blot analysis. By grouping the 581 clones corresponding to known **transcripts**, a study of the gene expression profile of the **heart** in the cardiovascular system can be achieved.

L66 ANSWER 48 OF 49 MEDLINE DUPLICATE 36
ACCESSION NUMBER: 97006147 MEDLINE
DOCUMENT NUMBER: 97006147 PubMed ID: 8853441
TITLE: Novel mouse embryonic renal marker gene products differentially expressed during kidney development.
AUTHOR: Kretzler M; Fan G; Rose D; Arend L J; Briggs J P; Holzman L
B
CORPORATE SOURCE: Department of Internal Medicine, University of Michigan Medical School, Ann Arbor 48109-0676, USA.
CONTRACT NUMBER: DK-37448 (NIDDK)
DK-39255 (NIDDK)
DK-40042 (NIDDK)
+

SOURCE: AMERICAN JOURNAL OF PHYSIOLOGY, (1996 Sep) 271 (3 Pt 2)
F770-7.
Journal code: 0370511. ISSN: 0002-9513.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-H15283; GENBANK-H32355; GENBANK-M10329;
GENBANK-N20517; GENBANK-X77398
ENTRY MONTH: 199612
ENTRY DATE: Entered STN: 19970128
Last Updated on STN: 19970128
Entered Medline: 19961205

AB Investigators approaching the problem of renal organogenesis have been hampered by a paucity of suitable molecular markers that specify distinct developmental phenotypes. To identify such markers, differential display-polymerase chain reaction (DD-PCR) was used to survey the temporal

pattern of gene expression in mouse **kidney** at 11.5, 13.5, 15.5, and 17.5 days after conception and in the adult **kidney**. Twenty-two differentially expressed amplification products were identified, isolated, and sequenced. Seventeen clones showed no significant similarity with previously reported nucleotide sequences: two were similar to two housekeeping gene products, and three were similar to human or rat expressed **sequence tags**. To confirm the differential **expression patterns** observed by DD-PCR, semiquantitative reverse transcription-PCR was performed using sequence-specific oligonucleotide primers. Nineteen of 22 clones were differentially expressed during **kidney** development [mouse embryonic renal marker (MERM) sequences 1-19]. The value of MERMs as developmental markers was further assessed in mouse metanephric organ culture, where the pattern of MERM **transcript** expression mimicked that observed in vivo. Therefore, the DD-PCR method permitted development of a panel of marker sequences that can be used to characterize renal developmental processes and that may allow the identification of novel, functionally relevant gene products.

L66 ANSWER 49 OF 49 MEDLINE DUPLICATE 37
ACCESSION NUMBER: 96163883 MEDLINE
DOCUMENT NUMBER: 96163883 PubMed ID: 8586430
TITLE: Analysis of expressed sequence tags from a fetal human heart cDNA library.
AUTHOR: Hwang D M; Fung Y W; Wang R X; Laurensen C M; Ng S H; Lam W Y; Tsui K W; Fung K P; Waye M; Lee C Y; +
CORPORATE SOURCE: Laboratory of Molecular Cardiology, Toronto Hospital, University of Toronto, Ontario, Canada.
SOURCE: GENOMICS, (1995 Nov 20) 30 (2) 293-8.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-R30692; GENBANK-R30693; GENBANK-R30694;
GENBANK-R30695; GENBANK-R30696; GENBANK-R30697;
GENBANK-R30698; GENBANK-R30699; GENBANK-R30700;
GENBANK-R30701; GENBANK-R30702; GENBANK-R30703;
GENBANK-R30704; GENBANK-R30705; GENBANK-R30706;
GENBANK-R30707; GENBANK-R30708; GENBANK-R30709;
GENBANK-R30710; GENBANK-R30711; GENBANK-R30712;
GENBANK-R30713; GENBANK-R30714; GENBANK-R30715;
GENBANK-R30716; GENBANK-R30717; GENBANK-R30718;

GENBANK-R30719; GENBANK-R30720; GENBANK-R30721; +
ENTRY MONTH: 199603
ENTRY DATE: Entered STN: 19960404
Last Updated on STN: 19960404
Entered Medline: 19960325

AB Single-pass sequencing of randomly selected **cDNA** clones to generate expressed **sequence tags (ESTs)** has been widely used to identify novel genes and to study gene expression in

a variety of tissues. We have generated 2244 **ESTs** from a human fetal **heart** library (GenBank Accession Nos. R30692-30774 and R56965-58824), which we present in this report. Of these, 51.7% showed no homology to known genes or were similar only to other **ESTs**, while 48.4% demonstrated homology to known **transcripts**. A total of 764 **ESTs** corresponding to known genes were used to study gene **expression patterns** in the fetal **heart** and to analyze differences in these patterns from those observed in the adult **heart**. These analyses demonstrate the utility of **ESTs** and sequence-tagged clones in comparative studies of gene expression in the cardiovascular system, and they reveal that differential gene expression underlies the structural and functional characteristics of the developing **heart**.

=>

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
19:04:09
ON 08 JUL 2002

L1 13496 S EST
L2 34 S L1(S) (NO#(W)CORRELAT?)
L3 21 DUP REM L2 (13 DUPLICATES REMOVED)
L4 3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5 1972 S L4(S) (PROTEIN OR PEPTIDE)
L6 1748 S L5(S) (EXPRESS?)
L7 775 S L6(S)DATABASE#
L8 355 DUP REM L7 (420 DUPLICATES REMOVED)
L9 96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN)
L10 47 S L8(S)GENBANK
L11 87 S L8(S) (HEART OR BONE OR BRAIN)
L12 137 S L11 OR L9
L13 1 S L12 AND (NO#(W)EXPRESS?)
L14 67 S L12(S) (TRANSCRI?)
L15 86 S L8(S)NORTHERN
L16 50 S L1(S) (NO#(2W)CORRELAT?)
L17 16 S L16 NOT L2
L18 12 DUP REM L17 (4 DUPLICATES REMOVED)
L19 54 S L1(S) (NO#(3W)CORRELAT?)
L20 0 S L19 NOT L1
L21 20 S L19 NOT L2
L22 4 S L21 NOT L16

FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002

L23 13496 S EST OR (SEQUENCE(W)TAG#)
L24 234 S L23 AND DATABASE#/TI
L25 0 S L24 AND (NO(3W)CORRELAT?)
L26 234 S L24(S)DATABASE#
L27 2221 S L23(S)DATABASE#

L28 4 S L27(S) (NO#(3W)CORRELAT?)
 L29 1174 S L23(S) (BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVA
 L30 310 S L29(S)NORTHERN
 L31 133 S L30 AND DATABASE#
 L32 78 DUP REM L31 (55 DUPLICATES REMOVED)
 L33 1072 S L23(S) (PREDICT? OR ANTICIPAT?)
 L34 22 S L33 AND DATABASE#/TI
 L35 13 DUP REM L34 (9 DUPLICATES REMOVED)
 L36 22 S L34(S)DATABASE#
 L37 2221 S L23(S)DATABASE#
 L38 612 S L37(S)TISSUE
 L39 58 S L38(S)PROSTATE
 L40 10 S L39 AND PREDICT?
 L41 6 DUP REM L40 (4 DUPLICATES REMOVED)
 L42 1 S L23(S) (CANNOT(3W)PREDICT)
 L43 13596 S L23 OR DBEST
 L44 6719 S L43(S)EXPRESS?
 L45 192 S L44(S)BLAST
 L46 47 S L45(S)PREDICT?
 L47 27 DUP REM L46 (20 DUPLICATES REMOVED)
 L48 2 S L43(S)RELIED
 L49 1 S L43(S) (("NOT" OR CANNOT) (W)PREDICT?)
 L50 0 S L43(S) (CANNOT(W)ANTICIPATE)
 L51 797 S L43(S)TRANSCRIPTS
 L52 28 S L43(S) ((NO(W)EXPRESSION) OR ("NOT" (W)EXPRESSED))
 L53 17 DUP REM L52 (11 DUPLICATES REMOVED)
 L54 546 S L43 AND (EXPRESSION(A)PATTERN#)
 L55 15 S L54 AND DATABASE#/TI
 L56 9 DUP REM L55 (6 DUPLICATES REMOVED)
 L57 239 S L43 AND DATABASE#/TI
 L58 5 S L57 AND PREDICT
 L59 3 DUP REM L58 (2 DUPLICATES REMOVED)
 L60 1735 S L43(S)LIBRAR?
 L61 34 S L60(S)PREDICT
 L62 19 DUP REM L61 (15 DUPLICATES REMOVED)
 L63 4276 S L43(S) (MRNA OR NORTHERN OR CDNA OR TRANSCRIPT#)
 L64 335 S L63(S) (EXPRESSION(A)PATTERN#)
 L65 86 S L64(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
 L66 49 DUP REM L65 (37 DUPLICATES REMOVED)

=> s s l43(s) (expression(a)pattern#)

MISSING OPERATOR S L43

The search profile that was entered contains terms or nested terms that are not separated by a logical operator.

=> s l43(s) (expression(a)pattern#)

L67 430 L43(S) (EXPRESSION(A) PATTERN#)

=> s l67 and database#/ti

L68 12 L67 AND DATABASE#/TI

=> dup rem l68

PROCESSING COMPLETED FOR L68

L69 6 DUP REM L68 (6 DUPLICATES REMOVED)

=> d ibib abs tot

L69 ANSWER 1 OF 6

MEDLINE

DUPLICATE 1

ACCESSION NUMBER: 2002185034 MEDLINE

DOCUMENT NUMBER: 21917691 PubMed ID: 11920606

TITLE: Identification of cancer/testis genes by database

mining and mRNA expression analysis.

AUTHOR: Scanlan Matthew J; Gordon Claudia M; Williamson Barbara;
Lee Sang-Yull; Chen Yao-Tseng; Stockert Elisabeth;
Jungbluth Achim; Ritter Gerd; Jager Dirk; Jager Elke;
Knuth
Alexander; Old Lloyd J

CORPORATE SOURCE: Ludwig Institute for Cancer Research, New York Branch at
Memorial Sloan-Kettering Cancer Center, New York, NY
10021,
USA.. scanlanm@mskcc.org

SOURCE: INTERNATIONAL JOURNAL OF CANCER, (2002 Apr 1) 98 (4)
485-92.
Journal code: 0042124. ISSN: 0020-7136.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200205

ENTRY DATE: Entered STN: 20020403
Last Updated on STN: 20020511
Entered Medline: 20020510

AB Cancer/testis (CT) antigens are immunogenic proteins expressed
predominantly in gametogenic tissue and cancer; they are considered
promising target molecules for cancer vaccines. The identification of new
CT genes is essential to the development of polyvalent cancer vaccines
designed to overcome tumor heterogeneity and antigen loss. In the current
study, a search for new CT genes was conducted by mining the Unigene
database for gene clusters that contain expressed **sequence**
tags derived solely from both normal testis and tumor-derived cDNA
libraries. This search identified 1,325 different
cancer/testis-associated
Unigene clusters. The mRNA **expression pattern** of 73
cancer/testis-associated Unigene clusters was assessed by reverse
transcriptase polymerase chain reaction. Three gene products,
CT15/Hs.177959, CT16/Hs.245431 and CT17/Hs.178062, were detected only in
testis and in tumor tissue. CT15 is equivalent to ADAM2/fertilin-beta.
CT16, an uncharacterized gene product, has homology (30-50%) to members
of
the GAGE gene family and is 89% identical to CT16.2/Hs.293317, indicating
that CT16 and CT16.2 are members of a new GAGE gene family. The
uncharacterized gene product, CT17, has homology (30%) to phospholipase
A1. RT-PCR analysis showed that CT15 is expressed exclusively in renal
cancer, whereas CT16 and CT17 are expressed in a range of human cancers.
Real-time RT-PCR analysis of newly defined CT genes and the prototype CT
antigens, MAGE-3 and NY-ESO-1, revealed low levels (less than 3% of the
level detected in testis) of CT15, CT16 and NY-ESO-1 in a limited range
of
normal, non-gametogenic tissues. This study demonstrates the merits of
database mining with respect to the identification of tissue-restricted
gene products expressed in cancer.
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L69 ANSWER 2 OF 6

MEDLINE

DUPLICATE 2

ACCESSION NUMBER: 2001075345 MEDLINE

DOCUMENT NUMBER: 20566896 PubMed ID: 11114628

TITLE: Strategy for identification of novel glucose transporter
family members by using internet-based genomic
databases.

AUTHOR: Phay J E; Hussain H B; Moley J F

CORPORATE SOURCE: Washington University School of Medicine and the St Louis
Veteran's Administration Medical Center, St Louis, MO,

USA.

SOURCE: SURGERY, (2000 Dec) 128 (6) 946-51.
Journal code: 0417347. ISSN: 0039-6060.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals

ENTRY MONTH: 200101

ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010103

AB BACKGROUND: We previously reported that medullary thyroid carcinomas and pheochromocytomas avidly take up the glucose analog fluoro-deoxyglucose on positron emission tomography but do not express any of the known human facilitative glucose transporters. We therefore hypothesized that a novel glucose transporter is responsible for glucose uptake in these tumors. METHODS: Internet-based Expressed **Sequence Tags** and high throughput genome sequence databases were screened for novel sequences homologous to the known glucose transporters. Derived clones were used to screen cDNA libraries. Sequence comparison and hydrophobic analysis of the putative proteins were performed. RESULTS: We identified

2 novel genes (GLUT8 and GLUT9) that are members of the facilitative glucose transporter family. The putative GLUT8 and GLUT9 proteins have 44% and

31% sequence identity to GLUT5 and GLUT3, respectively. Hydrophobic analysis showed both have exofacial and transmembrane domains consistent with a hexose transporter. CONCLUSIONS: By using the Expressed **Sequence Tags** database, we identified novel members of the glucose transporter family. Further work will establish function and **expression patterns** in medullary thyroid carcinomas and pheochromocytomas. Internet-based genomic databases allow rapid screening and identification of candidate sequences of novel members of human gene families.

L69 ANSWER 3 OF 6 MEDLINE DUPLICATE 3

ACCESSION NUMBER: 2000063237 MEDLINE

DOCUMENT NUMBER: 20063237 PubMed ID: 10592203

TITLE: BodyMap: a human and mouse gene expression **database**

AUTHOR: Hishiki T; Kawamoto S; Morishita S; Okubo K

CORPORATE SOURCE: Institute for Molecular and Cellular Biology, Osaka University, 1-3 Yamadaoka, Suita, Osaka 565-0871, Japan.

SOURCE: NUCLEIC ACIDS RESEARCH, (2000 Jan 1) 28 (1) 136-8.
Journal code: 0411011. ISSN: 0305-1048.

PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200002

ENTRY DATE: Entered STN: 20000314
Last Updated on STN: 20000314
Entered Medline: 20000225

AB BodyMap is a human and mouse gene expression database that has been maintained since 1993. It is based on site-directed 3'-**ESTs** collected from non-biased cDNA libraries constructed at Osaka University and contains >270 000 sequences from 60 human and 38 mouse tissues. The site-directed nature of the **sequence tags** allows unequivocal grouping of tags representing the same transcript and provides

abundance information for each transcript in different parts of the body. Our collection of **ESTs** was compared periodically with other public databases for cross referencing. The histological resolution of source tissues and unique cloning strategy that minimized cloning bias enabled BodyMap to support three unique mRNA based experiments in silico. First, the recurrence information for clones in each library provides a rough estimate of the mRNA composition of each source tissue. Second, a user can search the entire data set with nucleotide sequences or keywords to assess **expression patterns** of particular genes. Third, and most important, BodyMap allows a user to select genes that

have

a desired **expression pattern** in humans and mice.

BodyMap is accessible through the WWW at <http://bodymap.ims.u-tokyo.ac.jp>

L69 ANSWER 4 OF 6 MEDLINE DUPLICATE 4
 ACCESSION NUMBER: 1999063661 MEDLINE
 DOCUMENT NUMBER: 99063661 PubMed ID: 9847150
 TITLE: The Mouse Genome Database (MGD): genetic and genomic information about the laboratory mouse. The Mouse Genome Database Group.
 AUTHOR: Blake J A; Richardson J E; Davisson M T; Eppig J T
 CORPORATE SOURCE: The Jackson Laboratory, 600 Main Street, Bar Harbor, ME 04609, USA.. jblake@informatics.jax.org
 CONTRACT NUMBER: HG00330 (NHGRI)
 SOURCE: NUCLEIC ACIDS RESEARCH, (1999 Jan 1) 27 (1) 95-8. Journal code: 0411011. ISSN: 0305-1048.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199903
 ENTRY DATE: Entered STN: 19990326
 Last Updated on STN: 20000303
 Entered Medline: 19990316
 AB The Mouse Genome Database (MGD) focuses on the integration of mapping, homology, polymorphism and molecular data about the laboratory mouse. Detailed descriptions of genes including their chromosomal location, gene function, disease associations, mutant phenotypes, molecular polymorphisms and links to representative sequences including **ESTs** are integrated within MGD. The association of information from experiment to gene to genome requires careful coordination and implementation of standardized vocabularies, unique nomenclature constructions, and detailed information derived from multiple sources. This information is linked to other public databases that focus on additional information such as **expression patterns**, sequences, bibliographic details and large mapping panel data. Scientists participate in the curation of MGD data by generating the Chromosome Committee Reports, consulting on gene family nomenclature revisions, and providing descriptions of mouse strain characteristics and of new mutant phenotypes. MGD is accessible at <http://www.informatics.jax.org>

L69 ANSWER 5 OF 6 MEDLINE DUPLICATE 5
 ACCESSION NUMBER: 97049974 MEDLINE
 DOCUMENT NUMBER: 97049974 PubMed ID: 8894702
 TITLE: Characterization of the human ABC superfamily: isolation and mapping of 21 new genes using the expressed sequence tags database.
 AUTHOR: Allikmets R; Gerrard B; Hutchinson A; Dean M
 CORPORATE SOURCE: Laboratory of Viral Carcinogenesis, National Cancer

Institute, Frederick Cancer Research and Development
Center, MD 21702, USA.

SOURCE: HUMAN MOLECULAR GENETICS, (1996 Oct) 5 (10) 1649-55.
Journal code: 9208958. ISSN: 0964-6906.

PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-U66672; GENBANK-U66692

ENTRY MONTH: 199702

ENTRY DATE: Entered STN: 19970219
Last Updated on STN: 19970219
Entered Medline: 19970204

AB As an approach to characterizing all human ATP-binding cassette (ABC) superfamily genes, a search of the human expressed **sequence tag** (EST) database was performed using sequences from known ABC genes. A total of 105 clones, containing sequences of potential ABC genes, were identified, representing 21 distinct genes. This brings the total number of characterized human ABC genes from 12 to 33. The new ABC genes were mapped by PCR on somatic cell and radiation hybrid panels and yeast artificial chromosomes (YACs). The genes are located on human chromosomes 1, 2, 3, 4, 6, 7, 10, 12, 13, 14, 16, 17 and X; at locations distinct from previously mapped members of the superfamily. The characterized genes display extensive diversity in sequence and **expression pattern** and this information was utilized to determine potential structural, functional and evolutionary relationships to previously characterized members of the ABC superfamily.

L69 ANSWER 6 OF 6 MEDLINE DUPLICATE 6

ACCESSION NUMBER: 95284468 MEDLINE

DOCUMENT NUMBER: 95284468 PubMed ID: 7766993

TITLE: Characterization and mapping of three new mammalian ATP-binding transporter genes from an EST **database**

AUTHOR: Allikmets R; Gerrard B; Glavac D; Ravnik-Glavac M; Jenkins N A; Gilbert D J; Copeland N G; Modi W; Dean M

CORPORATE SOURCE: Laboratory of Viral Carcinogenesis, National Cancer Institute, Frederick Cancer Research and Development Center, Maryland 21702-1201, USA.

CONTRACT NUMBER: N0-CO-74101 (NCI)

SOURCE: MAMMALIAN GENOME, (1995 Feb) 6 (2) 114-7.
Journal code: 9100916. ISSN: 0938-8990.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-U18235; GENBANK-U18236; GENBANK-U18237

ENTRY MONTH: 199507

ENTRY DATE: Entered STN: 19950713
Last Updated on STN: 19950713
Entered Medline: 19950705

AB Analysis of the human expressed **sequence tag** (EST) database identified four clones that contain sequences of previously uncharacterized genes, members of the ATP-binding cassette (ABC) superfamily. Two new ABC genes (EST20237, 31252) are located at Chromosome (Chr) 1q42 and 1q25 respectively in humans, as determined by FISH; at locations distinct from previously mapped genes of this superfamily. Two additional clones, **EST** 600 and **EST** 1596, were found to represent different ATP-binding domains of the same gene, ABC2. This gene was localized to 9q34 in humans by FISH and to the proximal region of Chr 2 in mice by linkage analysis. All genes display

extensive diversity in sequence and **expression pattern**
 . We present several approaches to characterizing **EST** clones and demonstrate that the analysis of **EST** clones from different tissues is a powerful approach to identify new members of important gene families. Some drawbacks of using **EST** databases, including chimerism of cDNA clones, are discussed.

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT 19:04:09

ON 08 JUL 2002

```
L1      13496 S EST
L2      34 S L1(S) (NO#(W) CORRELAT?)
L3      21 DUP REM L2 (13 DUPLICATES REMOVED)
L4      3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5      1972 S L4(S) (PROTEIN OR PEPTIDE)
L6      1748 S L5(S) (EXPRESS?)
L7      775 S L6(S) DATABASE#
L8      355 DUP REM L7 (420 DUPLICATES REMOVED)
L9      96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
L10     47 S L8(S) GENBANK
L11     87 S L8(S) (HEART OR BONE OR BRAIN)
L12     137 S L11 OR L9
L13      1 S L12 AND (NO#(W) EXPRESS?)
L14     67 S L12(S) (TRANSCRI?)
L15     86 S L8(S) NORTHERN
L16     50 S L1(S) (NO#(2W) CORRELAT?)
L17     16 S L16 NOT L2
L18     12 DUP REM L17 (4 DUPLICATES REMOVED)
L19     54 S L1(S) (NO#(3W) CORRELAT?)
L20      0 S L19 NOT L1
L21     20 S L19 NOT L2
L22      4 S L21 NOT L16
```

FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002

```
L23     13496 S EST OR (SEQUENCE(W) TAG#)
L24     234 S L23 AND DATABASE#/TI
L25      0 S L24 AND (NO(3W) CORRELAT?)
L26     234 S L24(S) DATABASE#
L27     2221 S L23(S) DATABASE#
L28      4 S L27(S) (NO#(3W) CORRELAT?)
L29     1174 S L23(S) (BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVA
L30     310 S L29(S) NORTHERN
L31     133 S L30 AND DATABASE#
L32      78 DUP REM L31 (55 DUPLICATES REMOVED)
L33     1072 S L23(S) (PREDICT? OR ANTICIPAT?)
L34      22 S L33 AND DATABASE#/TI
L35      13 DUP REM L34 (9 DUPLICATES REMOVED)
L36      22 S L34(S) DATABASE#
L37     2221 S L23(S) DATABASE#
L38     612 S L37(S) TISSUE
L39      58 S L38(S) PROSTATE
L40      10 S L39 AND PREDICT?
L41      6 DUP REM L40 (4 DUPLICATES REMOVED)
L42      1 S L23(S) (CANNOT(3W) PREDICT)
L43     13596 S L23 OR DBEST
L44     6719 S L43(S) EXPRESS?
```

L45 192 S L44(S)BLAST
 L46 47 S L45(S)PREDICT?
 L47 27 DUP REM L46 (20 DUPLICATES REMOVED)
 L48 2 S L43(S)RELIED
 L49 1 S L43(S) (("NOT" OR CANNOT) (W) PREDICT?)
 L50 0 S L43(S) (CANNOT(W) ANTICIPATE)
 L51 797 S L43(S)TRANSCRIPTS
 L52 28 S L43(S) ((NO(W)EXPRESSION) OR ("NOT"(W)EXPRESSED))
 L53 17 DUP REM L52 (11 DUPLICATES REMOVED)
 L54 546 S L43 AND (EXPRESSION(A)PATTERN#)
 L55 15 S L54 AND DATABASE#/TI
 L56 9 DUP REM L55 (6 DUPLICATES REMOVED)
 L57 239 S L43 AND DATABASE#/TI
 L58 5 S L57 AND PREDICT
 L59 3 DUP REM L58 (2 DUPLICATES REMOVED)
 L60 1735 S L43(S)LIBRAR?
 L61 34 S L60(S)PREDICT
 L62 19 DUP REM L61 (15 DUPLICATES REMOVED)
 L63 4276 S L43(S) (MRNA OR NORTHERN OR CDNA OR TRANSCRIPT#)
 L64 335 S L63(S) (EXPRESSION(A)PATTERN#)
 L65 86 S L64(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
 L66 49 DUP REM L65 (37 DUPLICATES REMOVED)
 L67 430 S L43(S) (EXPRESSION(A)PATTERN#)
 L68 12 S L67 AND DATABASE#/TI
 L69 6 DUP REM L68 (6 DUPLICATES REMOVED)

=> s l23(3a)predict?

L70 99 L23(3A) PREDICT?

=> s l70(3a) (expression or transcription)

L71 2 L70(3A) (EXPRESSION OR TRANSCRIPTION)

=> d ibib abs tot

L71 ANSWER 1 OF 2 MEDLINE
 ACCESSION NUMBER: 2000304747 MEDLINE
 DOCUMENT NUMBER: 20304747 PubMed ID: 10843799
 TITLE: Identification of differentially expressed genes in
 cardiac hypertrophy by analysis of expressed sequence tags.
 AUTHOR: Hwang D M; Dempsey A A; Lee C Y; Liew C C
 CORPORATE SOURCE: The Cardiac Gene Unit, Department of Laboratory Medicine
 and Pathobiology, The Centre for Cardiovascular Research,
 The Toronto Hospital, Toronto, Ontario, M5G 1L5, Canada.
 SOURCE: GENOMICS, (2000 May 15) 66 (1) 1-14.
 Journal code: 8800135. ISSN: 0888-7543.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200007
 ENTRY DATE: Entered STN: 20000728
 Last Updated on STN: 20000728
 Entered Medline: 20000720

AB Cardiac hypertrophy is an adaptive response to chronic hemodynamic
 overload. We employed a whole-genome approach using expressed sequence
 tags (ESTs) to characterize gene transcription and identify new genes
 overexpressed in cardiac hypertrophy. Analysis of general transcription
 patterns revealed a proportional increase in transcripts related to
 cell/organism defense and a decrease in transcripts related to cell
 structure and motility in hypertrophic hearts compared to normal hearts.

Detailed comparison of individual gene expression identified 64 genes potentially overexpressed in hypertrophy, of 232 candidate genes derived from a set of 77,692 cardiac ESTs, including 47,856 ESTs generated in our laboratory. Of these, 29 were good candidates ($P < 0.0002$) and 35 were weaker candidates ($P < 0.005$). RT-PCR of a number of these candidate genes

demonstrated correspondence of **EST-based predictions** of gene **expression** with in vitro levels. Consistent with an organ under various stresses, up to one-half of the good candidates predicted to exhibit differential expression were genes potentially involved in stress response. Analyses of general transcription patterns and of single-gene expression levels were also suggestive of increased protein synthesis in the hypertrophic myocardium. Overall, these results depict a scenario compatible with current understanding of cardiac hypertrophy. However, the identification of several genes not previously known to exhibit increased expression in cardiac hypertrophy (e.g., prostaglandin D synthases; CD59 antigen) also suggests a number of new avenues for further investigation. These data demonstrate the utility of genome-based resources for investigating questions of cardiovascular biology and medicine.

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L71 ANSWER 2 OF 2 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2000:335010 BIOSIS
DOCUMENT NUMBER: PREV200000335010
TITLE: Identification of differentially expressed genes in cardiac hypertrophy by analysis of expressed sequence tags.
AUTHOR(S): Hwang, David M.; Dempsey, Adam A.; Lee, Cheuk-Yu; Liew, Choong-Chin (1)
CORPORATE SOURCE: (1) Department of Laboratory Medicine and Pathobiology, Banting Institute, University of Toronto, 100 College Street, Toronto, ON, M5G 1L5 Canada
SOURCE: Genomics, (May 15, 2000) Vol. 66, No. 1, pp. 1-14. print. ISSN: 0888-7543.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Cardiac hypertrophy is an adaptive response to chronic hemodynamic overload. We employed a whole-genome approach using expressed sequence tags (ESTs) to characterize gene transcription and identify new genes overexpressed in cardiac hypertrophy. Analysis of general transcription patterns revealed a proportional increase in transcripts related to cell/organism defense and a decrease in transcripts related to cell structure and motility in hypertrophic hearts compared to normal hearts. Detailed comparison of individual gene expression identified 64 genes potentially overexpressed in hypertrophy, of 232 candidate genes derived from a set of 77,692 cardiac ESTs, including 47,856 ESTs generated in our laboratory. Of these, 29 were good candidates ($P < 0.0002$) and 35 were weaker candidates ($P < 0.005$). RT-PCR of a number of these candidate genes

demonstrated correspondence of **EST-based predictions** of gene **expression** with in vitro levels. Consistent with an organ under various stresses, up to one-half of the good candidates predicted to exhibit differential expression were genes potentially involved in stress response. Analyses of general transcription patterns and of single-gene expression levels were also suggestive of increased protein synthesis in the hypertrophic myocardium. Overall, these results depict a scenario compatible with current understanding of cardiac hypertrophy. However, the identification of several genes not previously known to exhibit increased expression in cardiac hypertrophy (e.g.,

prostaglandin D synthases; CD59 antigen) also suggests a number of new avenues for further investigation. These data demonstrate the utility of genome-based resources for investigating questions of cardiovascular biology and medicine.

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
19:04:09
ON 08 JUL 2002

L1 13496 S EST
L2 34 S L1(S) (NO#(W) CORRELAT?)
L3 21 DUP REM L2 (13 DUPLICATES REMOVED)
L4 3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5 1972 S L4(S) (PROTEIN OR PEPTIDE)
L6 1748 S L5(S) (EXPRESS?)
L7 775 S L6(S) DATABASE#
L8 355 DUP REM L7 (420 DUPLICATES REMOVED)
L9 96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN)
L10 47 S L8(S) GENBANK
L11 87 S L8(S) (HEART OR BONE OR BRAIN)
L12 137 S L11 OR L9
L13 1 S L12 AND (NO#(W) EXPRESS?)
L14 67 S L12(S) (TRANSCRI?)
L15 86 S L8(S) NORTHERN
L16 50 S L1(S) (NO#(2W) CORRELAT?)
L17 16 S L16 NOT L2
L18 12 DUP REM L17 (4 DUPLICATES REMOVED)
L19 54 S L1(S) (NO#(3W) CORRELAT?)
L20 0 S L19 NOT L1
L21 20 S L19 NOT L2
L22 4 S L21 NOT L16

FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002

L23 13496 S EST OR (SEQUENCE(W) TAG#)
L24 234 S L23 AND DATABASE#/TI
L25 0 S L24 AND (NO(3W) CORRELAT?)
L26 234 S L24(S) DATABASE#
L27 2221 S L23(S) DATABASE#
L28 4 S L27(S) (NO#(3W) CORRELAT?)
L29 1174 S L23(S) (BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVA)
L30 310 S L29(S) NORTHERN
L31 133 S L30 AND DATABASE#
L32 78 DUP REM L31 (55 DUPLICATES REMOVED)
L33 1072 S L23(S) (PREDICT? OR ANTICIPAT?)
L34 22 S L33 AND DATABASE#/TI
L35 13 DUP REM L34 (9 DUPLICATES REMOVED)
L36 22 S L34(S) DATABASE#
L37 2221 S L23(S) DATABASE#
L38 612 S L37(S) TISSUE
L39 58 S L38(S) PROSTATE
L40 10 S L39 AND PREDICT?
L41 6 DUP REM L40 (4 DUPLICATES REMOVED)
L42 1 S L23(S) (CANNOT(3W) PREDICT)
L43 13596 S L23 OR DBEST
L44 6719 S L43(S) EXPRESS?
L45 192 S L44(S) BLAST
L46 47 S L45(S) PREDICT?

L47 27 DUP REM L46 (20 DUPLICATES REMOVED)
 L48 2 S L43(S) RELIED
 L49 1 S L43(S) (("NOT" OR CANNOT) (W) PREDICT?)
 L50 0 S L43(S) (CANNOT(W) ANTICIPATE)
 L51 797 S L43(S) TRANSCRIPTS
 L52 28 S L43(S) ((NO(W) EXPRESSION) OR ("NOT" (W) EXPRESSED))
 L53 17 DUP REM L52 (11 DUPLICATES REMOVED)
 L54 546 S L43 AND (EXPRESSION(A) PATTERN#)
 L55 15 S L54 AND DATABASE#/TI
 L56 9 DUP REM L55 (6 DUPLICATES REMOVED)
 L57 239 S L43 AND DATABASE#/TI
 L58 5 S L57 AND PREDICT
 L59 3 DUP REM L58 (2 DUPLICATES REMOVED)
 L60 1735 S L43(S) LIBRAR?
 L61 34 S L60(S) PREDICT
 L62 19 DUP REM L61 (15 DUPLICATES REMOVED)
 L63 4276 S L43(S) (MRNA OR NORTHERN OR CDNA OR TRANSCRIPT#)
 L64 335 S L63(S) (EXPRESSION(A) PATTERN#)
 L65 86 S L64(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
 L66 49 DUP REM L65 (37 DUPLICATES REMOVED)
 L67 430 S L43(S) (EXPRESSION(A) PATTERN#)
 L68 12 S L67 AND DATABASE#/TI
 L69 6 DUP REM L68 (6 DUPLICATES REMOVED)
 L70 99 S L23(3A) PREDICT?
 L71 2 S L70(3A) (EXPRESSION OR TRANSCRIPTION)

=> l43(5a)predict?

L43(5A)PREDICT? IS NOT A RECOGNIZED COMMAND

The previous command name entered was not recognized by the system.

For a list of commands available to you in the current file, enter
 "HELP COMMANDS" at an arrow prompt (=>).

=> s l43(5a)predict?

L72 152 L43(5A) PREDICT?

=> s l72(5a)(expression or transcription)

L73 3 L72(5A) (EXPRESSION OR TRANSCRIPTION)

=> s l73 not l71

L74 1 L73 NOT L71

=> d ibib abs

L74 ANSWER 1 OF 1 MEDLINE
 ACCESSION NUMBER: 2001453697 MEDLINE
 DOCUMENT NUMBER: 21390742 PubMed ID: 11499904
 TITLE: Identification of two down-regulated genes in rat liver
 allografts by mRNA differential display.
 AUTHOR: Lin Y C; Goto S; Pan T L; Hong Y R; Lin C L; Lord R;
 Chiang K C; Lai C Y; Tseng H P; Hsu L W; Iwashita S; Kitano S;
 Chen C L
 CORPORATE SOURCE: Department of Surgery, Chang Gung Memorial Hospital,
 Niao-Sung, Kaohsiung, Taiwan.
 SOURCE: TRANSPLANT INTERNATIONAL, (2001 Jun) 14 (3) 153-8.
 Journal code: 8908516. ISSN: 0934-0874.
 PUB. COUNTRY: Germany; Germany, Federal Republic of
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200201

ENTRY DATE: Entered STN: 20010814
 Last Updated on STN: 20020125
 Entered Medline: 20020111

AB Total RNA differential display (DD) using random primers was performed
 for rat orthotopic liver transplantation (OLT) models. DA (RT1a) donor livers
 were transplanted into DA, PVG (RT1c), and LEW (RT1l) recipients: (1)
 syngeneic OLT (DA-DA): no rejection occurs; (2) allogeneic OLT (DA-PVG):
 rejection occurs, but is naturally overcome without immunosuppression;
 (3) allogeneic OLT (DA-LEW): animals die of acute rejection within 14 days.
 cDNA was isolated from selected bands, re-amplified for sequencing, and
 confirmed by Northern blots. Two down-regulated genes were observed in
 day-7 allogeneic OLT livers (DA-PVG, DA-LEW), while they were
 consistently
 expressed in day-7 syngeneic OLT (DA-DA) livers. These two genes were
 identified as alpha-glutathione sulfotransferase (alpha-GST) Ya gene and
 estrogen sulfotransferase (EST), respectively. Northern blots confirmed
 that their expression was down-regulated in OLT (DA-PVG) livers on days
 7-26 and gradually restored. The mRNA **expression** of GST and
 EST may be good markers to **predict** rejection or
 induction of tolerance.

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
 19:04:09
 ON 08 JUL 2002

L1 13496 S EST
 L2 34 S L1(S) (NO#(W) CORRELAT?)
 L3 21 DUP REM L2 (13 DUPLICATES REMOVED)
 L4 3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
 L5 1972 S L4(S) (PROTEIN OR PEPTIDE)
 L6 1748 S L5(S) (EXPRESS?)
 L7 775 S L6(S) DATABASE#
 L8 355 DUP REM L7 (420 DUPLICATES REMOVED)
 L9 96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
 L10 47 S L8(S) GENBANK
 L11 87 S L8(S) (HEART OR BONE OR BRAIN)
 L12 137 S L11 OR L9
 L13 1 S L12 AND (NO#(W) EXPRESS?)
 L14 67 S L12(S) (TRANSCRI?)
 L15 86 S L8(S) NORTHERN
 L16 50 S L1(S) (NO#(2W) CORRELAT?)
 L17 16 S L16 NOT L2
 L18 12 DUP REM L17 (4 DUPLICATES REMOVED)
 L19 54 S L1(S) (NO#(3W) CORRELAT?)
 L20 0 S L19 NOT L1
 L21 20 S L19 NOT L2
 L22 4 S L21 NOT L16

FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002

L23 13496 S EST OR (SEQUENCE(W) TAG#)
 L24 234 S L23 AND DATABASE#/TI
 L25 0 S L24 AND (NO(3W) CORRELAT?)
 L26 234 S L24(S) DATABASE#
 L27 2221 S L23(S) DATABASE#
 L28 4 S L27(S) (NO#(3W) CORRELAT?)

L29 1174 S L23(S) (BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVA
 L30 310 S L29(S)NORTHERN
 L31 133 S L30 AND DATABASE#
 L32 78 DUP REM L31 (55 DUPLICATES REMOVED)
 L33 1072 S L23(S) (PREDICT? OR ANTICIPAT?)
 L34 22 S L33 AND DATABASE#/TI
 L35 13 DUP REM L34 (9 DUPLICATES REMOVED)
 L36 22 S L34(S)DATABASE#
 L37 2221 S L23(S)DATABASE#
 L38 612 S L37(S)TISSUE
 L39 58 S L38(S)PROSTATE
 L40 10 S L39 AND PREDICT?
 L41 6 DUP REM L40 (4 DUPLICATES REMOVED)
 L42 1 S L23(S) (CANNOT(3W)PREDICT)
 L43 13596 S L23 OR DBEST
 L44 6719 S L43(S)EXPRESS?
 L45 192 S L44(S)BLAST
 L46 47 S L45(S)PREDICT?
 L47 27 DUP REM L46 (20 DUPLICATES REMOVED)
 L48 2 S L43(S)RELIED
 L49 1 S L43(S) ((("NOT" OR CANNOT) (W) PREDICT?))
 L50 0 S L43(S) (CANNOT(W)ANTICIPATE)
 L51 797 S L43(S)TRANSCRIPTS
 L52 28 S L43(S) ((NO(W)EXPRESSION) OR ("NOT" (W) EXPRESSED))
 L53 17 DUP REM L52 (11 DUPLICATES REMOVED)
 L54 546 S L43 AND (EXPRESSION(A)PATTERN#)
 L55 15 S L54 AND DATABASE#/TI
 L56 9 DUP REM L55 (6 DUPLICATES REMOVED)
 L57 239 S L43 AND DATABASE#/TI
 L58 5 S L57 AND PREDICT
 L59 3 DUP REM L58 (2 DUPLICATES REMOVED)
 L60 1735 S L43(S)LIBRAR?
 L61 34 S L60(S)PREDICT
 L62 19 DUP REM L61 (15 DUPLICATES REMOVED)
 L63 4276 S L43(S) (MRNA OR NORTHERN OR CDNA OR TRANSCRIPT#)
 L64 335 S L63(S) (EXPRESSION(A)PATTERN#)
 L65 86 S L64(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
 L66 49 DUP REM L65 (37 DUPLICATES REMOVED)
 L67 430 S L43(S) (EXPRESSION(A)PATTERN#)
 L68 12 S L67 AND DATABASE#/TI
 L69 6 DUP REM L68 (6 DUPLICATES REMOVED)
 L70 99 S L23(3A)PREDICT?
 L71 2 S L70(3A) (EXPRESSION OR TRANSCRIPTION)
 L72 152 S L43(5A)PREDICT?
 L73 3 S L72(5A) (EXPRESSION OR TRANSCRIPTION)
 L74 1 S L73 NOT L71

=> s l43(s)hypothetical

L75 64 L43(S) HYPOTHETICAL

=> s l75(s)(express? or transci?)

L76 55 L75(S) (EXPRESS? OR TRANSCI?)

=> dup rem l76

PROCESSING COMPLETED FOR L76

L77 34 DUP REM L76 (21 DUPLICATES REMOVED)

=> d ibib abs tot

L77 ANSWER 1 OF 34 MEDLINE

ACCESSION NUMBER: 2002261011 MEDLINE

DUPLICATE 1

DOCUMENT NUMBER: 21995865 PubMed ID: 12000731
TITLE: Mapping and gene expression profile of the minimally overrepresented 8q24 region in prostate cancer.
AUTHOR: Tsuchiya Norihiko; Kondo Yasushi; Takahashi Atsushi; Pawar Hemant; Qian Junqi; Sato Kazunari; Lieber Michael M; Jenkins Robert B
CORPORATE SOURCE: Department of Urology, Mayo Clinic, Rochester, Minnesota 55905, USA.
CONTRACT NUMBER: CA15083 (NCI)
SOURCE: AMERICAN JOURNAL OF PATHOLOGY, (2002 May) 160 (5) 1799-806.

Journal code: 0370502. ISSN: 0002-9440.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 200206
ENTRY DATE: Entered STN: 20020510
Last Updated on STN: 20020605
Entered Medline: 20020604

AB We have recently reported that overrepresentation of 8q24 (c-myc) is associated with clinical progression in prostate cancer. In this study, we map the boundaries of the overrepresented region within 8q23-q24 using interphase fluorescent in situ hybridization analysis of paraffin-embedded prostate cancer specimens. One hundred primary prostate cancers and three prostate cancer cell lines were evaluated, and the minimally overrepresented region could be narrowed to the approximately 8.2-Mb region between D8S514 and H47317. This region includes c-myc and is wholly within 8q24. Eukaryotic translation initiation factor 3 subunit 3 does not seem to be overrepresented independent of c-myc in prostate cancer. The cell lines PC3 and DU145 have and do not have 8q24 overrepresentation, respectively. We then selected 39 **expressed sequence tags (ESTs)** within and surrounding the minimally overrepresented region and performed **expression** analysis using Northern blot hybridization. Five **ESTs**/genes including c-myc were overexpressed in both the PC3 cell line and DU145, but the PC3 to DU145 **expression** ratios were <2. Seven **ESTs** were overexpressed twofold or more in PC3 compared to DU145. This group included hyaluronan synthase 2, nephroblastoma-overexpressed gene, eukaryotic translation initiation factor 3 subunit 3, and an **EST** (R69368) encoding a **hypothetical** protein (BM009). These seven genes as well as c-myc are candidate target genes within the overrepresented 8q24 region and their overexpression may be associated with prostate cancer progression.

L77 ANSWER 2 OF 34 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:283669 BIOSIS
DOCUMENT NUMBER: PREV200200283669
TITLE: Expressed sequence tags from roots and nodule primordia of Lotus japonicus infected with Mesorhizobium loti.
AUTHOR(S): Poulsen, Carsten (1); Podenphant, Lone
CORPORATE SOURCE: (1) Department of Molecular and Structural Biology, Laboratory of Gene Expression, University of Aarhus, Gustav Wieds Vej 10, DK, Aarhus C: CHP@mbio.aau.dk Denmark
SOURCE: Molecular Plant-Microbe Interactions, (April, 2002) Vol. 15, No. 4, pp. 376-379. print.

ISSN: 0894-0282.

DOCUMENT TYPE: Article

LANGUAGE: English

AB Messenger RNA from young *Lotus japonicus* roots carrying root nodule primordia appearing after inoculation with *Mesorhizobium loti* bacteria were used to construct a cDNA **expression** library. Single-pass sequencing employing colony-polymerase chain reaction (PCR) and analysis of PCR products established a total of 2,397 new **expressed sequence tags (ESTs)**. We have putatively identified 1,236 known and 484 **hypothetical** proteins coded by the corresponding mRNAs. The remaining cDNAs are unknown (316) or redundant overlapping cDNAs (361). We hope that this batch of **ESTs** will assist in the recognition of plant genes involved during development of nitrogen-fixing root nodules.

L77 ANSWER 3 OF 34

MEDLINE

DUPLICATE 2

ACCESSION NUMBER: 2002229697 MEDLINE

DOCUMENT NUMBER: 21963940 PubMed ID: 11966884

TITLE: Leveraging genomic databases: from an *Aedes albopictus* mosquito cell line to the malaria vector *Anopheles gambiae* via the *Drosophila* genome project.

AUTHOR: Eccleston E D; Gerenday Anna; Fallon Ann M

CORPORATE SOURCE: ThermoFinnigan Protein Chemistry Unit, MicroChemical Facility, Academic Health Center, University of Minnesota, St. Paul, MN 55108, USA.

CONTRACT NUMBER: AI 36258 (NIAID)

AI 43971 (NIAID)

SOURCE: INSECT MOLECULAR BIOLOGY, (2002 Apr) 11 (2) 187-95.

Journal code: 9303579. ISSN: 0962-1075.

PUB. COUNTRY: England: United Kingdom

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200207

ENTRY DATE: Entered STN: 20020423

Last Updated on STN: 20020704

Entered Medline: 20020703

AB An important justification for genome sequencing efforts is the anticipation that data from model organisms will provide a framework for the more rapid analysis of other, less studied genomes. In this investigation, we sequenced an internal region of 25 amino acids from a

52

kDa protein that was differentially **expressed** in 20-hydroxyecdysone-treated *Aedes albopictus* cells in culture. Within the GenBank non-mouse and non-human **expressed sequence tag (EST)** database, this "Aedes peptide" uncovered a putative homology to **hypothetical** translation products from *Anopheles gambiae*, *Caenorhabditis elegans* and *Drosophila melanogaster*.

The

hypothetical translation product from *D. melanogaster*, which included 462 amino acids, uncovered five **expressed sequence tags (ESTs)** from the malaria vector, *Anopheles gambiae*. When the *Anopheles ESTs* were aligned against the **hypothetical** *Drosophila* protein, we found that in aggregate they covered 324 amino acids, with gaps measuring 19, 30, and 87 amino acids. To approximate the complete amino acid sequence, gaps between translation products from *Anopheles ESTs* were replaced with corresponding amino acids from *Drosophila* to arrive at a calculated mass of 51 104 and a pI of 5.84 for the mosquito protein, consistent with the position of the *Ae. albopictus* protein on two-dimensional polyacrylamide gels. Finally, tandem mass spectrometry of a tryptic digest of the 52 kDa

of Ae. albopictus protein revealed 33 peptides with masses within 1 Dalton of those predicted from an in silico digestion of the reconstructed Anopheles protein. In addition to providing the first direct evidence that a **hypothetical** protein in Drosophila is in fact translated, this analysis provides a general approach for maximizing recovery, from existing databases, of information that can facilitate prioritization of efforts among several candidate proteins.

L77 ANSWER 4 OF 34 MEDLINE DUPLICATE 3
 ACCESSION NUMBER: 2001271890 MEDLINE
 DOCUMENT NUMBER: 21223026 PubMed ID: 11322891
 TITLE: Molecular cloning and functional expression of rat liver cytosolic acetyl-CoA hydrolase.
 AUTHOR: Suematsu N; Okamoto K; Shibata K; Nakanishi Y; Isohashi F
 CORPORATE SOURCE: Department of Biochemistry, St Marianna University School of Medicine, Kanagawa, Japan.
 SOURCE: EUROPEAN JOURNAL OF BIOCHEMISTRY, (2001 May) 268 (9) 2700-9.
 PUB. COUNTRY: Journal code: 0107600. ISSN: 0014-2956.
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AB040609
 ENTRY MONTH: 200106
 ENTRY DATE: Entered STN: 20010611
 Last Updated on STN: 20010611
 Entered Medline: 20010607

AB A cytosolic acetyl-CoA hydrolase (CACH) was purified from rat liver to homogeneity by a new method using Triton X-100 as a stabilizer. We digested the purified enzyme with an endopeptidase and determined the N-terminal amino-acid sequences of the two proteolytic fragments. From the sequence data, we designed probes for RT-PCR, and amplified CACH cDNA from rat liver mRNA. The CACH cDNA contains a 1668-bp ORF encoding a protein of 556 amino-acid residues (62 017 Da). Recombinant **expression** of the cDNA in insect cells resulted in overproduction of functional acetyl-CoA hydrolase with comparable acyl-CoA chain-length specificity and Michaelis constant for acetyl-CoA to those of the native CACH. Database searching shows no homology to other known proteins, but reveals high similarities to two mouse **expressed sequence tags** (91% and 93% homology) and human mRNA for KIAA0707 **hypothetical** protein (50% homology) of unknown function.

L77 ANSWER 5 OF 34 MEDLINE DUPLICATE 4
 ACCESSION NUMBER: 2002015181 MEDLINE
 DOCUMENT NUMBER: 21317940 PubMed ID: 11425228
 TITLE: The proteome of maize leaves: use of gene sequences and expressed sequence tag data for identification of proteins with peptide mass fingerprints.
 AUTHOR: Porubleva L; Vander Velden K; Kothari S; Oliver D J; Chitnis P R
 CORPORATE SOURCE: Department of Biochemistry, Biophysics and Molecular Biology, Iowa State University, Ames 50011, USA.
 SOURCE: ELECTROPHORESIS, (2001 May) 22 (9) 1724-38.
 PUB. COUNTRY: Journal code: 8204476. ISSN: 0173-0835.
 Germany: Germany, Federal Republic of

Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20020121
Last Updated on STN: 20020121
Entered Medline: 20011204

AB As a first step in establishing a proteome database for maize, we have embarked on the identification of the leaf proteins resolved on two-dimensional (2-D) gels. We detected nearly 900 spots on the gels with a pH 4-7 gradient and over 200 spots on the gels with a pH 6-11 gradient when the proteins were visualized with colloidal Coomassie blue. Peptide mass fingerprints for 300 protein spots were obtained with matrix assisted laser desorption/ionization-time of flight (MALDI-TOF) mass spectrometer and 149 protein spots were identified using the protein databases. We also searched the pdbEST databases to identify the leaf proteins and verified 66% of the protein spots that had been identified using the protein databases. Sixty-seven additional protein spots were identified from **expressed sequence tags (ESTs)**. Many abundant leaf proteins are present in multiple spots. Functions of over 50% of the abundant leaf proteins are either unknown or **hypothetical**. Our results show that **EST** databases in conjunction with peptide mass fingerprints can be used for identifying proteins from organisms with incomplete genome sequence information.

L77 ANSWER 6 OF 34 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:526231 BIOSIS
DOCUMENT NUMBER: PREV200100526231
TITLE: Random sequencing of cDNAs and identification of mRNAs.
AUTHOR(S): Anderson, James V. (1); Horvath, David P.
CORPORATE SOURCE: (1) Biosciences Research Laboratory, Plant Science Research, U.S. Department of Agriculture, Agricultural Research Service, 1605 Albrecht Boulevard, Fargo, ND, 58105: andersjv@fargo.ars.usda.gov USA
SOURCE: Weed Science, (September October, 2001) Vol. 49, No. 5, pp. 590-597. print.
ISSN: 0043-1745.

DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

AB As a first step toward developing a genomics-based research program to study growth and development of underground adventitious shoot buds of leafy spurge, we initiated a leafy spurge **expressed sequence tag (EST)** database. From the approximately 2,000 clones randomly isolated from a cDNA library made from a population containing growth-induced underground adventitious shoot buds, we have obtained **ESTs** for 1,105 cDNAs. Approximately 29% of the leafy spurge **EST** database consists of **expressed** genes of unknown identity (**hypothetical** proteins), and 10% represents ribosomal proteins. The remaining 60% of the database is composed of **expressed** genes that show BLASTX sequence identity scores of gtoreq80 with known GenBank accessions. Clones showing sequence identity to a Histone H3, a gibberellic acid-responsive gene, Tubulin, and a light-harvesting chlorophyll a/b-binding protein were shown to be differentially **expressed** in underground adventitious shoot buds of leafy spurge after breaking of dormancy. RNA encoding a putative

cyclin-dependent protein kinase (CDK)-activating kinase, a gene associated with cell division, and Scarecrow-like 7, a gene involved in GA signaling, were present at similar levels in dormant and growth-induced underground adventitious shoot buds. These data show how even a small **EST** database can be used to develop a genomics-based research program that will help us identify genes responsive to or involved in the mechanisms controlling underground adventitious shoot bud growth and development.

L77 ANSWER 7 OF 34 MEDLINE
 ACCESSION NUMBER: 2001312137 MEDLINE
 DOCUMENT NUMBER: 21278998 PubMed ID: 11385108
 TITLE: A set of 840 mouse oocyte genes with well-matched human homologues.
 AUTHOR: Stanton J L; Green D P
 CORPORATE SOURCE: Department of Anatomy and Structural Biology, University of Otago, Medical School, P.O.Box 913, Dunedin, New Zealand.
 SOURCE: MOLECULAR HUMAN REPRODUCTION, (2001 Jun) 7 (6) 521-43.
 Journal code: 9513710. ISSN: 1360-9947.
 PUB. COUNTRY: England: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200108
 ENTRY DATE: Entered STN: 20010903
 Last Updated on STN: 20010903
 Entered Medline: 20010830

AB GenBank contains 14 477 **expressed sequence tags (EST)** derived from mouse oocyte cDNA libraries: 3499 of these are from two unfertilized oocyte libraries and 10 978 are from two fertilized oocyte libraries. Gene **expression** profiles were obtained for these libraries by matching library **EST** to UniGene clusters. The 14 477 **EST** identified 4226 UNIGENES: These were screened using HomoloGene to identify 1386 homologous UniGene clusters in two other species with one of the matches being human. Within these human matches, 840 encoded named proteins, 223 encoded **hypothetical** proteins, and 323 encoded clustered **EST**. The set of named genes provides the first step in establishing a database of genes **expressed** in mouse oocytes and, by extension, human oocytes.

L77 ANSWER 8 OF 34 MEDLINE DUPLICATE 5
 ACCESSION NUMBER: 2002048325 MEDLINE
 DOCUMENT NUMBER: 21630798 PubMed ID: 11775060
 TITLE: 'VIT1', a novel gene associated with vitiligo.
 AUTHOR: Le Poole I C; Sarangarajan R; Zhao Y; Stennett L S; Brown T
 L; Sheth P; Miki T; Boissy R E
 CORPORATE SOURCE: Department of Pathology, Loyola University Chicago, Illinois 60513, USA.. ilepool@lumc.edu
 CONTRACT NUMBER: AR46115 (NIAMS)
 SOURCE: PIGMENT CELL RESEARCH, (2001 Dec) 14 (6) 475-84.
 Journal code: 8800247. ISSN: 0893-5785.
 PUB. COUNTRY: Denmark
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AL117620; GENBANK-U73737
 ENTRY MONTH: 200206

ENTRY DATE: Entered STN: 20020125
Last Updated on STN: 20020627
Entered Medline: 20020626

AB To define genes associated with the pigmentary disorder vitiligo, gene **expression** was compared in non-lesional melanocytes cultured from three vitiligo patients and from three control melanocyte cultures by differential display. A basic local alignment search tool search did not reveal homology of six differentially **expressed** cDNA fragments to previously identified **expressed sequence tags**; thus, one was used to screen a melanocyte cDNA library. The underlying VIT1 gene maps to chromosome 2p16. The 3' portion of the VIT1 message is complementary to the 3' end of hMSH6 mRNA, enabling the formation of RNA-RNA hybrids, which may interfere with G/T mismatch repair function. Moreover, the aligned cDNA sequence revealed an open reading frame identical to a **hypothetical** protein **expressed** in brain, with a similarity to Drosophila calmodulin, and containing a zinc-finger motif partially identical to N-recognin. **Expression** of ORF mRNA was confirmed for multiple skin cell types, suggesting its importance for skin physiology.

L77 ANSWER 9 OF 34 MEDLINE DUPLICATE 6
ACCESSION NUMBER: 2002057218 MEDLINE
DOCUMENT NUMBER: 21643879 PubMed ID: 11784032
TITLE: Systematic screening and expression analysis of the head organizer genes in Xenopus embryos.
AUTHOR: Shibata M; Itoh M; Ohmori S Y; Shinga J; Taira M
CORPORATE SOURCE: Department of Biological Sciences, Graduate School of Science, University of Tokyo, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan.
SOURCE: DEVELOPMENTAL BIOLOGY, (2001 Nov 15) 239 (2) 241-56. Journal code: 0372762. ISSN: 0012-1606.
PUB. COUNTRY: United States
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200201
ENTRY DATE: Entered STN: 20020125
Last Updated on STN: 20020131
Entered Medline: 20020130

AB We describe here a systematic screen of an anterior endomesoderm (AEM) cDNA library to isolate novel genes which are **expressed** in the head organizer region. After removing clones which hybridized to labeled cDNA probes synthesized with total RNA from a trunk region of tailbud embryos, the 5' ends of 1039 randomly picked cDNA clones were sequenced to make **expressed sequence tags** (ESTs), which formed 754 tentative unique clusters. Those clusters were compared against public databases and classified according to similarities found to other genes and gene products. Of them, 151 clusters were identified as known Xenopus genes, including eight organizer-specific ones (5.3%). Gene **expression** pattern screening was performed for 198 unique clones, which were selected because they either have no known function or are predicted to be developmental regulators in other species. The screen revealed nine possible organizer-specific clones (4.5%), four of which appeared to be **expressed** in the head organizer region. Detailed **expression** analysis from gastrula to neurula stages

showed that these four genes named crescent, P7E4 (homologous to human **hypothetical** genes), P8F7 (an unclassified gene), and P17F11 (homologous to human and Arabidopsis **hypothetical** genes) demarcate spatiotemporally distinct subregions of the AEM corresponding to the head organizer region. These results indicate that our screening strategy is effective in isolating novel region-specific genes.
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L77 ANSWER 10 OF 34 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:463029 BIOSIS

DOCUMENT NUMBER: PREV200100463029

TITLE: SAND, a new protein family: From nucleic acid to protein structure and function prediction.

AUTHOR(S): Cottage, Amanda; Edwards, Yvonne J. K.; Elgar, Greg (1)

CORPORATE SOURCE: (1) UK Human Genome Mapping Project Resource Centre, Hinxton, Wellcome Trust Genome Campus, Cambridge, CB10

1SB:

gelgar@hgmp.mrc.ac.uk UK

SOURCE: Comparative and Functional Genomics, (August, 2001) Vol. 2,

No. 4, pp. 226-235. print.

ISSN: 1531-6912.

DOCUMENT TYPE: Article

LANGUAGE: English

SUMMARY LANGUAGE: English

AB As a result of genome, **EST** and cDNA sequencing projects, there are huge numbers of predicted and/or partially characterised protein sequences compared with a relatively small number of proteins with experimentally determined function and structure. Thus, there is a considerable attention focused on the accurate prediction of gene function and structure from sequence by using bioinformatics. In the course of our analysis of genomic sequence from Fugu rubripes, we identified a novel gene, SAND, with significant sequence identity to **hypothetical** proteins predicted in Saccharomyces cerevisiae, Schizosaccharomyces pombe, Caenorhabditis elegans, a Drosophila melanogaster gene, and mouse and human cDNAs. Here we identify a further SAND homologue in human and Arabidopsis thaliana by use of standard computational tools. We describe the genomic organisation of SAND in these evolutionarily divergent species and identify sequence homologues from **EST** database searches confirming the **expression** of SAND in over 20 different eukaryotes. We confirm the **expression** of two different SAND paralogues in mammals and determine **expression** of one SAND in other vertebrates and eukaryotes. Furthermore, we predict structural properties of SAND, and characterise conserved sequence motifs in this protein family.

L77 ANSWER 11 OF 34 MEDLINE

ACCESSION NUMBER: 2002319820 IN-PROCESS

DOCUMENT NUMBER: 22057596 PubMed ID: 12063399

TITLE: Comparative mapping of five coding DNA sequences on cattle chromosomes 7 and 25.

AUTHOR: Goldammer T; Kata S R; Brunner R M; Schwerin M; Womack J E

CORPORATE SOURCE: Department of Veterinary Pathobiology, Texas A&M University, College Station, TX (USA).

SOURCE: CYTOGENETICS AND CELL GENETICS, (2001) 95 (3-4) 192-5.
Journal code: 0367735. ISSN: 0301-0171.

PUB. COUNTRY: Switzerland

Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020614
Last Updated on STN: 20020614

AB Comparative mapping of four genes and one unknown coding DNA sequence in breakpoint positions of bovine chromosomes (BTA) 7 and 25 are presented. Performing a genome data base search five bovine **expressed sequence tags** from the MARC library matched with human genes coding for the general transcription factor IIIC polypeptide 1 (GTF3C1), the **hypothetical** protein KIAA0556, the interleukin 4 receptor (IL4R), the regulatory factor X-associated ankyrin-containing protein (RFXANK), and with an unknown human coding sequence partially homologous to the genomic cosmid clone R30923. Loci for these sequences were COMPASS predicted on BTA7 or BTA18 and to BTA18 or BTA25. Mapping

was performed in a cattle-hamster somatic hybrid cell panel and a cattle-hamster 5000 rad whole genome radiation hybrid panel. GTF3C1, KIAA0556 and IL4R were assigned to the centromere region of BTA25 and RFXANK and R30923 close to the centromere of BTA7. The assignments contribute to the identification of evolutionary chromosome break points between human chromosomes 16 and 19 and BTA7, BTA18, and BTA25. Copyright 2002 S. Karger AG, Basel

L77 ANSWER 12 OF 34 MEDLINE DUPLICATE 7
ACCESSION NUMBER: 2001106564 MEDLINE
DOCUMENT NUMBER: 20574776 PubMed ID: 11125074
TITLE: trEST, trGEN and Hits: access to databases of predicted protein sequences.
AUTHOR: Pagni M; Iseli C; Junier T; Falquet L; Jongeneel V; Bucher P
CORPORATE SOURCE: Swiss Institute of Bioinformatics, Ludwig Institute for Cancer Research, Chemin des Boveresses 155, CH-1066, Epalinges s/Lausanne, Switzerland.
SOURCE: NUCLEIC ACIDS RESEARCH, (2001 Jan 1) 29 (1) 148-51.
JOURNAL code: 0411011. ISSN: 1362-4962.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200102
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010521
Entered Medline: 20010208

AB High throughput genome (HTG) and **expressed sequence tag (EST)** sequences are currently the most abundant nucleotide sequence classes in the public database. The large volume, high degree of fragmentation and lack of gene structure annotations prevent efficient and effective searches of HTG and **EST** data for protein sequence homologies by standard search methods. Here, we briefly describe three newly developed resources that should make discovery of interesting genes in these sequence classes easier in the future, especially to biologists not having access to a powerful local bioinformatics environment. trEST and trGEN are regularly regenerated databases of **hypothetical** protein sequences predicted from **EST** and HTG sequences, respectively. Hits is a web-based data retrieval and analysis system providing access to precomputed matches between protein sequences (including sequences from trEST and trGEN) and patterns and profiles from Prosite and Pfam. The three resources can be accessed via the Hits home page (<http://hits.isb-sib.ch>).

L77 ANSWER 13 OF 34 MEDLINE

ACCESSION NUMBER: 2002319812 IN-PROCESS

DOCUMENT NUMBER: 22057588 PubMed ID: 12063391

TITLE: Localization, genomic organization, and alternative transcription of a novel human SAM-dependent methyltransferase gene on chromosome 2p22-->p21.

AUTHOR: Zhang Y; Gorrry M C; Hart P S; Pettenati M J; Wang L; Marks J J; Lu X; Hart T C

CORPORATE SOURCE: Center for Craniofacial and Dental Genetics, University of Pittsburgh School of Dental Medicine, Pittsburgh PA

(USA).

SOURCE: CYTOGENETICS AND CELL GENETICS, (2001) 95 (3-4) 146-52.
Journal code: 0367735. ISSN: 0301-0171.

PUB. COUNTRY: Switzerland
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals

ENTRY DATE: Entered STN: 20020614

Last Updated on STN: 20020614

AB As part of our studies to identify the gene responsible for hereditary gingival fibromatosis, GINGF (OMIM 135300), we have identified and cloned a novel human gene that contains the highly conserved methyltransferase domain characteristic of S-adenosylmethionine-dependent methyltransferases. We localized this gene (C2orf8 encoding 288L6 SAM-methyltransferase) to chromosome 2p22-->p21 by FISH, and sublocalized it to BAC RP11 288L6 flanked by D2S2238 and D2S2331. Computational analysis of aligned **ESTs** identified ten exons in the **hypothetical** C2orf8 gene. Results of RACE analyses in placenta identified multiple transcripts of this gene with heterogeneity at the 5'-UTR. Alternative transcription and tissue specific **expression** of C2orf8 were detected by RT-PCR and Northern blot analyses. C2orf8 is **expressed** in a variety of tissues including brain, colon, gingiva, heart, kidney, liver, lung, placenta, small intestine, spleen, and thymus.

Open reading frame analysis of the alternative transcripts identified a shared coding region spanning exons 6-10. This ORF consists of 732 nucleotides encoding a putative 244 amino acid protein. Bioinformational searches of both C2orf8 and the putative protein product identified three methyltransferase motifs conserved across many prokaryotic and eukaryotic species. Sequence analyses of C2orf8 excluded coding region mutations as causative of GINGF.

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L77 ANSWER 14 OF 34 MEDLINE

DUPLICATE 8

ACCESSION NUMBER: 2001208519 MEDLINE

DOCUMENT NUMBER: 21177060 PubMed ID: 11281453

TITLE: Isolation and characterization of the UBASH3A gene on 21q22.3 encoding a potential nuclear protein with a novel combination of domains.

AUTHOR: Wattenhofer M; Shibuya K; Kudoh J; Lyle R; Michaud J; Rossier C; Kawasaki K; Asakawa S; Minoshima S; Berry A; Bonne-Tamir B; Shimizu N; Antonarakis S E; Scott H S

CORPORATE SOURCE: Division of Medical Genetics Centre Medical Universitaire 1, Geneve, Switzerland.

SOURCE: HUMAN GENETICS, (2001 Feb) 108 (2) 140-7.
Journal code: 7613873. ISSN: 0340-6717.

PUB. COUNTRY: Germany: Germany, Federal Republic of
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AJ277750; GENBANK-AP001623; GENBANK-AP001624;
GENBANK-AP001746; GENBANK-AP001747

ENTRY MONTH: 200104

ENTRY DATE: Entered STN: 20010417
Last Updated on STN: 20010417
Entered Medline: 20010412

AB In order to identify candidate genes for Down syndrome phenotypes or monogenic disorders that map to human chromosome 21q22.3, we have used genomic sequence and **expressed sequence tags** mapping to an autosomal recessive deafness (DFNB10) critical region to isolate a novel 2.5-kb cDNA that maps between TFF1 and D21S49. A semi-quantitative reverse transcription/polymerase chain reaction method revealed that UBASH3A gene **expression** is limited to only a few tissues, with its highest **expression** in spleen, peripheral blood leukocytes, and bone marrow. The putative 661-amino-acid protein shows considerable homology to a **hypothetical** protein from *Drosophila melanogaster* but only domain homologies to other organisms. Both the human

and *D. melanogaster* proteins contain protein-protein interaction domains, viz., SH3 and ubiquitin-associated (UBA) domains, in addition to a novel domain also containing a nuclear localization signal. This is the first protein described containing both UBA and SH3 domains. The gene, thus called UBASH3A, spans 40 kb and is divided into 15 exons. Mutation analysis excluded UBASH3A as being responsible for DFNB10.

L77 ANSWER 15 OF 34 MEDLINE DUPLICATE 9
ACCESSION NUMBER: 2001443642 MEDLINE
DOCUMENT NUMBER: 21382160 PubMed ID: 11488641
TITLE: Genomic analysis of differentially expressed genes in liver
and biliary epithelial cells of patients with primary biliary cirrhosis.
AUTHOR: Tanaka A; Leung P S; Kenny T P; Au-Young J; Prindiville T; Coppel R L; Ansari A A; Gershwin M E
CORPORATE SOURCE: Division of Rheumatology, Allergy and Clinical Immunology, Department of Internal Medicine, University of California at Davis, CA 95616, USA.
CONTRACT NUMBER: DK39588 (NIDDK)
SOURCE: JOURNAL OF AUTOIMMUNITY, (2001 Aug) 17 (1) 89-98.
Journal code: 8812164. ISSN: 0896-8411.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20010813
Last Updated on STN: 20020121
Entered Medline: 20011204

AB The characterization of differentially **expressed** genes provides a powerful tool for identifying molecules that may be involved in the pathogenesis of disease. We have used two independent techniques to identify overexpressed transcripts in bile duct cells and in liver from patients with primary biliary cirrhosis (PBC). In the first method, we used suppressive subtractive hybridization to compare mRNA from isolated PBC bile duct epithelial cells (BECs) to normal BECs and identified 71 clones as transcribed at higher levels in PBC-BECs. Amongst these clones, 62/71 had matches in a non-redundant nucleotide database and 9/71 had matches in an **EST** database. Of the 62 clones, 51/62 include a complexity of genes involved in cell proliferation, signal transduction, transcription regulation, RNA processing, carbohydrate metabolism and **hypothetical**/unknown proteins; 4/62 were identified as

interstitial collagenase and collagenase precursors, 4/62 as ribosomal proteins, 3/62 as mitochondrial DNA. The mitochondrial cDNA sequences included cytochrome c oxidase, Wnt-13, and the pHL gene, a c-myc oncogene containing coxIII sequence. In the second method, we constructed cDNA libraries from three different PBC livers and sequenced a total of 12,324 independent clones. These 12,324 clones underwent virtual subtraction with

2,814,148 independent clones from Incyte LifeSeq libraries. Twenty one sequences were identified as unique to PBC liver. Collectively, these approaches identified a number of genes involved in signalling, RNA processing, mitochondrial function, inflammation, and fibrosis. Interestingly, both Wnt-13 and Notch transcripts are overexpressed in PBC liver. Further studies are needed to focus on the significance of these genes during the natural history of disease.

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L77 ANSWER 16 OF 34 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2001:324417 BIOSIS

DOCUMENT NUMBER: PREV200100324417

TITLE: Identification of MLA1 a member of a novel family of adaptor and scaffold genes expressed in myeloma and leukemias.

AUTHOR(S): Claudio, Jaime (1); Falcioni, Nathan (1); Zhu, Yuan Xiao (1); Stewart, A. Keith (1)

CORPORATE SOURCE: (1) Experimental Therapeutics, University Health Network, Toronto, ON Canada

SOURCE: Blood, (November 16, 2000) Vol. 96, No. 11 Part 1, pp. 472a. print.

Meeting Info.: 42nd Annual Meeting of the American Society of Hematology San Francisco, California, USA December 01-05, 2000 American Society of Hematology
. ISSN: 0006-4971.

DOCUMENT TYPE: Conference

LANGUAGE: English

SUMMARY LANGUAGE: English

AB In our transcriptional study of genes **expressed** in myeloma, we identified a clone that by Blast analysis in **dbEST** appeared to have restricted **expression** in hematopoietic cells such as macrophages, hematopoietic progenitors, T cells and germinal center B cells. Northern analysis demonstrated that this gene is **expressed** as a 2.2 kb transcript in hematopoietic malignancies including myeloid

and

T cell leukemias, myeloma and in bone marrow, heart, brain, placenta and lung on a multiple tissue blot. Full length sequencing of cDNA clones revealed a novel gene which we called Myeloma and Leukemia Adaptor 1 (MLA1). MLA1 encodes a 441 amino acid protein containing two domains frequently associated with signaling molecules. An SH3 motif is predicted in the middle half of the protein and a SAM domain is located toward the carboxy-terminal end. The presence of SAM and SH3, or SAM and SH2 domains in a protein is often indicative of adaptor or scaffolding functions. The SH3 domain of MLA1 is homologous to the SH3 in CRK and its SAM domain is identical to those in a family of uncharacterized putative scaffold and adaptor proteins. There are three predicted consensus nuclear

localization

signals and tyrosine kinase phosphorylation motif. MLA1 is a member of a novel gene family of putative adaptors and scaffold proteins. This family includes 2 uncharacterized **hypothetical** proteins dJ753P9.2

(MLA2) and KIAA0790. These proteins show strong similarity throughout but highest homology is observed in both the SH3 and SAM domain regions. Genomic sequence analysis of BAC clones from chromosome 21 suggests that MLA1 spans 50 kb and consists of at least 9 exons. MLA1 maps to human

chromosome 21q11.2 in a region that is frequently disrupted by translocation events in hematopoietic malignancies. A polyclonal antibody detected a protein of approximately 49.5 kDa in myeloma cell lines. Western analysis of lysates from myeloma cell lines detected a doublet protein band in some cell lines. Immunocytochemistry staining localizes MLA1 protein **expression** to the nucleus. In order to identify potential interacting proteins, we used immunoprecipitation in combination

with western analysis of lysates from Jurkat T cells and OCIMy4 myeloma cells. Our result indicates that MLA1 does not interact with HPK1, a hematopoietic **expressed** Crk interacting serine-threonine protein kinase. Although binding partners and function are as yet unknown we hypothesize that MLA1 may be analogous to adaptors that function by mediating interactions between proteins involved in signal transduction cascades.

L77 ANSWER 17 OF 34 MEDLINE
ACCESSION NUMBER: 2001085369 MEDLINE
DOCUMENT NUMBER: 20441420 PubMed ID: 10987136
TITLE: Analysis of expressed sequence tags from Brassica rapa L. ssp. pekinensis.
AUTHOR: Lim J Y; Shin C S; Chung E J; Kim J S; Kim H U; Oh S J; Choi W B; Ryou C S; Kim J B; Kwon M S; Chung T Y; Song S I;
J; Kim J K; Nahm B H; Hwang Y S; Eun M Y; Lee J S; Cheong J Choi Y D
CORPORATE SOURCE: School of Agricultural Biotechnology, Seoul National University, Suwon, Korea.
SOURCE: MOLECULES AND CELLS, (2000 Aug 31) 10 (4) 399-404. Journal code: 9610936. ISSN: 1016-8478.
PUB. COUNTRY: KOREA (SOUTH)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200101
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010118

AB Non-redundant **expressed sequence tags** (**ESTs**) were generated from six different organs at various developmental stages of Chinese cabbage, Brassica rapa L. ssp. pekinensis.

Of the 1,295 **ESTs**, 915 (71%) showed significantly high homology in nucleotide or deduced amino acid sequences with other sequences deposited in databases, while 380 did not show similarity to any sequences. Briefly, 598 **ESTs** matched with proteins of identified biological function, 177 with **hypothetical** proteins or non-annotated Arabidopsis genome sequences, and 140 with other **ESTs**. About 82% of the top-scored matching sequences were from Arabidopsis or Brassica, but overall 558 (43%) **ESTs** matched with Arabidopsis **ESTs** at the nucleotide sequence level. This observation strongly supports the idea that gene-**expression** profiles of Chinese cabbage differ from that of Arabidopsis, despite their

genome structures being similar to each other. Moreover, sequence analyses

of 21 Brassica **ESTs** revealed that their primary structure is different from those of corresponding annotated sequences of Arabidopsis genes. Our data suggest that direct prediction of Brassica gene **expression** pattern based on the information from Arabidopsis

genome research has some limitations. Thus, information obtained from the Brassica **EST** study is useful not only for understanding of unique developmental processes of the plant, but also for the study of Arabidopsis genome structure.

L77 ANSWER 18 OF 34 MEDLINE DUPLICATE 10
 ACCESSION NUMBER: 2001181863 MEDLINE
 DOCUMENT NUMBER: 21098486 PubMed ID: 11173868
 TITLE: EST mining of the UniGene dataset to identify retina-specific genes.
 AUTHOR: Stohr H; Mah N; Schulz H L; Gehrig A; Frohlich S; Weber B
 H
 CORPORATE SOURCE: Institut fur Humangenetik, Biozentrum, Universitat Wurzburg, Wurzburg , Germany.
 SOURCE: CYTOGENETICS AND CELL GENETICS, (2000) 91 (1-4) 267-77. Journal code: 0367735. ISSN: 0301-0171.
 PUB. COUNTRY: Switzerland
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF295725; GENBANK-AF295730
 ENTRY MONTH: 200103
 ENTRY DATE: Entered STN: 20010404
 Last Updated on STN: 20020125
 Entered Medline: 20010329

AB Age-related macular degeneration (AMD) is a multifactorial disorder affecting the visual system with a high prevalence among the elderly population but with no effective therapy available at present. To better understand the pathogenesis of this disorder, the identification of the genetic factors and the determination of their contribution to AMD is needed. Towards this goal, we are pursuing a strategy that makes use of the **EST** data processed in the UniGene database and aims at the generation of a comprehensive catalogue of genes preferentially active in the human retina. Subsequently, these genes will be systematically assessed in AMD. We performed a retina **EST** sampling and obtained a total of 673 clusters containing only retina **ESTs** as well as 568 clusters with at least 30% of the **ESTs** in each cluster originating from retina cDNA libraries. Of these, 180 representative **EST** clusters with varying retina and non-retina **EST** contents were analyzed for their in vitro **expression**. This approach identified 39 transcripts with retina-specific **expression**. One of these genes (C18orf2) mapping to chromosome 18 was further characterized. Multiple C18orf2 transcripts display a complex pattern of differential splicing in the human retina. The various isoforms encode **hypothetical** polypeptides with no homologies to known proteins or protein motifs.
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L77 ANSWER 19 OF 34 MEDLINE DUPLICATE 11
 ACCESSION NUMBER: 2001076993 MEDLINE
 DOCUMENT NUMBER: 20510011 PubMed ID: 11054555
 TITLE: Human allantoicase gene: cDNA cloning, genomic organization and chromosome localization.
 AUTHOR: Vigetti D; Monetti C; Acquati F; Taramelli R; Bernardini G
 CORPORATE SOURCE: Dipartimento di Biologia Strutturale e Funzionale, Universita degli Studi dell'Insubria, Via J. H. Dunant 3, I-21100, Varese, Italy.
 SOURCE: GENE, (2000 Oct 3) 256 (1-2) 253-60. Journal code: 7706761. ISSN: 0378-1119.
 PUB. COUNTRY: Netherlands

Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF215924
ENTRY MONTH: 200101
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010111

AB Uric-acid-degrading enzymes (uricase, allantoinase, allantoicase, ureidoglycolate lyase and urease) were lost during vertebrate evolution and the causes for this loss are still unclear. We have recently cloned the first vertebrate allantoicase cDNA from the amphibian *Xenopus laevis*. Surprisingly, we have found some mammalian **expressed sequence tags (ESTs)** that show high similarity with *Xenopus* allantoicase cDNA. From a human fetal spleen cDNA library and adult kidney **EST** clone, we have obtained a 1790 nucleotide long cDNA. The 3' end of this sequence reveals a substantial high identity with the corresponding portion of *Xenopus* allantoicase cDNA. In contrast, at the 5' end the human sequence diverges from that of *Xenopus*; since no continuous open reading frame can be found in this region, the **hypothetical** human protein appears truncated at its N-terminus. We proposed that such a transcript could be due to an incorrect splicing mechanism that introduces an intron portion at the 5' end of human cDNA. Allantoicase cDNA is **expressed** in adult testis, prostate, kidney and fetal spleen. By comparison with available genomic sequences deposited in database, we have determined that the human allantoicase gene consists of five exons and spans 8kb. We have also mapped the gene in chromosome 2.

L77 ANSWER 20 OF 34 MEDLINE

ACCESSION NUMBER: 2000290991 MEDLINE
DOCUMENT NUMBER: 20290991 PubMed ID: 10828591
TITLE: cDNA cloning and genomic structure of a novel gene (C11orf9) localized to chromosome 11q12-->q13.1 which encodes a highly conserved, potential membrane-associated protein.
AUTHOR: Stohr H; Marquardt A; White K; Weber B H
CORPORATE SOURCE: Institut fur Humangenetik, Universitat Wurzburg, Germany.
SOURCE: CYTOGENETICS AND CELL GENETICS, (2000) 88 (3-4) 211-6.
Journal code: 0367735. ISSN: 0301-0171.
PUB. COUNTRY: Switzerland
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200006
ENTRY DATE: Entered STN: 20000706
Last Updated on STN: 20000706
Entered Medline: 20000626

AB We have cloned and characterized a novel gene (C11orf9) mapping to chromosome 11q12-->q13.1. The transcript was initially identified as a partial cDNA sequence in the course of constructing a transcript map of the region between markers D11S1765 and uteroglobin known to encompass the gene causing Best disease. Using a combination of **EST** mapping, computational exon prediction, RT-PCR, and 5'-RACE its 5.7-kb full-length cDNA sequence was subsequently obtained. The C11orf9 gene consists of 26 exons spanning 33.1 kb of genomic DNA and is located about 4.3 kb

centromeric to FEN1. Biocomputational analysis predicts that its conceptual translation product of 1,111 amino acids contains two transmembrane helices as well as two proline-rich regions. Alignment reveals significant homology to **hypothetical** peptides from several other species including *C. elegans* and *D. melanogaster*, indicating a high degree of conservation throughout evolution. Northern Blot and RT-PCR analyses demonstrate widespread **expression** of a single transcript but varying degrees of abundance among the individual tissues tested. Mutation analysis of the entire coding sequence excluded C11orf9 as the Best disease gene.
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L77 ANSWER 21 OF 34 MEDLINE
 ACCESSION NUMBER: 2001095149 MEDLINE
 DOCUMENT NUMBER: 20363093 PubMed ID: 10907847
 TITLE: A large scale analysis of cDNA in *Arabidopsis thaliana*: generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries.
 AUTHOR: Asamizu E; Nakamura Y; Sato S; Tabata S
 CORPORATE SOURCE: Kazusa DNA Research Institute, Kisarazu, Chiba, Japan.
 SOURCE: DNA RESEARCH, (2000 Jun 30) 7 (3) 175-80.
 Journal code: 9423827. ISSN: 1340-2838.
 PUB. COUNTRY: Japan
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AB038710; GENBANK-AB038711; GENBANK-AB038712;
 GENBANK-AB038713; GENBANK-AB038714; GENBANK-AB038715;
 GENBANK-AB038716; GENBANK-AB038717; GENBANK-AB038718;
 GENBANK-AB038719; GENBANK-AB038720; GENBANK-AB038721;
 GENBANK-AB038722; GENBANK-AB038723; GENBANK-AB038724;
 GENBANK-AB038725; GENBANK-AB038726; GENBANK-AV439465;
 GENBANK-AV439466; GENBANK-AV439467; GENBANK-AV439468;
 GENBANK-AV439469; GENBANK-AV439470; GENBANK-AV439471;
 GENBANK-AV439472; GENBANK-AV439473; GENBANK-AV439474;
 GENBANK-AV439475; GENBANK-AV439476; GENBANK-AV439477; +
 ENTRY MONTH: 200102
 ENTRY DATE: Entered STN: 20010322
 Last Updated on STN: 20010322
 Entered Medline: 20010201
 AB For comprehensive analysis of genes **expressed** in the model dicotyledonous plant, *Arabidopsis thaliana*, **expressed sequence tags (ESTs)** were accumulated. Normalized and size-selected cDNA libraries were constructed from aboveground organs, flower buds, roots, green siliques and liquid-cultured seedlings, respectively, and a total of 14,026 5'-end **ESTs** and 39,207 3'-end **ESTs** were obtained. The 3'-end **ESTs** could be clustered into 12,028 non-redundant groups. Similarity search of the non-redundant **ESTs** against the public non-redundant protein database indicated that 4816 groups show similarity to genes of known function, 1864 to **hypothetical** genes, and the remaining 5348 are novel sequences. Gene coverage by the non-redundant **ESTs** was analyzed using the annotated genomic sequences of approximately 10 Mb on chromosomes 3 and 5. A total of 923 regions were hit by at least one **EST**, among which only 499 regions were hit by the **ESTs** deposited in the public database. The result indicates that the **EST** source generated in this project complements the **EST** data in the public database and facilitates new gene discovery.

L77 ANSWER 22 OF 34 MEDLINE
 ACCESSION NUMBER: 2000433820 MEDLINE
 DOCUMENT NUMBER: 20277479 PubMed ID: 10819328
 TITLE: Generation of 7137 non-redundant expressed sequence tags from a legume, *Lotus japonicus*.
 AUTHOR: Asamizu E; Nakamura Y; Sato S; Tabata S
 CORPORATE SOURCE: Kazusa DNA Research Institute, Kisarazu, Chiba, Japan.
 SOURCE: DNA RESEARCH, (2000 Apr 28) 7 (2) 127-30.
 Journal code: 9423827. ISSN: 1340-2838.
 PUB. COUNTRY: Japan
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AV406328; GENBANK-AV406329; GENBANK-AV406330;
 GENBANK-AV406331; GENBANK-AV406332; GENBANK-AV406333;
 GENBANK-AV406334; GENBANK-AV406335; GENBANK-AV406336;
 GENBANK-AV406337; GENBANK-AV406338; GENBANK-AV406339;
 GENBANK-AV406340; GENBANK-AV406341; GENBANK-AV406342;
 GENBANK-AV406343; GENBANK-AV406344; GENBANK-AV406345;
 GENBANK-AV406346; GENBANK-AV406347; GENBANK-AV406348;
 GENBANK-AV406349; GENBANK-AV406350; GENBANK-AV406351;
 GENBANK-AV406352; GENBANK-AV406353; GENBANK-AV406354;
 GENBANK-AV406355; GENBANK-AV406356; GENBANK-AV406357; +
 ENTRY MONTH: 200009
 ENTRY DATE: Entered STN: 20000928
 Last Updated on STN: 20000928
 Entered Medline: 20000921

AB For comprehensive analysis of genes **expressed** in a model legume, *Lotus japonicus*, a total of 22,983 5' end **expressed sequence tags (ESTs)** were accumulated from normalized and size-selected cDNA libraries constructed from young (2 weeks old) plants. The **EST** sequences were clustered into 7137 non-redundant groups. Similarity search against public non-redundant protein database indicated that 3302 groups showed similarity to genes of known function, 1143 groups to **hypothetical** genes, and 2692 were novel sequences. Homologues of 5 nodule-specific genes which have been reported in other legume species were contained in the collected **ESTs**, suggesting that the **EST** source generated in this study will become a useful tool for identification of genes related to legume-specific biological processes. The sequence data of individual **ESTs** are available at the web site: <http://www.kazusa.or.jp/en/plant/lotus/EST/>.

L77 ANSWER 23 OF 34 MEDLINE DUPLICATE 12
 ACCESSION NUMBER: 2001012870 MEDLINE
 DOCUMENT NUMBER: 20374020 PubMed ID: 10919380
 TITLE: A group of expressed cDNA sequences from the wheat fungal leaf blotch pathogen, *Mycosphaerella graminicola* (*Septoria tritici*).
 AUTHOR: Keon J; Bailey A; Hargreaves J
 CORPORATE SOURCE: IACR-Long Ashton Research Station, University of Bristol, United Kingdom.
 SOURCE: FUNGAL GENETICS AND BIOLOGY, (2000 Mar) 29 (2) 118-33.
 Journal code: 9607601. ISSN: 1087-1845.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AW067761; GENBANK-AW067762; GENBANK-AW067763;
 GENBANK-AW067764; GENBANK-AW067765; GENBANK-AW179955;
 GENBANK-AW179956; GENBANK-AW179957; GENBANK-AW179958;

GENBANK-AW179959; GENBANK-AW179960; GENBANK-AW179961;
GENBANK-AW179962; GENBANK-AW179963; GENBANK-AW179964;
GENBANK-AW179965; GENBANK-AW179966; GENBANK-AW179967;
GENBANK-AW179968; GENBANK-AW179969; GENBANK-AW179970;
GENBANK-AW179971; GENBANK-AW179972; GENBANK-AW179973;
GENBANK-AW179974; GENBANK-AW179975; GENBANK-AW179976;
GENBANK-AW179977; GENBANK-AW179978; GENBANK-AW179979; +

ENTRY MONTH: 200010
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001031

AB A group of **expressed sequence tags (ESTs)** from the wheat fungal pathogen *Mycosphaerella graminicola* utilizing ammonium as a nitrogen source has been analyzed. Single pass sequences of complementary DNAs from 986 clones were determined. Contig analysis and sequence comparisons allowed 704 unique **ESTs** (unigenes) to be identified, of which 148 appeared as multiple copies. Searches of the nrdb95 protein database at EMBL using the BLAST2x algorithm revealed 407 (57.8%) sequences that generated high to moderate high scoring pairs with proteins of known and unknown function. The rest of the sequences (297) showed either weak or no similarities to database entries. Among the unigenes with assigned function, 26.7% were involved

in primary metabolism and 17.9% were associated with protein and RNA metabolism. Fewer clones were ascribed roles in signal transduction (4.9%), transport and secretion (6.1%), cell structure (3.1%), and cell division (3.6%). Approximately 18.1% of the identities found were to **hypothetical** or unknown proteins mainly from the yeasts *Saccharomyces cerevisiae* and *Schizosaccharomyces pombe*. Comparison of the 297 sequences with no clear function to other fungal **ESTs** in the public domain revealed 12 sequences that had high to moderate similarity to *Neurospora crassa*, *Emericella* (*Aspergillus*) *nidulans*, or *Magnaporthe grisea* sequences.

L77 ANSWER 24 OF 34 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:514713 BIOSIS
DOCUMENT NUMBER: PREV200100514713
TITLE: Analysis of the filarial parasite *Brugia malayi* adult male stage EST clusters for novel gene identification.
AUTHOR(S): Kamal, Ibrahim H. (1); Ganatra, Mehul B. (1); Foster, Jeremy M. (1); Moran, Laurie S. (1); Ware, Jennifer L. (1);
Guiliano, David; Blaxter, Mark L.; Helmy, Hanan; Slatk, Barton E. (1); Ramzy, Reda M.
CORPORATE SOURCE: (1) New England Biolabs, Inc., Beverly, MA USA
SOURCE: International Genome Sequencing and Analysis Conference, (2000) Vol. 12, pp. 70-71. print.
Meeting Info.: 12th International Genome Sequencing and Analysis Conference Miami Beach, Florida, USA September 12-15, 2000
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English
AB The current database of *Brugia malayi* (a filarial nematode responsible for lymphatic elephantiasis) contains DNA sequences of more than 22,000 **expressed sequence tags (ESTs)** providing a resource for identifying new genes and determining their functions. The *B. malayi* adult male cDNA library was selected for detailed analysis. A total of 1611 **ESTs** from *B. malayi* adult male stage

were identified, clustered by a sequence similarity algorithm and assembled into 1356 separate clusters. All the sequences have been submitted to **dbEST**/GenBank. These clusters of the Filarial database version 2.0 (FilDB v. 2.0) were analyzed using BLAST search for the identification of novel genes. Comparison of these clusters with GenBank database identified 151 clusters hitting the free living nematode *Caenorhabditis elegans*, 90 clusters hitting other organisms and 704 as novel genes which have no significant similarities in the database. The remaining 411 clusters, (30%) are not included in these analyses since they are shorter than 200 bp in length and contain more than 10% Ns (aNybase). Members of many gene families, including cytoskeletal house keeping proteins, GTB-binding proteins, and house keeping enzymes were identified. Other identified genes include RAS-related signaling protein, calcium activated potassium channel protein, aspartyl and cysteine proteases, sex determining gene (*her-1*) and major sperm protein. About

50%

of the clusters that hit the *C. elegans* database have similarity to **hypothetical** or predicted proteins. Among those novel genes (52%) there is a set of potentially *Brugia* specific targets for immunotherapy and drug development. The variety and redundancy of **ESTs** in this study suggest that the cDNA library reflects *in vivo* gene **expression**. A large scale **EST** effort should uncover many new genes and provide information about genes involved in the biochemical pathways of the nematode. As this approach is expanded to the analysis of **ESTs** from other *B. malayi* stages, other genes involved in development and/or pathogenicity are likely to be revealed.

L77 ANSWER 25 OF 34 MEDLINE DUPLICATE 13
 ACCESSION NUMBER: 1999348308 MEDLINE
 DOCUMENT NUMBER: 99348308 PubMed ID: 10419491
 TITLE: The dihydrolipoamide S-acetyltransferase subunit of the mitochondrial pyruvate dehydrogenase complex from maize contains a single lipoyl domain.
 AUTHOR: Thelen J J; Muszynski M G; David N R; Luethy M H; Elthon T E; Miernyk J A; Randall D D
 CORPORATE SOURCE: Department of Biochemistry, University of Missouri, Columbia, Missouri 65211, USA.
 SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1999 Jul 30) 274 (31) 21769-75.
 PUB. COUNTRY: United States
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF135014
 ENTRY MONTH: 199908
 ENTRY DATE: Entered STN: 19990827
 Last Updated on STN: 19990827
 Entered Medline: 19990819
 AB The dihydrolipoamide S-acetyltransferase (E2) subunit of the maize mitochondrial pyruvate dehydrogenase complex (PDC) was postulated to contain a single lipoyl domain based upon molecular mass and N-terminal protein sequence (Thelen, J. J., Miernyk, J. A., and Randall, D. D. (1998) Plant Physiol. 116, 1443-1450). This sequence was used to identify a cDNA from a maize **expressed sequence tag** data base. The deduced amino acid sequence of the full-length cDNA was greater than 30% identical to other E2s and contained a single lipoyl domain. Mature maize E2 was **expressed** in *Escherichia coli* and purified to a specific activity of 191 units mg(-1). The purified recombinant protein had a native mass of approximately 2.7 MDa and assembled into a

29-nm pentagonal dodecahedron as visualized by electron microscopy. Immunoblot analysis of mitochondrial proteins from various plants, using a monoclonal antibody against the maize E2, revealed 50-54-kDa cross-reacting polypeptides in all samples. A larger protein (76 kDa) was also recognized in an enriched pea mitochondrial PDC preparation, indicating two distinct E2s. The presence of a single lipoyl-domain E2 in *Arabidopsis thaliana* was confirmed by identifying a gene encoding a **hypothetical** protein with 62% amino acid identity to the maize homologue. These data suggest that all plant mitochondrial PDCs contain an E2 with a single lipoyl domain. Additionally, *A. thaliana* and other dicots

possess a second E2, which contains two lipoyl domains and is only 33% identical at the amino acid level to the smaller isoform. The reason two distinct E2s exist in dicotyledon plants is uncertain, although the variability between these isoforms, particularly within the subunit-binding domain, suggests different roles in assembly and/or function of the plant mitochondrial PDC.

L77 ANSWER 26 OF 34 MEDLINE DUPLICATE 14
 ACCESSION NUMBER: 1999269920 MEDLINE
 DOCUMENT NUMBER: 99269920 PubMed ID: 10337626
 TITLE: The 5' region of the COX4 gene contains a novel overlapping gene, NOC4.
 AUTHOR: Bachman N J; Wu W; Schmidt T R; Grossman L I; Lomax M I
 CORPORATE SOURCE: Department of Anatomy and Cell Biology, University of Michigan, Ann Arbor 48109-0616, USA.
 CONTRACT NUMBER: GM48800 (NIGMS)
 SOURCE: MAMMALIAN GENOME, (1999 May) 10 (5) 506-12.
 Journal code: 9100916. ISSN: 0938-8990.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF005888; GENBANK-AF005889; GENBANK-AF052621
 ENTRY MONTH: 199907
 ENTRY DATE: Entered STN: 19990715
 Last Updated on STN: 20000922
 Entered Medline: 19990708
 AB We identified a novel human gene, NOC4 (Neighbor Of COX4), located 5' to COX4, the gene for cytochrome c oxidase subunit IV, on Chr 16q32-ter. Transcripts from this gene were identified among human **expressed sequence tags**. A full-length, 1.06-kb human retinal NOC4 cDNA encoded a 24-kDa, 210-amino acid **hypothetical** protein of unknown function. Northern hybridization analysis of human RNAs from various tissues detected NOC4 transcripts of 2.2 and 1.4 kb in all tissues examined, suggesting that NOC4 **expression** is ubiquitous. Transcription of both the COX4 and NOC4 genes initiates within a 250-bp intergenic promoter and occurs in opposite directions. The bidirectional promoter is G + C-rich, lacks TATA and CCAAT elements, and contains multiple potential binding sites for Sp1 and NRF-2/GABP. Two of the NRF-2/GABP sites are located within 14-bp direct repeats, a conserved feature of mammalian COX4 promoters. The NOC4 and COX4 genes are also linked in the rat, mouse, and bovine genomes. A NOC4-GFP fusion protein is located in both the nucleus and the cytoplasm, including the mitochondria.

L77 ANSWER 27 OF 34 MEDLINE

ACCESSION NUMBER: 1999296366 MEDLINE
 DOCUMENT NUMBER: 99296366 PubMed ID: 10366717
 TITLE: Identification of a 24 kDa intrinsic membrane protein from mammalian peroxisomes.
 AUTHOR: Reguenga C; Oliveira M E; Gouveia A M; Eckerskorn C; Sa-Miranda C; Azevedo J E
 CORPORATE SOURCE: Unidade de Neurobiologia Genetica do Instituto de Biologia Molecular e Celular, Universidade do Porto, Porto, Portugal.
 SOURCE: BIOCHIMICA ET BIOPHYSICA ACTA, (1999 Jun 9) 1445 (3) 337-41.
 Journal code: 0217513. ISSN: 0006-3002.
 PUB. COUNTRY: Netherlands
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF072864
 ENTRY MONTH: 199907
 ENTRY DATE: Entered STN: 19990730
 Last Updated on STN: 19990730
 Entered Medline: 19990719

AB A 24 kDa protein from rat liver peroxisomal membrane was isolated and subjected to Edman degradation. Using the N-terminal sequence of this polypeptide we have identified several rat and human **expressed sequence tags** in the GenBank Database. The complete sequence of a human cDNA clone was determined. The open reading frame encodes an extremely basic protein 212 amino acid residues long. A high similarity between this mammalian protein and **hypothetical** proteins from *Caenorhabditis elegans* and *Neurospora crassa* was found. Hydropathy analysis reveals the existence of two putative membrane-spanning domains in conserved regions of the three homologous proteins.

L77 ANSWER 28 OF 34 MEDLINE DUPLICATE 15
 ACCESSION NUMBER: 1999041962 MEDLINE
 DOCUMENT NUMBER: 99041962 PubMed ID: 9822667
 TITLE: Cadmium-regulated genes from the nematode *Caenorhabditis elegans*. Identification and cloning of new cadmium-responsive genes by differential display.
 AUTHOR: Liao V H; Freedman J H
 CORPORATE SOURCE: Nicholas School of the Environment, Duke University, Durham, North Carolina 27708, USA.
 CONTRACT NUMBER: CA 61337 (NCI)
 SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1998 Nov 27) 273 (48) 31962-70.
 Journal code: 2985121R. ISSN: 0021-9258.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF071353; GENBANK-AF071354; GENBANK-AF071355;
 GENBANK-AF071356; GENBANK-AF071357; GENBANK-AF071358;
 GENBANK-AF071359; GENBANK-AF071360; GENBANK-AF071361;
 GENBANK-AF071362; GENBANK-AF071363; GENBANK-AF071364;
 GENBANK-AF071365; GENBANK-AF071366; GENBANK-AF071367;
 GENBANK-AF071368; GENBANK-AF071369; GENBANK-AF071370;
 GENBANK-AF071371; GENBANK-AF071372; GENBANK-AF071373;
 GENBANK-AF071374; GENBANK-AF071375; GENBANK-AF071376;
 GENBANK-AF071377; GENBANK-AF071378; GENBANK-AF071379;
 GENBANK-AF071380; GENBANK-AF071381; GENBANK-AF071382
 ENTRY MONTH: 199812

ENTRY DATE: Entered STN: 19990115

Last Updated on STN: 20000303

Entered Medline: 19981223

AB The transition metal cadmium is a pervasive and persistent environmental contaminant that has been shown to be both a human toxicant and carcinogen. To inhibit cadmium-induced damage, cells respond by

increasing

the **expression** of genes encoding stress-response proteins. In most cases, the mechanism by which cadmium affects the **expression** of these genes remains unknown. It has been demonstrated in several instances that cadmium activates gene transcription through signal transduction pathways, mediated by protein kinase C, cAMP-dependent protein kinase, or calmodulin. A codicil is that cadmium should influence the **expression** of numerous genes. To investigate the ability of cadmium to affect gene transcription, the differential display technique was used to analyze gene **expression** in the nematode *Caenorhabditis elegans*. Forty-nine cDNAs whose steady-state levels of **expression** change 2-6-fold in response to cadmium exposure were identified. The nucleotide sequences of the majority of the

differentially

expressed cDNAs are identical to those of *C. elegans* cosmids, yeast artificial chromosomes, **expressed sequence tags**, or predicted genes. The translated amino acid sequences of several clones are identical to *C. elegans* metallothionein-1, HSP70, collagens, and rRNAs. In addition, *C. elegans* homologues of pyruvate carboxylase, DNA gyrase, beta-adrenergic receptor kinase, and human **hypothetical** protein KIAA0174 were identified. The translated amino acid sequences of the remaining differentially **expressed** cDNAs encode novel proteins.

L77 ANSWER 29 OF 34

MEDLINE

DUPLICATE 16

ACCESSION NUMBER: 1999043884 MEDLINE

DOCUMENT NUMBER: 99043884 PubMed ID: 9826334

TITLE: Large-scale identification of virulence genes from *Streptococcus pneumoniae*.

AUTHOR: Polissi A; Pontiggia A; Feger G; Altieri M; Mottl H; Ferrari L; Simon D

CORPORATE SOURCE: Department of Microbiology, Medicine Research Centre, Glaxo

SOURCE: Wellcome S.p.A., 37100 Verona, Italy.

INFECTION AND IMMUNITY, (1998 Dec) 66 (12) 5620-9.
Journal code: 0246127. ISSN: 0019-9567.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199812

ENTRY DATE: Entered STN: 19990115

Last Updated on STN: 19990115

Entered Medline: 19981224

AB *Streptococcus pneumoniae* is the major cause of bacterial pneumonia, and it

is also responsible for otitis media and meningitis in children. Apart from the capsule, the virulence factors of this pathogen are not completely understood. Recent technical advances in the field of bacterial

pathogenesis (in vivo **expression** technology and signature-tagged mutagenesis [STM]) have allowed a large-scale identification of virulence genes. We have adapted to *S. pneumoniae* the STM technique, originally used

for the discovery of *Salmonella* genes involved in pathogenicity. A library

a of pneumococcal chromosomal fragments (400 to 600 bp) was constructed in suicide plasmid vector carrying unique DNA **sequence tags** and a chloramphenicol resistance marker. The recent clinical isolate G54 was transformed with this library. Chloramphenicol-resistant mutants were obtained by homologous recombination, resulting in genes inactivated by insertion of the suicide vector carrying a unique tag. In a mouse pneumonia model, 1.250 candidate clones were screened; 200 of these were not recovered from the lungs were therefore considered virulence-attenuated mutants. The regions flanking the chloramphenicol gene of the attenuated mutants were amplified by inverse PCR and sequenced. The sequence analysis showed that the 200 mutants had insertions in 126 different genes that could be grouped in six classes: (i) known pneumococcal virulence genes; (ii) genes involved in metabolic pathways; (iii) genes encoding proteases; (iv) genes coding for ATP binding cassette transporters; (v) genes encoding proteins involved in DNA recombination/repair; and (vi) DNA sequences that showed similarity to **hypothetical** genes with unknown function. To evaluate the virulence attenuation for each mutant, all 126 clones were individually analyzed in a mouse septicemia model. Not all mutants selected in the pneumonia model were confirmed in septicemia, thus indicating the existence of virulence factors specific for pneumonia.

L77 ANSWER 30 OF 34 MEDLINE DUPLICATE 17
 ACCESSION NUMBER: 1998126437 MEDLINE
 DOCUMENT NUMBER: 98126437 PubMed ID: 9465297
 TITLE: Characterization of a novel gene, C21orf2, on human chromosome 21q22.3 and its exclusion as the APECED gene by mutation analysis.
 AUTHOR: Scott H S; Kyriakou D S; Peterson P; Heino M; Tahtinen M; Krohn K; Chen H; Rossier C; Lalioti M D; Antonarakis S E
 CORPORATE SOURCE: Department of Genetics and Microbiology, University of Geneva Medical School, Switzerland..
 SOURCE: GENOMICS, (1998 Jan 1) 47 (1) 64-70.
 PUB. COUNTRY: United States
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-Y11392
 ENTRY MONTH: 199804
 ENTRY DATE: Entered STN: 19980430
 Last Updated on STN: 19980430
 Entered Medline: 19980420
 AB Exon trapping was performed from a partial cosmid, PAC, and P1 clone contig from human chromosome 21 between MX1 and 21qter to identify genes that may be involved in the pathogenesis of Down syndrome or several of the genetic diseases that map to chromosome 21q22.3. One 19-bp exon showed identity to three **ESTs**. The complete sequence of the **EST** clones, RT-PCR, and cDNA library screening were used to determine the full-length cDNA sequence of 2.2 kb with an open reading frame of 256-amino-acids. The putative 256-amino-acid peptide has homology with a **hypothetical** Caenorhabditis elegans protein of unknown function. Northern blot analysis of this gene, termed C21orf2 (chromosome 21 open reading frame 2), revealed two ubiquitously **expressed** mRNAs of 2.2 and 1.2 kb produced by use of alternative polyadenylation sites. Hybridization of the **EST** clones to a cosmid contig in chromosome 21q22.3 mapped C21orf2 just distal to PFKL, a critical mapping region for

several genetic diseases. Comparison to publicly available genomic sequence, and additional data, revealed that the gene is split into seven exons over 10.5 kb, further refining the mapping position to only 1.2 kb distal to PFKL with the direction of transcription toward the centromere. The 5'UTR is contiguous with D21S400, and intron 2 contains a 52-bp VNTR polymorphism. Given its mapping position, C21orf2 is a candidate for involvement in disorders including autoimmune polyglandular disease type

I

(also called autoimmune polyendocrinopathy candidiasis ectodermal dystrophy or APECED) and the autosomal nonsyndromic deafness loci, DFNB8 and DFNB10. Mutation analysis using sequencing of RT-PCR and genomic DNA-derived PCR products, SSCP, and Southern and Northern blot analyses

in

APECED patients excluded C21orf2 as the gene for APECED.

L77 ANSWER 31 OF 34 MEDLINE DUPLICATE 18
ACCESSION NUMBER: 97197972 MEDLINE
DOCUMENT NUMBER: 97197972 PubMed ID: 9046088
TITLE: The sequence of a 36.7 kb segment on the left arm of chromosome IV from *Saccharomyces cerevisiae* reveals 20 non-overlapping open reading frames (ORFs) including SIT4, FAD1, NAM1, RNA11, SIR2, NAT1, PRP9, ACT2 and MPS1 and 11 new ORFs.
AUTHOR: Saren A M; Laamanen P; Lejarcegui J B; Paulin L
CORPORATE SOURCE: DNA Synthesis and Sequencing Laboratory, Institute of Biotechnology, University of Helsinki, Finland.
SOURCE: YEAST, (1997 Jan) 13 (1) 65-71.
JOURNAL CODE: 8607637. ISSN: 0749-503X.
PUB. COUNTRY: ENGLAND: United Kingdom
JOURNAL; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-Z71781
ENTRY MONTH: 199705
ENTRY DATE: Entered STN: 19970514
Last Updated on STN: 19970514
Entered Medline: 19970505
AB A 36,688 bp fragment from the left arm of chromosome IV of *saccharomyces cerevisiae* was sequenced. Sequence analysis identified 20 complete non-overlapping open reading frames (ORFs) of at least 100 amino acids. Nine of these correspond to previously identified and sequenced genes: SIT4/PH1, FAD1, NAM1/MTF2, RNA11, SIR2/MAR1, NAT1/AAA1, PRP9, ACT2 and MPS1/RPK1. Three ORFs show homology to previously sequenced genes. One ORF exhibits a **hypothetical yabO/yceC/YfiI** family signature and one has the ATP-dependent helicase signature of the DEAD and DEAH box families. Six ORFs show no appreciable homology to any proteins in the database. One of these is identical to yeast **expressed sequence tags** and therefore corresponds to and **expressed** gene. In addition, two partial ORFs and 11 ORFs that are totally internal and are not likely to be functional were detected.

L77 ANSWER 32 OF 34 MEDLINE DUPLICATE 19
ACCESSION NUMBER: 96359148 MEDLINE
DOCUMENT NUMBER: 96359148 PubMed ID: 8703114
TITLE: Cloning and comparative mapping of a gene from the commonly deleted region of DiGeorge and Velocardiofacial syndromes conserved in *C. elegans*.
AUTHOR: Rizzu P; Lindsay E A; Taylor C; O'Donnell H; Levy A; Scambler P; Baldini A

CORPORATE SOURCE: Department of Molecular and Human Genetics, Baylor College of Medicine, 1 Baylor Plaza, T936, Houston, Texas 77030, USA.

CONTRACT NUMBER: HG00210 (NHGRI)

SOURCE: MAMMALIAN GENOME, (1996 Sep) 7 (9) 639-43.
Journal code: 9100916. ISSN: 0938-8990.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-L78010

ENTRY MONTH: 199610

ENTRY DATE: Entered STN: 19961025
Last Updated on STN: 19980206
Entered Medline: 19961017

AB We have identified and cloned a gene, ES2, encoding a putative 476 amino acid protein with a predicted Mr of 52,568. The gene is localized within the DiGeorge/Velocardiofacial syndrome locus on 22q11.2 and is deleted in all the patients in which a deletion within 22q11 could be demonstrated, with the exception of one patient. ES2 is **expressed** in all the tissues studied. Sequence comparison showed identity with five **ESTs** and at the amino acid level the sequence was highly similar to, and collinear with, a **hypothetical** C. elegans protein of unknown function. Mutation analysis was performed in 16 patients without deletion, but no mutation has been found. The cDNA sequence is conserved in mouse and is localized on MMU16B1-B3, known to contain a syntenic group in common with HSA 22q11.2.

L77 ANSWER 33 OF 34 MEDLINE DUPLICATE 20

ACCESSION NUMBER: 97032601 MEDLINE

DOCUMENT NUMBER: 97032601 PubMed ID: 8875867

TITLE: A modular domain of NifU, a nitrogen fixation cluster protein, is highly conserved in evolution.

AUTHOR: Hwang D M; Dempsey A; Tan K T; Liew C C

CORPORATE SOURCE: Department of Clinical Biochemistry, The Centre for Cardiovascular Research, The Toronto Hospital, University of Toronto, Canada.

SOURCE: JOURNAL OF MOLECULAR EVOLUTION, (1996 Nov) 43 (5) 536-40.

Journal code: 0360051. ISSN: 0022-2844.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-U47101

ENTRY MONTH: 199702

ENTRY DATE: Entered STN: 19970305
Last Updated on STN: 19970305
Entered Medline: 19970214

AB hnifU, a gene exhibiting similarity to nifU genes of nitrogen fixation gene clusters, was identified in the course of **expressed sequence tag (EST)** generation from a human fetal heart cDNA library. Northern blot of human tissues and polymerase chain reaction (PCR) using human genomic DNA verified that the hnifU gene represented a human gene rather than a microbial contaminant of the cDNA library. Conceptual translation of the hnifU cDNA yielded a protein product bearing 77% and 70% amino acid identity to NifU-like **hypothetical** proteins from Haemophilus influenzae and Saccharomyces cerevisiae, respectively, and 40-44% identity to the N-terminal regions of NifU proteins from several diazotrophs (i.e.,

nitrogen-fixing organisms). Pairwise determination of amino acid identities between the NifU-like proteins of nondiazotrophs showed that these NifU-like proteins exhibited higher sequence identity to each other (63-77%) than to the diazotrophic NifU proteins (40-48%). Further, the NifU-like proteins of non-nitrogen-fixing organisms were similar only to the N-terminal region of diazotrophic NifU proteins and therefore identified a novel modular domain in these NifU proteins. These findings support the hypothesis that NifU is indeed a modular protein. The high degree of sequence similarity between NifU-like proteins from species as divergent as humans and *H. influenzae* suggests that these proteins

perform

some basic cellular function and may be among the most highly conserved proteins.

L77 ANSWER 34 OF 34 MEDLINE DUPLICATE 21
ACCESSION NUMBER: 96021609 MEDLINE
DOCUMENT NUMBER: 96021609 PubMed ID: 8533473
TITLE: A 29.425 kb segment on the left arm of yeast chromosome XV contains more than twice as many unknown as known open reading frames.
AUTHOR: Zumstein E; Pearson B M; Kalogeropoulos A; Schweizer M
CORPORATE SOURCE: Institute of Food Research, Genetics & Microbiology Department, Norwich Research Park, Colney, U.K.
SOURCE: YEAST, (1995 Aug) 11 (10) 975-86.
Journal code: 8607637. ISSN: 0749-503X.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M73270; GENBANK-X83121
ENTRY MONTH: 199601
ENTRY DATE: Entered STN: 19960220
Last Updated on STN: 19960220
Entered Medline: 19960126

AB The nucleotide sequence of a 29.425 kb fragment localized on the left arm of chromosome XV from *Saccharomyces cerevisiae* has been determined. The sequence contains 13 open reading frames (ORFs) of which four encode the known genes ADH1, COQ3, MSH2 and RCF4. Predictions are made concerning the

functions of the unknown ORFs. Some of the ORFs contain sequences similar to **expressed sequence tags (EST)** found in the database made available by TIGR. In particular, the highly **expressed** ADH1 gene is represented in this database by no less than 20 **EST** sequences. Two ARS sequences and a putative functional GCN4 motif have also been detected. One ORF (O0953) containing nine putative transmembrane segments is similar to a **hypothetical** membrane protein of *Arabidopsis thaliana*. Characteristic features of the other ORFs include ATP/GTP binding sites, a fungal Zn(2)-Cys(6) binuclear centre, an endoplasmic reticulum targeting sequence, a beta-transducin repeat signature and in two instances, good similarity to the prokaryotic lipoprotein signal peptide motif.

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
19:04:09
ON 08 JUL 2002
L1 13496 S EST

L2 34 S L1(S) (NO#(W) CORRELAT?)
 L3 21 DUP REM L2 (13 DUPLICATES REMOVED)
 L4 3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
 L5 1972 S L4(S) (PROTEIN OR PEPTIDE)
 L6 1748 S L5(S) (EXPRESS?)
 L7 775 S L6(S) DATABASE#
 L8 355 DUP REM L7 (420 DUPLICATES REMOVED)
 L9 96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN)
 L10 47 S L8(S) GENBANK
 L11 87 S L8(S) (HEART OR BONE OR BRAIN)
 L12 137 S L11 OR L9
 L13 1 S L12 AND (NO#(W) EXPRESS?)
 L14 67 S L12(S) (TRANSCRI?)
 L15 86 S L8(S) NORTHERN
 L16 50 S L1(S) (NO#(2W) CORRELAT?)
 L17 16 S L16 NOT L2
 L18 12 DUP REM L17 (4 DUPLICATES REMOVED)
 L19 54 S L1(S) (NO#(3W) CORRELAT?)
 L20 0 S L19 NOT L1
 L21 20 S L19 NOT L2
 L22 4 S L21 NOT L16

FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002

L23 13496 S EST OR (SEQUENCE(W) TAG#)
 L24 234 S L23 AND DATABASE#/TI
 L25 0 S L24 AND (NO(3W) CORRELAT?)
 L26 234 S L24(S) DATABASE#
 L27 2221 S L23(S) DATABASE#
 L28 4 S L27(S) (NO#(3W) CORRELAT?)
 L29 1174 S L23(S) (BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVA)
 L30 310 S L29(S) NORTHERN
 L31 133 S L30 AND DATABASE#
 L32 78 DUP REM L31 (55 DUPLICATES REMOVED)
 L33 1072 S L23(S) (PREDICT? OR ANTICIPAT?)
 L34 22 S L33 AND DATABASE#/TI
 L35 13 DUP REM L34 (9 DUPLICATES REMOVED)
 L36 22 S L34(S) DATABASE#
 L37 2221 S L23(S) DATABASE#
 L38 612 S L37(S) TISSUE
 L39 58 S L38(S) PROSTATE
 L40 10 S L39 AND PREDICT?
 L41 6 DUP REM L40 (4 DUPLICATES REMOVED)
 L42 1 S L23(S) (CANNOT(3W) PREDICT)
 L43 13596 S L23 OR DBEST
 L44 6719 S L43(S) EXPRESS?
 L45 192 S L44(S) BLAST
 L46 47 S L45(S) PREDICT?
 L47 27 DUP REM L46 (20 DUPLICATES REMOVED)
 L48 2 S L43(S) RELIED
 L49 1 S L43(S) (("NOT" OR CANNOT) (W) PREDICT?)
 L50 0 S L43(S) (CANNOT(W) ANTICIPATE)
 L51 797 S L43(S) TRANSCRIPTS
 L52 28 S L43(S) ((NO(W) EXPRESSION) OR ("NOT" (W) EXPRESSED))
 L53 17 DUP REM L52 (11 DUPLICATES REMOVED)
 L54 546 S L43 AND (EXPRESSION(A) PATTERN#)
 L55 15 S L54 AND DATABASE#/TI
 L56 9 DUP REM L55 (6 DUPLICATES REMOVED)
 L57 239 S L43 AND DATABASE#/TI
 L58 5 S L57 AND PREDICT
 L59 3 DUP REM L58 (2 DUPLICATES REMOVED)
 L60 1735 S L43(S) LIBRAR?

L61 34 S L60(S) PREDICT
 L62 19 DUP REM L61 (15 DUPLICATES REMOVED)
 L63 4276 S L43(S) (MRNA OR NORTHERN OR CDNA OR TRANSCRIPT#)
 L64 335 S L63(S) (EXPRESSION(A) PATTERN#)
 L65 86 S L64(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
 L66 49 DUP REM L65 (37 DUPLICATES REMOVED)
 L67 430 S L43(S) (EXPRESSION(A) PATTERN#)
 L68 12 S L67 AND DATABASE#/TI
 L69 6 DUP REM L68 (6 DUPLICATES REMOVED)
 L70 99 S L23(3A) PREDICT?
 L71 2 S L70(3A) (EXPRESSION OR TRANSCRIPTION)
 L72 152 S L43(5A) PREDICT?
 L73 3 S L72(5A) (EXPRESSION OR TRANSCRIPTION)
 L74 1 S L73 NOT L71
 L75 64 S L43(S) HYPOTHETICAL
 L76 55 S L75(S) (EXPRESS? OR TRANSCI?)
 L77 34 DUP REM L76 (21 DUPLICATES REMOVED)

=> s l23(s l30(s) (expression(a) pattern#)
 MISSING OPERATOR 'L140(S'
 The search profile that was entered contains terms or
 nested terms that are not separated by a logical operator.

=> s l30(s) (expression(a) pattern#)
 L78 28 L30(S) (EXPRESSION(A) PATTERN#)

=> dup rem l78
 PROCESSING COMPLETED FOR L78
 L79 15 DUP REM L78 (13 DUPLICATES REMOVED)

=> d ibib abs tot

L79 ANSWER 1 OF 15 MEDLINE
 ACCESSION NUMBER: 2002353498 IN-PROCESS
 DOCUMENT NUMBER: 22091578 PubMed ID: 12096622
 TITLE: Mapping and expression analysis of a different expression
 cDNA fragment from lung adenocarcinoma cell line.
 AUTHOR: Fan Hong; Li Yu; Feng Hui-Chen; Lu Bing-Jie; Fu Song-Bin;
 Zhang Gui-Yin; Li Pu
 CORPORATE SOURCE: Laboratory of Medical Genetics, Ha'erbin Medical
 University, Ha'erbin 150086, China.
 SOURCE: I CHUAN HSUEH PAO. ACTA GENETICA SINICA, (2002 Jun) 29 (6)
 476-80.
 Journal code: 7900784. ISSN: 0379-4172.
 PUB. COUNTRY: China
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: Chinese
 FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
 ENTRY DATE: Entered STN: 20020705
 Last Updated on STN: 20020705

AB **Lung** cancer is one of the most common malignant tumors in
 humans. Metastasis is the basic biological feature of malignant tumors,
 which is the main cause of death. Molecular mechanism of metastasis is
 still unclear, although lots of studies have been done in tumor
 metastasis. To study and explore the molecular basis of metastasis in
lung cancer, and isolate tumor metastasis-related genes, two human
lung adenocarcinoma cell lines AGZY 83-a and Anip 973 were chosen
 as research materials. The Anip973 was derived from AGZY83-a, but
 manifested much higher metastasis potential than the parent line. Using
 mRNA differential display technique, an unknown cDNA fragment, OPB7-1,
 which is over-expressive in Anip973 cell line, was obtained. It was used

as a template to isolate its corresponding cDNA through dbEST searching and PCR. To search and clone **lung** adenocarcinoma metastasis-related candidate gene, and to explore the molecular basis of development of **lung** carcinoma, differential expression of OPB7-1 cDNA fragment among 9 human **lung** adenocarcinoma cell lines and 12 normal human tissues were detected using cell culture, cDNA clone, **Northern** blot analysis and bioinformation technology. Results showed that there were significant differences in OPB7-1 expression among 9 human **lung** adenocarcinoma cell lines. High expression tendency was observed in Anip973 cell line with high metastasis potential, TKB-18 cell line with high invasion potential and GLC-82 cell line with low differentiation potential. Besides, a bigger fragment can be found in Anip973 cell line on the **Northern** blot hybridization. The 3.0 kb transcriptions were found in various tissues. Over-expression in **heart** and skeletal muscle could be observed, whereas expression in spleen, liver, **kidney**, placental and **lung** could be found except colon, thyroid gland and small intestine. These manifests indicate that OPB7-1 gene has a wide-range expression in human multiple tissues. A 1.0 kb cDNA fragment was acquired by linking up **EST** fragments homologous match 5' end and PCR. BLAST analysis revealed that OPB7-1 gene has extremely low sequence identity with any known genes from GenBank and any sequences from **EST** database. The chromosomal localization of it was determined by RH location method. The OPB7-1 fragment was localized to chromosome 1p31-34. That OPB7-1 gene has an extensive **expression pattern**, may be a novel tumor gene related to **lung** carcinoma. Further research needs to be done to obtain the full-length cDNA of OPB7-1 gene. It will be helpful to investigate the expression in **lung** cancer cases and other tumor tissues for further determining the function of OPB7-1 gene in development of tumor.

L79 ANSWER 2 OF 15 MEDLINE DUPLICATE 1
 ACCESSION NUMBER: 2002132101 MEDLINE
 DOCUMENT NUMBER: 21856794 PubMed ID: 11867260
 TITLE: Digital expression profiles of the prostate androgen-response program.
 AUTHOR: Clegg Nigel; Eroglu Burak; Ferguson Camari; Arnold Hugh; Moorman Alec; Nelson Peter S
 CORPORATE SOURCE: Division of Human Biology, Fred Hutchinson Cancer Research Center, 1100 Fairview Avenue North, Seattle, WA 98109, USA.
 CONTRACT NUMBER: CA75173 (NCI)
 SOURCE: JOURNAL OF STEROID BIOCHEMISTRY AND MOLECULAR BIOLOGY, (2002 Jan) 80 (1) 13-23.
 Journal code: 9015483. ISSN: 0960-0760.
 PUB. COUNTRY: England: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200205
 ENTRY DATE: Entered STN: 20020228
 Last Updated on STN: 20020515
 Entered Medline: 20020514

AB The androgen receptor (AR) and cognate ligands regulate vital aspects of **prostate** cellular growth and function including proliferation, differentiation, apoptosis, lipid metabolism, and secretory action. In addition, the AR pathway also influences pathological processes of the **prostate** such as benign prostatic hypertrophy and **prostate** carcinogenesis. The pivotal role of androgens and the AR in **prostate** biology prompted this study with the objective of

identifying molecular mediators of androgen action. Our approach was designed to compare transcriptomes of the LNCaP **prostate** cancer cell line under conditions of androgen depletion and androgen stimulation by generating and comparing collections of expressed **sequence tags (ESTs)**. A total of 4400 **ESTs** were produced from LNCaP cDNA libraries and these **ESTs** assembled into 2486 distinct transcripts. Rigorous statistical analysis of the expression profiles indicated that 17 genes exhibited a high probability ($P > 0.9$) of androgen-regulated expression. **Northern** analysis confirmed that the expression of KLK3/PSA, FKBP5, KRT18, DKFZP564K247, DDX15, and HSP90 is regulated by androgen exposure. Of these, only KLK3/PSA is known to be androgen-regulated while the other genes represent new members of the androgen-response program in **prostate** epithelium. LNCaP gene expression profiles defined by two independent experiments using the serial analysis of gene expression (SAGE) method were compared with the **EST** profiles. Distinctly different **expression patterns** were produced from each dataset. These results are indicative of the sensitivity of the methods to experimental conditions and demonstrate the power and the statistical limitations of digital expression analyses.

L79 ANSWER 3 OF 15 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
 ACCESSION NUMBER: 2002:372790 BIOSIS
 DOCUMENT NUMBER: PREV200200372790
 TITLE: Cloning and characterization of human ubiquitin binding enzyme 2 cDNA.
 AUTHOR(S): Li Guangtao; Lu Hongyan; Zhou Yan; Jin Jian; Jiang Keyi; Peng Xiaozhong; Yuan Jiangang (1); Qiang Boqin
 CORPORATE SOURCE: (1) National Laboratory of Medical Molecular Biology, Institute of Basic Medical Sciences, CAMS and PUMC, Chinese
 SOURCE: National Human Genome Center, Beijing, 100005 China
 Chinese Medical Sciences Journal, (March, 2002) Vol. 17, No. 1, pp. 7-12. print.
 ISSN: 1001-9294.
 DOCUMENT TYPE: Article
 LANGUAGE: English
 AB Objective: To clone and identify the gene encoding human ubiquitin binding enzyme 2 and study its **expression pattern**. Methods: According to the sequence of human **EST**, which is highly homologous to the mouse ubiquitin binding/conjugating enzyme (E2), primers were synthesized to screen the human fetal brain cDNA library. The gene was analyzed by bioinformatics technique and its **expression pattern** was studied by using multiple-tissue **Northern** blot. Results: Two cDNA clones encoding human ubiquitin conjugating enzyme have been isolated and identified. Both containing the ubiquitin conjugating domain, the 2 cDNA clones are 88% identical in amino acid sequences and splicing isoforms to each other only with an exon excised to form the short sequence. They belong to a highly conserved and widely expressed E2 enzyme family. **Northern** blot shows that they are expressed exclusively in adult human **heart**, placenta, and pancreas but no transcripts can be detected in brain, **lung**, liver, skeletal muscle or **kidney**. Conclusions: The gene encoding human ubiquitin binding enzyme is expressed under temporal control. As a key enzyme in the degradation of proteins, ubiquitin conjugating enzymes play a central role in the expression regulation on the level of

post-translation.

L79 ANSWER 4 OF 15 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2001374577 MEDLINE
DOCUMENT NUMBER: 21324347 PubMed ID: 11431363
TITLE: Global analysis of gene expression in invasion by a lung cancer model.
AUTHOR: Chen J J; Peck K; Hong T M; Yang S C; Sher Y P; Shih J Y; Wu R; Cheng J L; Roffler S R; Wu C W; Yang P C
CORPORATE SOURCE: Department of Clinical Research, National Taiwan University
SOURCE: Hospital, Taipei, Taiwan 100, Republic of China.
CANCER RESEARCH, (2001 Jul 1) 61 (13) 5223-30.
Journal code: 2984705R. ISSN: 0008-5472.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200107
ENTRY DATE: Entered STN: 20010723
Last Updated on STN: 20010723
Entered Medline: 20010719
AB Metastasis is a complicated multistep process that involves interactions between cancer cells and their surrounding microenvironments. Previously, we have established a series of **lung** adenocarcinoma cell lines with varying degrees of invasiveness. Tracheal graft assay confirmed that cell lines with higher in vitro invasiveness had greater in vivo invasive potential. In this study, we used these model cell lines to identify invasion-associated genes using cDNA microarray with colorimetric detection. A more invasive subline, CL 1-5-F 4, derived from metastatic **lung** tumor of severe combined immunodeficient mice inoculated with CL 1-5 cells, was combined with CL 1-0, CL 1-1, and CL 1-5 in cDNA microarray screening. cDNA microarray membranes, each containing 9600 nonredundant expressed **sequence tag** clones, were used to identify differentially expressed genes in these cell lines. For statistical analysis, self-organizing map algorithm was performed to identify the **expression patterns**. Positive correlation between gene expression levels and cell line invasiveness was found in 2.9% of the 9600 putative genes. On the other hand, negative correlation was found in 3.3% of the genes. The trends of expression of some of the genes were also confirmed by **Northern** hybridization and flow cytometry. Our data demonstrated that genes related to cell adhesion, motility, angiogenesis, signal transduction, and some other expressed **sequence tag** genes may play significant roles in the metastasis process. These results substantiate the model system with which one can identify invasion-associated genes by using cDNA microarray and cancer cell lines of different invasiveness. This technique may allow us to explore complex interactions between multiple genes that orchestrate the process of cancer metastasis.

L79 ANSWER 5 OF 15 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 2001235535 MEDLINE
DOCUMENT NUMBER: 21134366 PubMed ID: 11237856
TITLE: Expression pattern and localization of beta,beta-carotene 15,15'-dioxygenase in different tissues.
AUTHOR: Wyss A; Wirtz G M; Woggon W D; Brugger R; Wyss M; Friedlein
CORPORATE SOURCE: A; Riss G; Bachmann H; Hunziker W
F. Hoffmann-La Roche Ltd., Vitamins & Fine Chemicals Division, 4070 Basel, Switzerland.. adrian.wyss@roche.com

SOURCE: BIOCHEMICAL JOURNAL, (2001 Mar 15) 354 (Pt 3) 521-9.
Journal code: 2984726R. ISSN: 0264-6021.
PUB. COUNTRY: England: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AJ271386; GENBANK-AW278064
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010517
Last Updated on STN: 20010517
Entered Medline: 20010503

AB Beta,beta-carotene 15,15'-dioxygenase cleaves beta,beta-carotene into two molecules of retinal, and is the key enzyme in the metabolism of beta,beta-carotene to vitamin A. The enzyme has been known for more than 40 years, yet all attempts to purify the protein to homogeneity have failed. Recently, the successful cloning and sequencing of an enzyme with beta,beta-carotene 15,15'-dioxygenase activity from chicken, as well as from *Drosophila*, has been reported. Here, we describe in detail our attempt to enrich the chicken beta,beta-carotene 15,15'-dioxygenase to such an extent as to allow determination of partial amino acid sequences, which were then used to design degenerate oligonucleotides. Screening of

a
chicken duodenal expression library yielded a full-length clone containing a coding sequence of 1578 bp. Functional expression in *Escherichia coli* and in eukaryotic cell lines confirmed that we had cloned the first vertebrate dioxygenase that cleaves beta,beta-carotene at the central 15,15'-double bond. By performing a sequence homology search, the cDNA sequence of the mouse homologue was found as an expressed **sequence tag (EST)** in the gene bank. At the amino-acid level, the degree of homology between the chicken and mouse sequences is 81%. Thus beta,beta-carotene 15,15'-dioxygenase can be considered as being an enzyme that is evolutionarily rather well conserved. We established the **expression pattern** of beta,beta-carotene 15,15'-dioxygenase in chicken and mouse tissues with a combination of **Northern** blots and in situ hybridization. The mRNA for beta,beta-carotene 15,15'-dioxygenase was localized primarily in duodenal villi, as well as in liver and in tubular structures of **lung** and **kidney**. These new findings demonstrate that beta,beta-carotene 15,15'-dioxygenase is also expressed in epithelial structures, where it serves to provide the tissue-specific vitamin A supply.

L79 ANSWER 6 OF 15 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 2002184690 MEDLINE
DOCUMENT NUMBER: 21914855 PubMed ID: 11917942
TITLE: Identification of a gene frequently mutated in prostate tumors.
AUTHOR: Reding D J; Zhang K Q; Salzman S A; Thomalla J V; Riepe R E; Suarez B K; Catalona W J; Burmester J K
CORPORATE SOURCE: Department of Hematology, Marshfield Clinic, WI, USA.
CONTRACT NUMBER: MH31302 (NIMH)
SOURCE: MEDICAL ONCOLOGY, (2001) 18 (3) 179-87.
Journal code: 9435512. ISSN: 1357-0560.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200204
ENTRY DATE: Entered STN: 20020403
Last Updated on STN: 20020424

Entered Medline: 20020423

AB Although **prostate** cancer is the second leading cause of cancer death for men in the United States, the genetics of tumor development are poorly understood. Several expressed sequence tagged genes (**ESTs**) that are expressed predominantly in the **prostate** have recently been identified, although their role in the development and maintenance

of

the **prostate** is unknown. Here, we demonstrate that the gene identified as UNIGENE cluster Hs. 104215, which codes for a message found predominantly in the **prostate**, may be important in tumor development. We name this gene PCan1 for **Prostate** Cancer gene 1. **Northern** blot experiments were performed using RNA isolated from tumor-derived cell lines and human **prostate** to determine the **expression pattern** of the gene. DNA sequencing was used to identify mutations that occurred in tumor tissue. By **Northern** blot analysis, this gene product was not detectable in LNCaP, DU 145, or PC-3 **prostate** cancer cell lines, although it was readily observed in RNA isolated from total **prostate** and from dissected central and peripheral regions of **prostate**. Sequence analysis of genomic DNA from LNCaP, DU 145, or PC-3 cells demonstrated a G/A polymorphism at position 193. Analysis of matched tumor-derived DNA and blood-derived DNA samples from 11 of 13 patients who had undergone a radical prostatectomy and who were homozygous for A in blood-derived DNA demonstrated mutation of position 193 in matched tumor samples resulting in G/A polymorphism. Sixteen additional patient samples were G/A polymorphic in both blood-derived DNA and tumor-derived DNA and two samples were GG in both blood-derived and tumor-derived DNA. Our results suggest that this gene may be a hot spot for mutation in **prostate** cancer, especially because our radiation hybrid mapping located this gene within a region identified in linkage mapping studies of affected

families

with **prostate** cancer. Loss of heterozygosity in **prostate** tumors has also been reported at the location of PCan1. Further studies

to

determine the functional role of this candidate tumor suppressor gene are warranted.

L79 ANSWER 7 OF 15

MEDLINE

DUPLICATE 5

ACCESSION NUMBER: 2001069529 MEDLINE

DOCUMENT NUMBER: 20525406 PubMed ID: 11071854

TITLE: Expression of an intracisternal A-particle-like element in rat ovary.

AUTHOR: Graham K M; Ko C; Park K S; Sarge K; Park-Sarge O K

CORPORATE SOURCE: Department of Physiology, University of Kentucky, Lexington, Kentucky 40536-0084, USA.

CONTRACT NUMBER: HD01135 (NICHD)

HD30719 (NICHD)

HD36879 (NICHD)

SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2000 Nov 11) 278 (1) 48-57.

Journal code: 0372516. ISSN: 0006-291X.

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200101

ENTRY DATE: Entered STN: 20010322

Last Updated on STN: 20010322

Entered Medline: 20010104

AB We have isolated a rat intracisternal-A particle element (IAP)-like element (IAP-LE) from ovarian granulosa cells that appears to be identical

to the rat **EST** clone AA964260. The compiled cDNA sequences contain several putative in-frame translation initiation codons with the largest capable of encoding a 365 amino acid protein with a reverse transcriptase domain in the N-terminus as well as a bipartite nuclear localization signal sequence in the middle. **Northern** blotting shows a major approximately 7 Kb transcript and a minor approximately 5

Kb

transcript that are abundantly expressed in the **ovary**. In situ hybridization histochemistry using **ovaries** from gonadotropin-treated immature rats and regularly cycling adult rats show that this transcript is predominantly localized to granulosa cells of all healthy follicles, including primary follicles, and to newly-formed and healthy corpora lutea. This cell-specific **expression pattern** of the IAP-LE gene is distinct from those of the several known retroviral elements, suggesting the potentially novel functional importance of the IAP-LE gene. Taken together, our results demonstrate abundant and cell-specific expression of a novel IAP-LE in rat granulosa cells.

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L79 ANSWER 8 OF 15 MEDLINE DUPLICATE 6
 ACCESSION NUMBER: 1999143102 MEDLINE
 DOCUMENT NUMBER: 99143102 PubMed ID: 9988682
 TITLE: Control of O-glycan branch formation. Molecular cloning of human cDNA encoding a novel beta1,6-N-acetylglucosaminyltransferase forming core 2 and core 4.
 AUTHOR: Schwientek T; Nomoto M; Lavery S B; Merkx G; van Kessel A G; Bennett E P; Hollingsworth M A; Clausen H
 CORPORATE SOURCE: School of Dentistry, University of Copenhagen, Norre Alle 20, 2200 Copenhagen N, Denmark.
 CONTRACT NUMBER: 1 RO1 CA66234 (NCI)
 1RO1 CA66234 (NCI)
 5 P41 RR05351 (NCRR)
 SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1999 Feb 19) 274 (8) 4504-12.
 Journal code: 2985121R. ISSN: 0021-9258.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 OTHER SOURCE: GENBANK-AF038650
 ENTRY MONTH: 199903
 ENTRY DATE: Entered STN: 19990326
 Last Updated on STN: 20000303
 Entered Medline: 19990318
 AB A novel human UDP-GlcNAc:Gal/GlcNAc beta1-3GalNAc alpha beta1, 6GlcNAc-transferase, designated C2/4GnT, was identified by BLAST analysis of expressed **sequence tags**. The sequence of C2/4GnT encoded a putative type II transmembrane protein with significant sequence similarity to human C2GnT and IGnT. Expression of the secreted form of C2/4GnT in insect cells showed that the gene product had UDP-N-acetyl-alpha-D-glucosamine:acceptor beta1, 6-N-acetylglucosaminyltransferase (beta1,6GlcNAc-transferase) activity. Analysis of substrate specificity revealed that the enzyme catalyzed O-glycan branch formation of the core 2 and core 4 type. NMR analyses of the product formed with core 3-para-nitrophenyl confirmed the product core 4-para-nitrophenyl. The coding region of C2/4GnT was contained in a single exon and located to chromosome 15q21.3. **Northern** analysis

revealed a restricted **expression pattern** of C2/4GnT mainly in colon, **kidney**, pancreas, and small intestine. No expression of C2/4GnT was detected in brain, **heart**, liver, **ovary**, placenta, spleen, thymus, and peripheral blood leukocytes. The expression of core 2 O-glycans has been correlated with cell differentiation processes and cancer. The results confirm the predicted existence of a beta1,6GlcNAc-transferase that functions in both core 2

and

core 4 O-glycan branch formation. The redundancy in beta1,6GlcNAc-transferases capable of forming core 2 O-glycans is important for understanding the mechanisms leading to specific changes in core 2 branching during cell development and malignant transformation.

L79 ANSWER 9 OF 15 MEDLINE DUPLICATE 7
ACCESSION NUMBER: 1999400797 MEDLINE
DOCUMENT NUMBER: 99400797 PubMed ID: 10471358
TITLE: Chromosomal, in silico and in vitro expression analysis of cardiovascular-based genes encoding zinc finger proteins.
AUTHOR: Dai K S; Liew C C
CORPORATE SOURCE: The Cardiac Gene Unit, Institute of Medical Science
Department of Laboratory Medicine and Pathobiology,
University of Toronto, Ontario, Canada.
SOURCE: JOURNAL OF MOLECULAR AND CELLULAR CARDIOLOGY, (1999 Sep)
31
(9) 1749-69.
Journal code: 0262322. ISSN: 0022-2828.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199910
ENTRY DATE: Entered STN: 19991014
Last Updated on STN: 19991014
Entered Medline: 19991004
AB Three hundred and sixty expressed **sequence tags** (**ESTs**) from human **heart** cDNA libraries corresponding to one hundred and twenty six unique zinc finger proteins (ZFPs) were annotated and classified into seven types of ZFPs as reported previously. Among these 126 cvbZFPs (cardiovascular-based ZFPs), the C(2)H(2)-type
and the C(2)C(2)-type are the two major ZFP types which account for more than 80% of ZFP genes present in the cardiovascular system. The **expression patterns** of 11 randomly selected ZFP genes (at least one for each type) in normal fetal, adult and hypertrophic
adult **hearts**, respectively, were determined using reverse transcriptase-polymerase chain reaction (RT-PCR) analysis. The results suggest that ZFPs may be involved in the processes of either
developmental control (downregulated or upregulated expression) or basic cellular functional regulation (constant expression). Interestingly, PAF-1 (peroxisome assembly factor-1), a C(3)HC(4)-type ZFP (RING domain-containing ZFP) showing a downregulated **expression pattern** in normal tissues was found to be upregulated in hypertrophic adult **heart**, suggesting a possible role for this fetal gene in the pathogenesis of cardiac hypertrophy. In silico **Northern** analysis of 15 tissues showed that over 90% of cvbZFPs demonstrate widespread tissue distribution, suggesting the vast majority of ZFPs are functionally shared among tissues. The potential importance
of transcriptional repressors in cardiovascular development and disease,
such

as HFHZ, was supported by the observation that one-third (39 of 126) of cvbZFPs possess this function. Of these, 26 are C(2)H(2)-type and the remaining 13 included 8 C(2)C(2)-type, 1 C(3)HC(4)-type, 1 C(2)HC(4)C(HD)-type, 2 C(3)H-type and 1 combination type. Of particular interest was the observation that ZFPs which contain a KRAB domain are the major subtype present (51.3% of the total repressors in cvbZFPs). Chromosomal distribution analysis showed that mapping loci of cvbZFP genes are concentrated on chromosomes 1, 3, 6, 8, 10, 11, 12, 19 and X. In particular, chromosome 19 appears to be enriched in ZFP genes with C(2)H(2)-type as the predominant type present. Overall, this report provides a fundamental initial step toward understanding the potential role of ZFPs in regulating cardiac development and disease.
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L79 ANSWER 10 OF 15 MEDLINE DUPLICATE 8
 ACCESSION NUMBER: 1999110977 MEDLINE
 DOCUMENT NUMBER: 99110977 PubMed ID: 9892814
 TITLE: mRNA differential display analysis of nephrotic kidney glomeruli.
 AUTHOR: Haltia A; Solin M; Luimula P; Kretzler M; Holthofer H
 CORPORATE SOURCE: Haartman Institute, Division of Bacteriology and Immunology, University of Helsinki, Finland.
 SOURCE: EXPERIMENTAL NEPHROLOGY, (1999 Jan-Feb) 7 (1) 52-8.
 Journal code: 9302239. ISSN: 1018-7782.
 PUB. COUNTRY: Switzerland
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199903
 ENTRY DATE: Entered STN: 19990316
 Last Updated on STN: 20020420
 Entered Medline: 19990301
 AB BACKGROUND: Differential display RT-PCR (DDRT-PCR) is a new powerful technique for identification and characterization of altered gene expression in eukaryotic cells and tissues. We studied here changes in **kidney** glomerular gene expression in patients with congenital nephrotic syndrome of the Finnish type (CNF), an inherited **kidney** disease with heavy proteinuria already in utero. METHODS: Using the DDRT-PCR approach and isolated glomeruli from removed human **kidneys**, we compared the gene **expression patterns** of normal human and CNF glomeruli. Differential expression of candidate genes was verified by **Northern** blotting, and the corresponding PCR fragments were sequenced and compared to known sequences in databanks. RESULTS: We found several genes and **sequence tags** with altered expression in nephrotic glomeruli including fragments with close homologies to cytochrome c oxidase subunit I, integrin-linked kinase, insulin-like growth factor II receptor and eotaxin, and also clones resembling ankyrin and cadherin-like consensus sequences. CONCLUSION: All the sequences identified are of interest in respect to pathogenesis of proteinuria. Furthermore, this study reveals potentially new members to known gene families with tissue and cell type-specific expression.

L79 ANSWER 11 OF 15 MEDLINE DUPLICATE 9
 ACCESSION NUMBER: 1998250717 MEDLINE
 DOCUMENT NUMBER: 98250717 PubMed ID: 9582303
 TITLE: A family of human beta3-galactosyltransferases.
 Characterization of four members of a
 UDP-galactose:beta-N-

acetyl-glucosamine/beta-nacetyl-galactosamine
beta-1,3-galactosyltransferase family.

AUTHOR: Amado M; Almeida R; Carneiro F; Levery S B; Holmes E H;
Nomoto M; Hollingsworth M A; Hassan H; Schwientek T;
Nielsen P A; Bennett E P; Clausen H

CORPORATE SOURCE: School of Dentistry, University of Copenhagen, Norre Alle
20, 2200 Copenhagen N, Denmark.

CONTRACT NUMBER: 1 RO1 CA66234 (NCI)
RO1 CA41521 (NCI)
RO1 CA70740 (NCI)
+

SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1998 May 22) 273 (21)
12770-8.
Journal code: 2985121R. ISSN: 0021-9258.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-Y15060; GENBANK-Y15061; GENBANK-Y15062

ENTRY MONTH: 199806

ENTRY DATE: Entered STN: 19980708
Last Updated on STN: 19980708
Entered Medline: 19980625

AB BLAST analysis of expressed **sequence tags** (**ESTs**) using the coding sequence of a human UDP-galactose:beta-N-acetyl-glucosamine beta-1, 3-galactosyltransferase, designated beta3Gal-T1, revealed no **ESTs** with identical sequences but a large number with similarity. Three different sets of overlapping **ESTs** with sequence similarities to beta3Gal-T1 were compiled, and complete coding regions of these genes were obtained. Expression of two of these genes in the Baculo virus system showed that one represented a UDP-galactose:beta-N-acetyl-glucosamine beta-1, 3-galactosyltransferase (beta3Gal-T2) with similar kinetic properties as beta3Gal-T1. Another gene represented a UDP-galactose:beta-N-acetyl-galactosamine beta-1, 3-galactosyltransferase (beta3Gal-T4) involved in GM1/GD1 ganglioside synthesis, and this gene was highly similar to a recently reported rat GD1 synthase (Miyazaki, H., Fukumoto, S., Okada, M., Hasegawa, T., and Furukawa, K. (1997) J. Biol. Chem. 272, 24794-24799). **Northern** analysis of mRNA from human organs with the four homologous cDNA revealed different **expression patterns**. beta3Gal-T1 mRNA was expressed in brain, beta3Gal-T2 was expressed in brain and heart, and beta3Gal-T3 and -T4 were more widely expressed. The coding regions for each of the four genes were contained in single exons. beta3Gal-T2, -T3, and -T4 were localized to 1q31, 3q25, and 6p21.3, respectively, by **EST** mapping. The results demonstrate the existence of a family of homologous beta3-galactosyltransferase genes.

L79 ANSWER 12 OF 15 MEDLINE DUPLICATE 10

ACCESSION NUMBER: 1998103635 MEDLINE

DOCUMENT NUMBER: 98103635 PubMed ID: 9443398

TITLE: Hevin, an antiadhesive extracellular matrix protein, is down-regulated in metastatic prostate adenocarcinoma.

AUTHOR: Nelson P S; Plymate S R; Wang K; True L D; Ware J L; Gan L;
Liu A Y; Hood L

CORPORATE SOURCE: Department of Molecular Biotechnology, University of Washington, Seattle 98195, USA.

SOURCE: CANCER RESEARCH, (1998 Jan 15) 58 (2) 232-6.

Journal code: 2984705R. ISSN: 0008-5472.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 199802

ENTRY DATE: Entered STN: 19980217
Last Updated on STN: 19980217
Entered Medline: 19980204

AB Hevin, a gene closely related to the extracellular matrix protein SPARC, is an acidic cysteine-rich glycoprotein shown to be important for the adhesion and trafficking of cells through the endothelium. Through the use of differential display and differential **EST** analysis, we identified Hevin as a gene whose transcription is down-regulated in transformed **prostate** epithelial cell lines and metastatic **prostate** adenocarcinoma. These results were confirmed by comparing expression levels between normal and neoplastic human **prostate** tissues using **Northern** analysis. In situ hybridization with an 35S-labeled antisense riboprobe demonstrated the loss of Hevin expression in metastatic **prostate** carcinoma. The **expression pattern** of Hevin in transformed and metastatic epithelium may provide further insights into the complex cell adhesion events involved in the metastatic progression of **prostate** carcinoma.

L79 ANSWER 13 OF 15 MEDLINE DUPLICATE 11

ACCESSION NUMBER: 1998234542 MEDLINE

DOCUMENT NUMBER: 98234542 PubMed ID: 9570947

TITLE: Divergently transcribed overlapping genes expressed in liver and kidney and located in the 11p15.5 imprinted domain.

AUTHOR: Cooper P R; Smilinich N J; Day C D; Nowak N J; Reid L H; Pearsall R S; Reece M; Prawitt D; Landers J; Housman D E; Winterpacht A; Zabel B U; Pelletier J; Weissman B E; Shows T B; Higgins M J

CORPORATE SOURCE: Department of Human Genetics, Roswell Park Cancer Institute, Buffalo, New York 14263, USA.

CONTRACT NUMBER: CA63176 (NCI)
CA63333 (NCI)
HG00333 (NHGRI)

SOURCE: GENOMICS, (1998 Apr 1) 49 (1) 38-51.
Journal code: 8800135. ISSN: 0888-7543.

PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AC001228; GENBANK-AF087428

ENTRY MONTH: 199806

ENTRY DATE: Entered STN: 19980708
Last Updated on STN: 20000512
Entered Medline: 19980625

AB Human chromosomal band 11p15.5 has been shown to contain genes involved in the development of several pediatric and adult tumors and in Beckwith-Wiedemann syndrome (BWS). Overlapping P1 artificial chromosome clones from this region have been used as templates for genomic sequencing in an effort to identify candidate genes for these disorders. PowerBLAST identified several matches with expressed **sequence tags (ESTs)** from fetal brain and liver cDNA libraries.

Northern blot analysis indicated that two of the genes identified by these ESTs encode transcripts of 1-1.5 kb with predominant expression in fetal and adult liver and kidney. With RT-PCR and RACE, full-length transcripts were isolated for these two genes, with the largest open reading frames encoding putative proteins of 253 and 424 amino acids. Database comparison of the predicted amino acid sequence of the larger transcript indicated homology to integral membrane organic cation transporters; hence, we designate this gene ORCTL2 (organic cation transporter-like 2). An expressed sequence polymorphism provided evidence that the ORCTL2 gene exhibits "leaky" imprinting in both human fetal kidney and human fetal liver. The mouse orthologue (Orctl2) was identified, and a similar polymorphism was used to demonstrate maternal-specific expression of this gene in fetal liver from interspecific F1 mice. The predicted protein of the smaller gene showed

no

significant similarity in the database. Northern and RACE analyses suggest that this gene may have multiple transcription start sites. Determination of the genomic structure in humans indicated that

the

5'-end of this transcript overlaps in divergent orientation with the first

two exons of ORCTL2, suggesting a possible role for antisense regulation of one gene by the other. We, therefore, provisionally name this second transcript ORCTL2S (ORCTL2-antisense). The expression patterns of these genes and the imprinted expression of ORCTL2 are suggestive of a possible role in the development of Wilms tumor (WT) and hepatoblastoma. Although SSCP analysis of 62 WT samples and 10 BWS patients did not result in the identification of any mutations in ORCTL2 or ORCTL2S, it will be important to examine their expression pattern in tumors and BWS patients, since epigenetic alteration at these loci may play a role in the etiology of these diseases.

L79 ANSWER 14 OF 15 MEDLINE DUPLICATE 12
 ACCESSION NUMBER: 97094765 MEDLINE
 DOCUMENT NUMBER: 97094765 PubMed ID: 8939999
 TITLE: Molecular cloning and characterization of human tissue inhibitor of metalloproteinase 4.
 AUTHOR: Greene J; Wang M; Liu Y E; Raymond L A; Rosen C; Shi Y E
 CORPORATE SOURCE: Human Genome Sciences, Inc., Rockville, Maryland 20850-3338, USA. aecom.yu.edu.
 CONTRACT NUMBER: CA68064-01 (NCI)
 SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1996 Nov 29) 271 (48) 30375-80.
 Journal code: 2985121R. ISSN: 0021-9258.
 PUB. COUNTRY: United States
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199701
 ENTRY DATE: Entered STN: 19970128
 Last Updated on STN: 20000303
 Entered Medline: 19970107
 AB The tissue inhibitors of metalloproteinases (TIMPs) constitute a family of proteins, of which three members have so far been described. Using the expressed sequence tag sequencing approach, we have identified a novel TIMP-related cDNA fragment and subsequently cloned a fourth human TIMP (TIMP-4) from a human heart cDNA library. The open reading frame encodes a 224-amino acid precursor including a 29-residue secretion signal. The predicted structure of the new protein shares 37% sequence identity with TIMP-1 and 51% identity with TIMP-2 and

-3. The protein has a predicted isoelectric point of 7.34. The open reading frame-directed expression of TIMP-4 protein in MDA-MB-435 human breast cancer cells showed metalloproteinase inhibitory activity on reverse zymography. By **Northern** analysis, only the adult **heart** showed abundant TIMP-4 transcripts with a 1.4-kilobase predominant transcript band; very low levels of the transcripts were detected in the **kidney**, placenta, colon, and testes, and no transcripts were detected in the liver, brain, **lung**, thymus, and spleen. This unique **expression pattern** suggests that TIMP-4 may function in a tissue-specific fashion in extracellular matrix homeostasis.

L79 ANSWER 15 OF 15 MEDLINE DUPLICATE 13
 ACCESSION NUMBER: 96375776 MEDLINE
 DOCUMENT NUMBER: 96375776 PubMed ID: 8782065
 TITLE: Identification of genes associated with myocardial development.
 AUTHOR: Fung Y W; Liew C C
 CORPORATE SOURCE: Department of Clinical Biochemistry, Toronto Hospital, University of Toronto, Canada.
 SOURCE: JOURNAL OF MOLECULAR AND CELLULAR CARDIOLOGY, (1996 Jun) 28
 (6) 1241-9.
 Journal code: 0262322. ISSN: 0022-2828.
 PUB. COUNTRY: ENGLAND: United Kingdom
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 199611
 ENTRY DATE: Entered STN: 19961219
 Last Updated on STN: 19961219
 Entered Medline: 19961127
 AB We are conducting a cDNA sequencing project using human **heart** cDNA libraries to study expression of genes in the human **heart**. From our human **heart** cDNA libraries, we have accumulated over 10,000 partial cDNA sequences (expressed **sequence tags** -**ESTs**) representing both the previously uncharacterized and known transcripts expressed in the human **heart** (Liew et al., 1994). Currently, we have applied dot blot hybridization as a rapid approach to determine the genes putatively involved in myocardial development. Differential **expression patterns** of gene transcripts represented by the cDNA clones can be revealed by comparing dot intensities on the autoradiographs, after hybridization with cDNA probes generated from neonatal and adult **heart** mRNAs, cDNA clones (1505) have been processed by dot blot hybridization, of which 924 and 581 represented novel and known transcripts respectively. Among the screened clones, about 1.4% were found to be differentially expressed during **heart** development. Further verification was accomplished by **Northern** blot analysis. By grouping the 581 clones corresponding to known transcripts, a study of the gene expression profile of the **heart** in the cardiovascular system can be achieved.

=>

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT 19:04:09

ON 08 JUL 2002

L1 13496 S EST
L2 34 S L1(S) (NO#(W) CORRELAT?)
L3 21 DUP REM L2 (13 DUPLICATES REMOVED)
L4 3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5 1972 S L4(S) (PROTEIN OR PEPTIDE)
L6 1748 S L5(S) (EXPRESS?)
L7 775 S L6(S) DATABASE#
L8 355 DUP REM L7 (420 DUPLICATES REMOVED)
L9 96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
L10 47 S L8(S) GENBANK
L11 87 S L8(S) (HEART OR BONE OR BRAIN)
L12 137 S L11 OR L9
L13 1 S L12 AND (NO#(W) EXPRESS?)
L14 67 S L12(S) (TRANSCRI?)
L15 86 S L8(S) NORTHERN
L16 50 S L1(S) (NO#(2W) CORRELAT?)
L17 16 S L16 NOT L2
L18 12 DUP REM L17 (4 DUPLICATES REMOVED)
L19 54 S L1(S) (NO#(3W) CORRELAT?)
L20 0 S L19 NOT L1
L21 20 S L19 NOT L2
L22 4 S L21 NOT L16

FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002

L23 13496 S EST OR (SEQUENCE(W) TAG#)
L24 234 S L23 AND DATABASE#/TI
L25 0 S L24 AND (NO(3W) CORRELAT?)
L26 234 S L24(S) DATABASE#
L27 2221 S L23(S) DATABASE#
L28 4 S L27(S) (NO#(3W) CORRELAT?)
L29 1174 S L23(S) (BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVA
L30 310 S L29(S) NORTHERN
L31 133 S L30 AND DATABASE#
L32 78 DUP REM L31 (55 DUPLICATES REMOVED)
L33 1072 S L23(S) (PREDICT? OR ANTICIPAT?)
L34 22 S L33 AND DATABASE#/TI
L35 13 DUP REM L34 (9 DUPLICATES REMOVED)
L36 22 S L34(S) DATABASE#
L37 2221 S L23(S) DATABASE#
L38 612 S L37(S) TISSUE
L39 58 S L38(S) PROSTATE
L40 10 S L39 AND PREDICT?
L41 6 DUP REM L40 (4 DUPLICATES REMOVED)
L42 1 S L23(S) (CANNOT(3W) PREDICT)
L43 13596 S L23 OR DBEST
L44 6719 S L43(S) EXPRESS?
L45 192 S L44(S) BLAST
L46 47 S L45(S) PREDICT?
L47 27 DUP REM L46 (20 DUPLICATES REMOVED)
L48 2 S L43(S) RELIED
L49 1 S L43(S) (("NOT" OR CANNOT) (W) PREDICT?)
L50 0 S L43(S) (CANNOT(W) ANTICIPATE)
L51 797 S L43(S) TRANSCRIPTS
L52 28 S L43(S) ((NO(W) EXPRESSION) OR ("NOT" (W) EXPRESSED))
L53 17 DUP REM L52 (11 DUPLICATES REMOVED)
L54 546 S L43 AND (EXPRESSION(A) PATTERN#)
L55 15 S L54 AND DATABASE#/TI
L56 9 DUP REM L55 (6 DUPLICATES REMOVED)
L57 239 S L43 AND DATABASE#/TI
L58 5 S L57 AND PREDICT

L59 3 DUP REM L58 (2 DUPLICATES REMOVED)
 L60 1735 S L43(S) LIBRAR?
 L61 34 S L60(S) PREDICT
 L62 19 DUP REM L61 (15 DUPLICATES REMOVED)
 L63 4276 S L43(S) (MRNA OR NORTHERN OR CDNA OR TRANSCRIPT#)
 L64 335 S L63(S) (EXPRESSION(A) PATTERN#)
 L65 86 S L64(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN)
 L66 49 DUP REM L65 (37 DUPLICATES REMOVED)
 L67 430 S L43(S) (EXPRESSION(A) PATTERN#)
 L68 12 S L67 AND DATABASE#/TI
 L69 6 DUP REM L68 (6 DUPLICATES REMOVED)
 L70 99 S L23(3A) PREDICT?
 L71 2 S L70(3A) (EXPRESSION OR TRANSCRIPTION)
 L72 152 S L43(5A) PREDICT?
 L73 3 S L72(5A) (EXPRESSION OR TRANSCRIPTION)
 L74 1 S L73 NOT L71
 L75 64 S L43(S) HYPOTHETICAL
 L76 55 S L75(S) (EXPRESS? OR TRANSCI?)
 L77 34 DUP REM L76 (21 DUPLICATES REMOVED)
 L78 28 S L30(S) (EXPRESSION(A) PATTERN#)
 L79 15 DUP REM L78 (13 DUPLICATES REMOVED)

=> s l23(s) ("not"(w) predictive)
 L80 0 L23(S) ("NOT"(W) PREDICTIVE)

=> s l23(s) (cannot(w) anticipate)
 L81 0 L23(S) (CANNOT(W) ANTICIPATE)

=> s database(a) mining
 L82 107 DATABASE(A) MINING

=> s l23 and l82
 L83 14 L23 AND L82

=> dup rem l83
 PROCESSING COMPLETED FOR L83
 L84 8 DUP REM L83 (6 DUPLICATES REMOVED)

=> d ibib abs tot

L84	ANSWER 1 OF 8	MEDLINE	DUPLICATE 1
ACCESSION NUMBER:	2002299254	IN-PROCESS	
DOCUMENT NUMBER:	22035872	PubMed ID: 12040005	
TITLE:	Identification of Gasz, an Evolutionarily Conserved Gene Expressed Exclusively in Germ Cells and Encoding a Protein with Four Ankyrin Repeats, a Sterile-alpha Motif, and a Basic Leucine Zipper.		
AUTHOR:	Yan Wei; Rajkovic Aleksandar; Viveiros Maria M; Burns Kathleen H; Eppig John J; Matzuk Martin M		
CORPORATE SOURCE:	Departments of Pathology (W.Y., M.M.M.), Department of Molecular and Cellular Biology (M.M.M.), Department of Molecular and Human Genetics (M.M.M., K.H.B.), Department of Obstetrics and Gynecology (A.R.), Baylor College of Medicine, Houston, Texas 77030.		
SOURCE:	MOLECULAR ENDOCRINOLOGY, (2002 Jun) 16 (6) 1168-84. Journal code: 8801431. ISSN: 0888-8809.		
PUB. COUNTRY:	United States Journal; Article; (JOURNAL ARTICLE)		
LANGUAGE:	English		
FILE SEGMENT:	IN-PROCESS; NONINDEXED; Priority Journals		
ENTRY DATE:	Entered STN: 20020602		

Last Updated on STN: 20020602

AB To discover causes of infertility and potential contraceptive targets, we used in silico subtraction and genomic **database mining** to identify conserved genes with germ cell-specific expression. In silico subtraction identified an expressed **sequence tag** (**EST**) present exclusively in a newborn mouse ovary library. The full-length cDNA sequence corresponding to this **EST** encodes a novel protein containing four ankyrin (ANK) repeats, a sterile-alpha motif (SAM), and a putative basic leucine zipper (bZIP) domain. Northern blot and semiquantitative RT-PCR analyses demonstrated that the mRNA is exclusively expressed in the mouse testis and ovary. The expression sites were localized by in situ hybridization to pachytene spermatocytes in the testis and oocytes in the ovary. Immunohistochemistry showed that the novel protein is localized to the cytoplasm in pachytene spermatocytes and early spermatids, oocytes at all stages of oogenesis, and in early preimplantation embryos. Based on its germ cell-specific expression and the presence of ANK, SAM, and basic leucine zipper domains, we have termed this novel protein GASZ. The mouse Gasz gene, which consists of 13 exons and spans 60 kb, is located on chromosome 6 between the Wnt2 and cystic fibrosis transmembrane conductance regulator (Cftr) genes. Using genomic **database mining**, orthologous genes encoding GASZ were identified in the rat, cow, baboon, chimpanzee, and human. Phylogenetic analyses reveal that the GASZ proteins are highly conserved among these species. Human and mouse GASZ proteins share 85.3% amino acid identity, and human and chimpanzee GASZ proteins differ by only 3 out of 475 amino acids. In humans, the GASZ gene resides on chromosome 7 and is similarly composed of 13 exons. Because both ANK repeats and the SAM domain function as protein-protein interaction modules that mediate signal transduction cascades in some systems, GASZ may represent an important cytoplasmic signal transducer that mediates protein-protein interactions during germ cell maturation in both males and females and during preimplantation embryogenesis.

L84 ANSWER 2 OF 8 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2002185034 MEDLINE
DOCUMENT NUMBER: 21917691 PubMed ID: 11920606
TITLE: Identification of cancer/testis genes by **database mining** and mRNA expression analysis.
AUTHOR: Scanlan Matthew J; Gordon Claudia M; Williamson Barbara; Lee Sang-Yull; Chen Yao-Tseng; Stockert Elisabeth; Jungbluth Achim; Ritter Gerd; Jager Dirk; Jager Elke; Knuth Alexander; Old Lloyd J
CORPORATE SOURCE: Ludwig Institute for Cancer Research, New York Branch at Memorial Sloan-Kettering Cancer Center, New York, NY 10021, USA.. scanlanm@mskcc.org
SOURCE: INTERNATIONAL JOURNAL OF CANCER, (2002 Apr 1) 98 (4) 485-92.
Journal code: 0042124. ISSN: 0020-7136.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200205
ENTRY DATE: Entered STN: 20020403
Last Updated on STN: 20020511

Entered Medline: 20020510

AB Cancer/testis (CT) antigens are immunogenic proteins expressed predominantly in gametogenic tissue and cancer; they are considered promising target molecules for cancer vaccines. The identification of new CT genes is essential to the development of polyvalent cancer vaccines designed to overcome tumor heterogeneity and antigen loss. In the current study, a search for new CT genes was conducted by mining the Unigene database for gene clusters that contain expressed **sequence tags** derived solely from both normal testis and tumor-derived cDNA libraries. This search identified 1,325 different

cancer/testis-associated

Unigene clusters. The mRNA expression pattern of 73 cancer/testis-associated Unigene clusters was assessed by reverse transcriptase polymerase chain reaction. Three gene products, CT15/Hs.177959, CT16/Hs.245431 and CT17/Hs.178062, were detected only in testis and in tumor tissue. CT15 is equivalent to ADAM2/fertilin-beta. CT16, an uncharacterized gene product, has homology (30-50%) to members of the

GAGE

gene family and is 89% identical to CT16.2/Hs.293317, indicating that

CT16

and CT16.2 are members of a new GAGE gene family. The uncharacterized

gene

product, CT17, has homology (30%) to phospholipase A1. RT-PCR analysis showed that CT15 is expressed exclusively in renal cancer, whereas CT16 and CT17 are expressed in a range of human cancers. Real-time RT-PCR analysis of newly defined CT genes and the prototype CT antigens, MAGE-3 and NY-ESO-1, revealed low levels (less than 3% of the level detected in testis) of CT15, CT16 and NY-ESO-1 in a limited range of normal, non-gametogenic tissues. This study demonstrates the merits of **database mining** with respect to the identification of tissue-restricted gene products expressed in cancer.
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L84 ANSWER 3 OF 8 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.

ACCESSION NUMBER: 2002:306446 BIOSIS

DOCUMENT NUMBER: PREV200200306446

TITLE: PAGE4 is a cytoplasmic protein that is expressed in normal prostate and in prostate cancers.

AUTHOR(S): Iavarone, Carlo; Wolfgang, Curt; Kumar, Vasantha; Duray, Paul; Willingham, Mark; Pastan, Ira; Bera, Tapan K. (1)

CORPORATE SOURCE: (1) Laboratory of Molecular Biology, Clinical Cancer Research, National Cancer Institute, NIH, 37 Convent

Drive,

MSC 4264, Building 37, Room 5106, Bethesda, MD,

20892-4264:

tkbera@helix.nih.gov USA

SOURCE: Molecular Cancer Therapeutics, (March, 2002) Vol. 1, No. 5,

pp. 329-335. <http://mct.aacrjournals.org/>. print.
ISSN: 1535-7163.

DOCUMENT TYPE: Article

LANGUAGE: English

AB PAGE4 is an X chromosome-linked cancer-testis antigen that was identified by expressed **sequence tags database mining** and a functional genomic approach. PAGE4 is preferentially expressed in normal male and female reproductive tissues and also in a variety of cancers including prostate. In the present study, we have used in situ hybridization to show that PAGE4 mRNA is expressed only in the epithelial cells of normal and prostate-cancer specimens. Analysis of the protein product encoded by the PAGE4 mRNA reveals that it encodes a Mr 16,000 protein and is detected in tissue extracts from both normal

prostate and prostate cancer. Cell fractionation analysis of PAGE4 protein indicates that PAGE4 is localized in the cytoplasm of the cell. Furthermore, cDNA microarray analysis indicates that the expression of lipoprotein lipase, a gene frequently deleted in prostate cancer, is down-regulated in a cell line that expresses PAGE4.

L84 ANSWER 4 OF 8 MEDLINE DUPLICATE 3
 ACCESSION NUMBER: 2001687112 MEDLINE
 DOCUMENT NUMBER: 21590336 PubMed ID: 11733002
 TITLE: A new siglec family member, siglec-10, is expressed in cells of the immune system and has signaling properties similar to CD33.
 AUTHOR: Whitney G; Wang S; Chang H; Cheng K Y; Lu P; Zhou X D; Yang W P; McKinnon M; Longphre M
 CORPORATE SOURCE: Inflammation and Pulmonary Drug Discovery Department, Bristol-Myers Squibb Pharmaceutical Research Institute, Princeton, NJ 08543-4000, USA.
 SOURCE: EUROPEAN JOURNAL OF BIOCHEMISTRY, (2001 Dec) 268 (23) 6083-96.
 Journal code: 0107600. ISSN: 0014-2956.
 PUB. COUNTRY: Germany: Germany, Federal Republic of
 Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200201
 ENTRY DATE: Entered STN: 20011205
 Last Updated on STN: 20020125
 Entered Medline: 20020116
 AB The siglecs (sialic acid-binding Ig-like lectins) are a distinct subset of the Ig superfamily with adhesion-molecule-like structure. We describe here a novel member of the siglec protein family that shares a similar structure including five Ig-like domains, a transmembrane domain, and a cytoplasmic tail containing two ITIM-signaling motifs. Siglec-10 was identified through **database mining** of an asthmatic eosinophil **EST** library. Using the Stanford G3 radiation hybrid panel we were able to localize the genomic sequence of siglec-10 within the cluster of genes on chromosome 19q13.3-4 that encode other siglec family members. We have demonstrated that siglec-10 is an immune system-restricted membrane-bound protein that is highly expressed in peripheral blood leukocytes as demonstrated by Northern, RT-PCR and flow cytometry. Binding assays determined that the extracellular domain of siglec-10 was capable of binding to peripheral blood leukocytes. The cytoplasmic tail of siglec-10 contains four tyrosines, two of which are embedded in ITIM-signaling motifs (Y597 and Y667) and are likely involved in intracellular signaling. The ability of tyrosine kinases to phosphorylate the cytoplasmic tyrosines was evaluated by kinase assay using wild-type siglec-10 cytoplasmic domain and Y-->F mutants. The majority of the phosphorylation could be attributed to Y597 and Y667. Further experiments with cell extracts suggest that SHP-1 interacts with Y667 and SHP-2 interacts with Y667 in addition to another tyrosine. This is very similar to CD33, which also binds the phosphatases SHP-1 and SHP-2, therefore siglec-10, as CD33, may be characterized as an inhibitory receptor.

L84 ANSWER 5 OF 8 MEDLINE DUPLICATE 4
 ACCESSION NUMBER: 2001543308 MEDLINE

DOCUMENT NUMBER: 21475973 PubMed ID: 11591886
TITLE: MRP8, a new member of ABC transporter superfamily, identified by **EST database mining** and gene prediction program, is highly expressed in breast cancer.
AUTHOR: Bera T K; Lee S; Salvatore G; Lee B; Pastan I
CORPORATE SOURCE: Laboratory of Molecular Biology, Division of Basic Sciences, National Cancer Institute, National Institutes of Health, Bethesda, Maryland 20892-4255, USA.
SOURCE: MOLECULAR MEDICINE, (2001 Aug) 7 (8) 509-16.
Journal code: 9501023. ISSN: 1076-1551.
PUB. COUNTRY: United States
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20011010
Last Updated on STN: 20020215
Entered Medline: 20020214

AB BACKGROUND: With the completion of the human draft genome sequence, efforts are now devoted to identifying new genes. We have developed a computer-based strategy that utilizes the **EST database** to identify new genes that could be targets for the immunotherapy of cancer or could be involved in the multistep process of cancer. MATERIALS AND METHODS: Utilizing our computer-based screening strategy, we identified a cluster of expressed **sequence tags (ESTs)** that are highly expressed in breast cancer. Northern blot and reverse transcriptase polymerase chain reaction (RT-PCR) analyses demonstrated the tissue specificity of the computer-generated cluster and comparison with the human genome sequence assisted in isolating a full-length cDNA clone. RESULTS: We identified a new gene that is highly expressed in breast cancer. This gene is expressed at moderate levels in normal breast and testis and at very low levels in liver, brain, and placenta. The gene has two major transcripts of 4.5 kb and 4.1 kb. The 4.5-kb transcript is very abundant in breast cancer, and has an open reading frame of 1382 amino acids. The predicted protein sequence of the 4.5-kb transcript reveals that it has high homology with MRP5, a member of multidrug resistant-associated protein family (MRP). There are seven reported members in the MRP family; we designate this gene as MRP8 (ABCC11). The 4.5-kb MRP8 transcript consists of 31 exons and is located in a genomic region of over 80.4 kb on chromosome 16q12.1. The smaller 4.1-kb transcript of MRP8 is found in testis and may initiate within intron 6 of the gene. CONCLUSION: The selective expression of MRP8 (ABCC11), a new member of ATP-binding cassette transporter superfamily could be a molecular target for the treatment of breast cancer.

L84 ANSWER 6 OF 8 MEDLINE DUPLICATE 5
ACCESSION NUMBER: 2001493705 MEDLINE
DOCUMENT NUMBER: 21427669 PubMed ID: 11536302
TITLE: GDEP, a new gene differentially expressed in normal prostate and prostate cancer.
AUTHOR: Olsson P; Bera T K; Essand M; Kumar V; Duray P; Vincent J; Lee B; Pastan I
CORPORATE SOURCE: Laboratory of Molecular Biology, Division of Basic Sciences, National Cancer Institute, National Institutes of Health, Bethesda, Maryland 20892-4255, USA.
SOURCE: PROSTATE, (2001 Sep 15) 48 (4) 231-41.
Journal code: 8101368. ISSN: 0270-4137.
PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200110
ENTRY DATE: Entered STN: 20010906
Last Updated on STN: 20011008
Entered Medline: 20011004

AB BACKGROUND: The database of human expressed **sequence tags** (dbEST) is a potential source for the identification of tissue specific genes. The database contains sequences that originate from

cdNA libraries from different tissues cell types and tumors. METHODS: Computer based analysis identified a cluster of sequence homologous **ESTs**, containing **ESTs** derived only from human prostate cdNA libraries. The tissue specificity was examined by multiple tissue RNA

dot blots and RT-PCR. The new RNA transcript was characterized using northern blot analysis, RACE-PCR, and a ribonuclease protection assay. RESULTS: We have identified a gene differentially expressed in prostate using **EST** database analysis and experimental studies. We name the gene GDEP for gene differentially expressed in prostate. The major GDEP transcript is about 520 bp long. GDEP RNA was detected in nine prostate tissue samples, four normal and five cancer. Expression in prostate epithelial cells was established by in situ hybridization. Weak expression was detected in the prostate cancer cell line LNCaP. In vitro transcription/translation indicate that the RNA encodes a small 34 amino acid protein. The major transcript consists of two exons with one large intron (> 15 kb). The GDEP gene was mapped to chromosome 4q21.1 by radiation hybrid mapping. CONCLUSIONS: Our data proves that tissue specific genes can be identified by **EST database mining**. The prostate specificity of GDEP expression indicates that GDEP may be useful in the diagnosis or treatment of prostate cancer. Published 2001 Wiley-Liss, Inc.

L84 ANSWER 7 OF 8 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:151910 BIOSIS
DOCUMENT NUMBER: PREV200200151910
TITLE: Cloning and characterization of zebrafish gp130.
AUTHOR(S): Layton, Judith E. (1); Hall, Nathan E. (1); Connell, Fiona (1); Varma, Sony (1); Fujiki, Kazuhiro; Lieschke, Graham J.

(1)
CORPORATE SOURCE: (1) Melbourne Tumour Biology Branch, Ludwig Institute for Cancer Research, Parkville, VIC Australia
SOURCE: Blood, (November 16, 2001) Vol. 98, No. 11 Part 2, pp. 134b. <http://www.bloodjournal.org/>. print.
Meeting Info.: 43rd Annual Meeting of the American Society of Hematology, Part 2 Orlando, Florida, USA December

07-11,
2001
ISSN: 0006-4971.

DOCUMENT TYPE: Conference
LANGUAGE: English

AB The transmembrane glycoprotein, gp130, is the shared signal transducing sub-unit of the interleukin-6 receptor family. The ligands for this receptor family, including interleukins 6 and 11, leukemia inhibitory factor, oncostatin M, ciliary neurotrophic factor and cardiotrophin-1, exhibit a broad range of biological activities. We have embraced zebrafish as a useful model for the genetic study of hematopoiesis and hence have been collecting molecular reagents to facilitate this work.

Database mining revealed an unannotated carp **EST** with similarity to gp130. Further sequencing of this clone (gift of Dr.

M.

Nakao, Fukuoka, Japan) confirmed it contained sequences encoding a gp130-like protein. A zebrafish kidney library (gift of Dr. L. Zon, Boston, U.S.A.) was screened at low stringency using these carp sequences as a probe, a partial cDNA clone of zebrafish gp130 was obtained, and

then

a probe corresponding to the 3' end of this used to recover a second clone. These overlapping clones combined to describe a 4663 nucleotide cDNA encoding an 859 amino acid sequence, predicted to be of similar structure to avian, frog and mammalian gp130, with amino acid sequence identity of 30-32% between these species. The carp translated **EST** sequence of 141 amino acids, corresponding to the transmembrane and adjacent cytoplasmic region, is 85% identical to the equivalent zebrafish sequence. This region of the zebrafish sequence is 47-55% identical to avian, frog and mammalian sequences. Although the zebrafish gp130 cytoplasmic domain is 77 residues shorter than the human, the Box 1, Box

2

and Box 3 conserved regions are present, as are the five tyrosine residues

that are critical for signaling. In a phylogenetic analysis including other mammalian and zebrafish hematopoietin receptor superfamily members, this zebrafish protein formed an outgroup with other gp130 proteins, supporting the hypothesis that this protein is a zebrafish gp130 ortholog despite its relatively low overall homology. Expression of gp130 in zebrafish embryos was examined by RT-PCR and appeared to be developmentally regulated. The tissue distribution of expression is being examined by in situ hybridization. We conclude that the hematopoietin receptor superfamily is conserved in zebrafish and infer that a family of ligands that signal via gp130 will also be present.

L84 ANSWER 8 OF 8 MEDLINE DUPLICATE 6
ACCESSION NUMBER: 2000493620 MEDLINE
DOCUMENT NUMBER: 20442530 PubMed ID: 10984454
TITLE: An ordered comparative map of the cattle and human
genomes.
AUTHOR: Band M R; Larson J H; Rebeiz M; Green C A; Heyen D W;
Donovan J; Windish R; Steining C; Mahyuddin P; Womack J E;
Lewin H A
CORPORATE SOURCE: Department of Animal Sciences, University of Illinois at
Urbana-Champaign, Urbana, Illinois 61801, USA.
SOURCE: GENOME RESEARCH, (2000 Sep) 10 (9) 1359-68.
Journal code: 9518021. ISSN: 1088-9051.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AW244888; GENBANK-AW244889; GENBANK-AW244890;
GENBANK-AW244891; GENBANK-AW244892; GENBANK-AW244893;
GENBANK-AW244894; GENBANK-AW244895; GENBANK-AW244896;
GENBANK-AW244897; GENBANK-AW261132; GENBANK-AW261133;
GENBANK-AW261134; GENBANK-AW261135; GENBANK-AW261136;
GENBANK-AW261137; GENBANK-AW261138; GENBANK-AW261139;
GENBANK-AW261140; GENBANK-AW261141; GENBANK-AW261142;
GENBANK-AW261143; GENBANK-AW261144; GENBANK-AW261145;
GENBANK-AW261146; GENBANK-AW261147; GENBANK-AW261148;
GENBANK-AW261149; GENBANK-AW261150; GENBANK-AW261151; +
ENTRY MONTH: 200010
ENTRY DATE: Entered STN: 20001027
Last Updated on STN: 20001027

Entered Medline: 20001017

AB A cattle-human whole-genome comparative map was constructed using parallel

radiation hybrid (RH) mapping in conjunction with **EST** sequencing, **database mining** for unmapped cattle genes, and a predictive bioinformatics approach (COMPASS) for targeting specific homologous regions. A total of 768 genes were placed on the RH map in addition to 319 microsatellites used as anchor markers. Of these, 638 had human orthologs with mapping data, thus permitting construction of an ordered comparative map. The large number of ordered loci revealed > or =105 conserved segments between the two genomes. The comparative map suggests that 41 translocation events, a minimum of 54 internal rearrangements, and repositioning of all but one centromere can account for the observed organizations of the cattle and human genomes. In addition, the COMPASS in silico mapping tool was shown to be 95% accurate in its ability to predict cattle chromosome location from random sequence data, demonstrating this tool to be valuable for efficient targeting of specific regions for detailed mapping. The comparative map generated will be a cornerstone for elucidating mammalian chromosome phylogeny and the identification of genes of agricultural importance."Ought we, for instance, to begin by discussing each separate species-in virtue of some common element of their nature, and proceed from this as a basis for the consideration of them separately?" from Aristotle, On the Parts of Animals, 350 B.C.E.

=> d history

(FILE 'HOME' ENTERED AT 19:03:47 ON 08 JUL 2002)

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
19:04:09
ON 08 JUL 2002

L1 13496 S EST
L2 34 S L1(S) (NO#(W) CORRELAT?)
L3 21 DUP REM L2 (13 DUPLICATES REMOVED)
L4 3375 S L1(S) (MRNA OR CDNA OR POLYNUCLEOTIDE#)
L5 1972 S L4(S) (PROTEIN OR PEPTIDE)
L6 1748 S L5(S) (EXPRESS?)
L7 775 S L6(S) DATABASE#
L8 355 DUP REM L7 (420 DUPLICATES REMOVED)
L9 96 S L8(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN)
L10 47 S L8(S) GENBANK
L11 87 S L8(S) (HEART OR BONE OR BRAIN)
L12 137 S L11 OR L9
L13 1 S L12 AND (NO#(W) EXPRESS?)
L14 67 S L12(S) (TRANSCRI?)
L15 86 S L8(S) NORTHERN
L16 50 S L1(S) (NO#(2W) CORRELAT?)
L17 16 S L16 NOT L2
L18 12 DUP REM L17 (4 DUPLICATES REMOVED)
L19 54 S L1(S) (NO#(3W) CORRELAT?)
L20 0 S L19 NOT L1
L21 20 S L19 NOT L2
L22 4 S L21 NOT L16

FILE 'MEDLINE, BIOSIS' ENTERED AT 20:42:05 ON 08 JUL 2002

L23 13496 S EST OR (SEQUENCE(W) TAG#)
L24 234 S L23 AND DATABASE#/TI
L25 0 S L24 AND (NO(3W) CORRELAT?)
L26 234 S L24(S) DATABASE#

L27 2221 S L23(S)DATABASE#
 L28 4 S L27(S) (NO#(3W)CORRELAT?)
 L29 1174 S L23(S) (BLADDER OR PROSTATE OR KIDNEY OR HEART OR LUNG OR OVA
 L30 310 S L29(S)NORTHERN
 L31 133 S L30 AND DATABASE#
 L32 78 DUP REM L31 (55 DUPLICATES REMOVED)
 L33 1072 S L23(S) (PREDICT? OR ANTICIPAT?)
 L34 22 S L33 AND DATABASE#/TI
 L35 13 DUP REM L34 (9 DUPLICATES REMOVED)
 L36 22 S L34(S)DATABASE#
 L37 2221 S L23(S)DATABASE#
 L38 612 S L37(S)TISSUE
 L39 58 S L38(S)PROSTATE
 L40 10 S L39 AND PREDICT?
 L41 6 DUP REM L40 (4 DUPLICATES REMOVED)
 L42 1 S L23(S) (CANNOT(3W)PREDICT)
 L43 13596 S L23 OR DBEST
 L44 6719 S L43(S)EXPRESS?
 L45 192 S L44(S)BLAST
 L46 47 S L45(S)PREDICT?
 L47 27 DUP REM L46 (20 DUPLICATES REMOVED)
 L48 2 S L43(S)RELIED
 L49 1 S L43(S) (("NOT" OR CANNOT) (W)PREDICT?)
 L50 0 S L43(S) (CANNOT(W)ANTICIPATE)
 L51 797 S L43(S)TRANSCRIPTS
 L52 28 S L43(S) ((NO(W)EXPRESSION) OR ("NOT"(W)EXPRESSED))
 L53 17 DUP REM L52 (11 DUPLICATES REMOVED)
 L54 546 S L43 AND (EXPRESSION(A)PATTERN#)
 L55 15 S L54 AND DATABASE#/TI
 L56 9 DUP REM L55 (6 DUPLICATES REMOVED)
 L57 239 S L43 AND DATABASE#/TI
 L58 5 S L57 AND PREDICT
 L59 3 DUP REM L58 (2 DUPLICATES REMOVED)
 L60 1735 S L43(S)LIBRAR?
 L61 34 S L60(S)PREDICT
 L62 19 DUP REM L61 (15 DUPLICATES REMOVED)
 L63 4276 S L43(S) (MRNA OR NORTHERN OR CDNA OR TRANSCRIPT#)
 L64 335 S L63(S) (EXPRESSION(A)PATTERN#)
 L65 86 S L64(S) (PROSTATE OR BLADDER OR LUNG OR KIDNEY OR BONE OR SKIN
 L66 49 DUP REM L65 (37 DUPLICATES REMOVED)
 L67 430 S L43(S) (EXPRESSION(A)PATTERN#)
 L68 12 S L67 AND DATABASE#/TI
 L69 6 DUP REM L68 (6 DUPLICATES REMOVED)
 L70 99 S L23(3A)PREDICT?
 L71 2 S L70(3A) (EXPRESSION OR TRANSCRIPTION)
 L72 152 S L43(5A)PREDICT?
 L73 3 S L72(5A) (EXPRESSION OR TRANSCRIPTION)
 L74 1 S L73 NOT L71
 L75 64 S L43(S)HYPOTHETICAL
 L76 55 S L75(S) (EXPRESS? OR TRANSCI?)
 L77 34 DUP REM L76 (21 DUPLICATES REMOVED)
 L78 28 S L30(S) (EXPRESSION(A)PATTERN#)
 L79 15 DUP REM L78 (13 DUPLICATES REMOVED)
 L80 0 S L23(S) ("NOT"(W)PREDICTIVE)
 L81 0 S L23(S) (CANNOT(W)ANTICIPATE)
 L82 107 S DATABASE(A)MINING
 L83 14 S L23 AND L82
 L84 8 DUP REM L83 (6 DUPLICATES REMOVED)

=> s ESTs

L85 2347 ESTS

=> s 185 and database/ti
L86 79 L85 AND DATABASE/TI

=> s 186 and (cannot(w)(anticipate or predict))
UNMATCHED LEFT PARENTHESIS 'AND (CANNOT'
The number of right parentheses in a query must be equal to the
number of left parentheses.

=> s 186 and (cannot(w)(anticipate or predict))
L87 0 L86 AND (CANNOT(W) (ANTICIPATE OR PREDICT))

=> s 186 and (expression(a)pattern#)
L88 4 L86 AND (EXPRESSION(A) PATTERN#)

=> dup rem 188
PROCESSING COMPLETED FOR L88
L89 2 DUP REM L88 (2 DUPLICATES REMOVED)

=> d ibib abs tot

L89 ANSWER 1 OF 2 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2000063237 MEDLINE
DOCUMENT NUMBER: 20063237 PubMed ID: 10592203
TITLE: BodyMap: a human and mouse gene expression database

AUTHOR: Hishiki T; Kawamoto S; Morishita S; Okubo K
CORPORATE SOURCE: Institute for Molecular and Cellular Biology, Osaka
University, 1-3 Yamadaoka, Suita, Osaka 565-0871, Japan.
SOURCE: NUCLEIC ACIDS RESEARCH, (2000 Jan 1) 28 (1) 136-8.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200002
ENTRY DATE: Entered STN: 20000314
Last Updated on STN: 20000314
Entered Medline: 20000225

AB BodyMap is a human and mouse gene expression database that has been
maintained since 1993. It is based on site-directed 3'-ESTs
collected from non-biased cDNA libraries constructed at Osaka University
and contains >270 000 sequences from 60 human and 38 mouse tissues. The
site-directed nature of the sequence tags allows unequivocal grouping of
tags representing the same transcript and provides abundance information
for each transcript in different parts of the body. Our collection of
ESTs was compared periodically with other public databases for
cross referencing. The histological resolution of source tissues and
unique cloning strategy that minimized cloning bias enabled BodyMap to
support three unique mRNA based experiments in silico. First, the
recurrence information for clones in each library provides a rough
estimate of the mRNA composition of each source tissue. Second, a user
can
search the entire data set with nucleotide sequences or keywords to
assess
expression patterns of particular genes. Third, and most
important, BodyMap allows a user to select genes that have a desired
expression pattern in humans and mice. BodyMap is
accessible through the WWW at <http://bodymap.ims.u-tokyo.ac.jp>

L89 ANSWER 2 OF 2 MEDLINE DUPLICATE 2